



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 182306

TO: Minh-Tam Davis
Location: rem/3A24/3C18
Art Unit: 1642
Monday, March 20, 2006
Case Serial Number: 09/856812

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518

barbara.obryen@uspto.gov

Search Notes

RUSH

Tam,

It wasn't possible to ~~g~~ do ~~the~~ a search to which would address your query exactly. I gave you the following searches to address it as best I could:

- Your:
- 1) - done exactly as requested
 - 2) - done exactly as requested
 - 3) - we can't specify only a few residues in an oligomer, or "NOT" a sequence out of an answer set. I gave you an oligomer search ^{of ~~sequence~~ Seq 1} with a size limitation of ≤ 9 aa, an oligomer search of Seq 1 with a size limitation of ≤ 93 aa, & an oligomer search of Seq 57. You will have to manually "NOT" out Seq 57 by comparing the Seq 1 oligomer search answers with the Seq 57 answers. You will also have to look at the Seq 1 answers to determine if they meet the aa specifications you provided.
 - 4) the nonapeptide described = XLYDGX EHL. I searched Seq 1 & found this peptide at positions 254-262. I then did an oligomer using this fragment.

(over)

5) Oligomer search of Seq1 already provided in 1)
Oligomer search of Seq 7, nt 334-918; ^{standard searches of} Seq 48, 49, 50 provided
so you can compare with the results of Seq1 & manually
"NOT" out Seq 7, nt 334-918 & Seq 48-50.

6) Provided oligomer search of Seq1, with size limitation
 ≤ 10 aa. You'll have to look through the results
to see if the aa limitations are met & to "NOT" out
Seq 57 (provided in part 3)c)

Please let me know if you have questions.

Barb

O'Bryen, Barbara

182306

From: Hale, Mary
Sent: Thursday, March 16, 2006 1:28 PM
To: O'Bryen, Barbara
Subject: FW: Rush search request for 09/856812

Importance: High

I think you should have this search, please attach the modification below from Minh-Tam. If you don't have it, let me know and I'll look for it.

Mary

-----Original Message-----

From: Chan, Christina
Sent: Thursday, March 16, 2006 1:25 PM
To: Davis, Minh-Tam; Hale, Mary
Subject: RE: Rush search request for 09/856812
Importance: High

Mary,

This case had been rushed by me this morning. Examiner needs to add more to the search. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Davis, Minh-Tam
Sent: Thursday, March 16, 2006 10:50 AM
To: Chan, Christina
Subject: FW: Rush search request for 09/856812

Please add:

- 6) A nonapeptide of SEQ ID NO:1, wherein the amino acid adjacent to the N-terminal amino acid is L, and the C-terminal amino acid is L, with size limitation for the sequences in the database to 10 amino acids, and wherein said nonapeptide is not the nonapeptide SEQ ID NO:57.

Thanks

-----Original Message-----

From: Davis, Minh-Tam
Sent: Wednesday, March 15, 2006 6:06 PM
To: Chan, Christina
Subject: Rush search request for 09/856812

Please search in commercial database, issued patent files and PGPUB:

1) SEQ ID NO:42 with size limitation of the sequences in the database to the size of the sequence. *9aa*

2) Oligomer search for SEQ ID NO:1. *aa*

3) A nonapeptide of SEQ ID NO:1, wherein the amino acid adjacent to the N-terminal amino acid is L, and the C-terminal amino acid is L, with and without size limitation for the sequences in the database to 9 amino acids, or to 93 amino acids, and wherein said nonapeptide is not the nonapeptide SEQ ID NO:57.

4) A nonapeptide of SEQ ID NO:1, wherein the amino acid adjacent to the N-terminal amino acid is L, the amino acid in position 3 is Y, the amino acid position 4 is D, the amino acid in position 5

x L²⁵⁶
Y D G X E H L
254 262

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is G, **and/or** the amino acid position 7 is E, **and/or** the amino acid position 8 is H, and the C-terminal amino acid is L, with size limitation for the sequence in the database to 9 amino acids.

5) ~~6~~ Oligomer search for SEQ ID NO:1, which oligomer is not encoded by nucleotides 334-918 of SEQ ID NO:7, **or** which is not SEQ ID NO:48, 49, 50.

Thank you.

MINH TAM DAVIS
ART UNIT 1642, ROOM 3A24, MB 3C18
272-0830

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 17, 2006, 22:45:25 ; Search time 184 Seconds
(without alignments)
881.145 Million cell updates/sec

Title: US-09-856-812B-1
Perfect score: 369
Sequence: 1 MPRAKRCQRCMPEDLOSQ.....DTTAVASASSATGFSFSYPE 369

Scoring table: OLIGO)
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 401289

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	2.4	9	2	Aar79845 Tumour re
2	9	2.4	9	2	Aar79846 Tumour re
3	9	2.4	9	2	Aar79847 Tumour re
4	9	2.4	9	2	Aay47277 Immunogen
5	9	2.4	9	3	Aay71528 Human MAG
6	9	2.4	9	3	Aay71528 Human MAG
7	9	2.4	9	3	Aay71487 Human MAG
8	9	2.4	9	3	Aay71491 Human MAG
9	9	2.4	9	3	Aay71492 Human MAG
10	9	2.4	9	3	Aay92269 MAGS-A1 a
11	9	2.4	9	4	Aab31307 Exemplary
12	9	2.4	9	4	Aab31323 Exemplary
13	9	2.4	9	5	Aao17088 Human mag
14	9	2.4	9	5	Aae31265 Human mag
15	9	2.4	9	5	Aae31269 Human mag
16	9	2.4	9	5	Aae31261 Human mag
17	9	2.4	9	5	Aae31268 Human mag
18	9	2.4	9	5	Aae31267 Human mag
19	9	2.4	9	5	Aae31270 Human mag
20	9	2.4	9	5	Aae31271 Human mag
21	9	2.4	9	5	Aae31259 Human mag
22	9	2.4	9	5	Aae31272 Human mag
23	9	2.4	9	5	Aae31401 Human MAG
24	9	2.4	9	5	Aae31215 Human mag
					Aae31263 Human mag

25	9	2.4	9	5	AAE31264	Human mag
26	9	2.4	9	5	AAE31257	Human mag
27	9	2.4	9	5	AAE31258	Human mag
28	9	2.4	9	5	AAE31262	Human mag
29	9	2.4	9	5	AAE31266	Human mag
30	9	2.4	9	5	AAE31217	Human mag
31	9	2.4	9	5	AAE31216	Human mag
32	9	2.4	9	6	ABU19876	MHC bindi
33	9	2.4	9	6	ABP74235	Human MAG
34	9	2.4	9	6	ABP74381	Human MAG
35	9	2.4	9	7	ADC09240	Epitope w
36	9	2.4	9	7	ADC09094	Epitope w
37	9	2.4	9	8	ADG89842	Immunogen
38	9	2.4	9	8	ADG89586	Class I H
39	9	2.4	9	8	ADG89571	Class I H
40	9	2.4	9	8	ADI19869	Human HLA
41	9	2.4	9	8	ADI19026	Human HLA
42	9	2.4	9	8	ADI47252	Anti-canc
43	9	2.4	9	8	ADI47251	Anti-canc
44	9	2.4	9	8	ADI47250	Anti-canc
45	9	2.4	9	8	ADJ58374	Peptide p

ALIGNMENTS

RESULT 1
AAR79845
ID AAR79845 standard; peptide; 9 AA.
XX
AC AAR79845;
XX
DT 08-MAY-1996 (first entry)
XX
DE Tumour rejection antigen peptide #9.
XX
KW Tumour rejection antigen; MAGE tumour rejection precursor; complex;
KW HLA-2; immunogen; antibody; cytolytic T cell clone.
XX
OS Synthetic.
XX
PN WO9525740-A1.
XX
PD 28-SEP-1995.
XX
PF 22-MAR-1995; 95WO-US003657.
XX
PR 24-MAR-1994; 94US-00217186.
PR 17-JUN-1994; 94US-00261160.
PR 15-AUG-1994; 94US-00290381.
XX
(LUDW-) LUDWIG INST CANCER RES.
PA (UYOX-) UNIV OXFORD.
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Townsend A, Bastin J, Boon-Falleur T, Van Der Bruggen P, Coulie P;
PI Gajewski T, Melief CJ, Visseren MW, Kast WM;
XX
WPI; 1995-344584/44.
XX
Isolated peptide(s) which complex with HLA-A2 - used as immunogens for
the prodn. of antibodies, or as targets for the generation of cytolytic T
cell clones.
XX
Claim 15; Page 23; 44pp; English.
XX
The peptides given in AAR79845-47 represent tumour rejection antigens
derived from MAGE tumour rejection precursor. These peptides form a
strong complex with HLA-2 which may be used diagnostically and as an
immunogen in the production of antibodies. They may also be used as
targets for the generation of cytolytic T cell clones. This cytolytic T
cell clone is used to treat a cancerous condition characterised by the
fact that the cancer cells present the HLA-2/ peptide complex on their

```

CC surface
XX Sequence 9 AA;
SQ Query Match 2.4%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 FLLFKYQMK 152
Db 1 FLLFKYQMK 9

RESULT 2
AAR79846
ID AAR79846 standard; peptide; 9 AA.
XX AC AAR79846;
XX DT 08-MAY-1996 (first entry)
XX DE Tumour rejection antigen peptide #10.
XX KW Tumour rejection antigen; MAGE tumour rejection precursor; complex;
XX KW HLA-2; immunogen; antibody; cytolytic T cell clone.
XX OS Synthetic.
XX PN WO9525740-A1.
XX PD 28-SEP-1995.
XX PF 22-MAR-1995; 95WO-US003657.
XX PR 24-MAR-1994; 94US-00217186.
XX PR 17-JUN-1994; 94US-00261160.
XX PR 15-AUG-1994; 94US-00290381.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PA (UYOX-) UNIV OXFORD.
XX PA (UYLE-) RIJKSUNIV LEIDEN.
XX PI Townsend A, Bastin J, Boon-Falleur T, Van Der Bruggen P, Coulie P;
XX PI Gajewski T, Melief CJ, Visseren MW, Kast WM;
XX DR WPI; 1995-344584/44.
XX PT Isolated peptide(s) which complex with HLA-A2 - used as immunogens for
XX PT the prodn. of antibodies, or as targets for the generation of cytolytic T
XX PT cell clones.
XX PS Claim 15; Page 23; 44pp; English.
XX CC The peptides given in AAR79845-47 represent tumour rejection antigens
XX CC derived from MAGE tumour rejection precursor. These peptides form a
XX CC strong complex with HLA-2 which may be used diagnostically and as an
XX CC immunogen in the production of antibodies. They may also be used as
XX CC targets for the generation of cytolytic T cell clones. This cytolytic T
XX CC cell clone is used to treat a cancerous condition characterised by the
XX CC fact that the cancer cells present the HLA-2/ peptide complex on their
XX CC surface
XX SQ Sequence 9 AA;

Query Match 2.4%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 FIEGYCTPE 243
Db 1 FIEGYCTPE 9

RESULT 4
AAY47277
ID AAY47277 standard; peptide; 9 AA.
XX AC AAY47277;
XX DT 01-DEC-1999 (first entry)
XX DE Immunogenic peptide having a human leukocyte antigen binding motif #1888.
XX KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX KW immune response; T cell activation; major histocompatibility complex;
XX KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;

Query Match 2.4%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GLEGAQAPL 32
Db 1 GLEGAQAPL 9

```

KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9945954-A1.
 XX
 XX 16-SEP-1999.
 PD
 XX
 XX 13-MAR-1998; 98WO-US005039.
 PF
 XX
 XX 13-MAR-1998; 98WO-US005039.
 PR
 XX
 XX (EPIM-) EPIMUNE INC.
 PA
 XX
 XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
 PI
 XX WPI; 1999-551214/46.
 DR
 XX
 XX New immunogenic peptides with HLA binding motif, useful in treatment and
 PT diagnosis of cancers and viral diseases.
 PT
 XX
 XX Claim 1; Page 101; 150pp; English.
 PS
 XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also known
 CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
 CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
 CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
 CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
 CC (CTLs) which destroy antigen-bearing cells are normally induced by an
 CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
 CC than the intact foreign antigen itself, and are particularly important in
 CC tumour rejection and in fighting viral infections. The peptides are
 CC therefore useful therapeutically to treat or prevent viral infections and
 CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
 CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
 CC elicit an immune response in individuals susceptible or otherwise at risk
 CC of viral infection or cancer, or used to treat chronic or acute
 CC conditions. They are also useful diagnostically, and can be used to
 CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
 CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
 CC patient. The polynucleotides encoding the immunogenic peptides are also
 CC useful therapeutically and for immunisation as above
 XX
 SQ Sequence 9 AA;

Query Match 2.4%; Score 9; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 YEFLMGPR 302
 DB 1 YEFLMGPR 9
 |||||

RESULT 5
 AAY71528
 ID AAY71528 standard; peptide; 9 AA.
 XX
 XX AAY71528;
 AC
 XX
 XX 12-OCT-2000 (first entry)
 DT
 XX
 XX Human MAGE-A10 nonapeptide-5.
 DE
 XX
 XX MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
 KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
 KW immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
 KW cancer; TNF; tumour necrosis factor; vaccine; cytostatic.
 XX
 XX Homo sapiens.
 OS

XX WO200032769-A2.
 PN
 XX
 PD 08-JUN-2000.
 XX
 XX 26-NOV-1999; 99WO-IB002018.
 PF
 XX
 XX 27-NOV-1998; 98GB-00026143.
 PR
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 XX
 XX Huang L, Van Pel A, Brasseur P, De Plaen E, Boon T;
 PI
 XX WPI; 2000-412317/35.
 DR
 XX
 XX Novel polypeptides expressed in tumor cells useful for treating cancers
 PT have an ability to complex with a major histocompatibility complex
 PT molecule and comprises a specific unbroken amino acid sequence.
 PT
 XX
 XX Example 3; Page 31; 80pp; English.
 PS
 XX The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
 CC decapeptide sequences, that function as tumour rejection antigens (TRA).
 CC These peptides are capable of forming a complex with major
 CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
 CC Antigen), that are recognised by T-lymphocytes and elicit an immune
 CC response from cytolytic T-lymphocytes (CTL). They function as an immune
 CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
 CC therapy and diagnosis of tumours and are effective in controlling or
 CC preventing tumour growth. The present peptide sequence is the human MAGE-
 CC A10 nonapeptide-5, that corresponds to residues 183-191 of the MAGE-A10
 CC protein. This peptide conform to the HLA-A2.1 peptide binding motif and
 CC can serve as a tumour rejection antigen (TRA). This peptide failed to
 CC confer recognition by the CTLs even after LB1751-EBV cells were treated
 CC with monoclonal antibody MA2.1
 XX
 XX Sequence 9 AA;

Query Match 2.4%; Score 9; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 MLLVFGIDV 191
 DB 1 MLLVFGIDV 9
 |||||

RESULT 6
 AAY71487
 ID AAY71487 standard; peptide; 9 AA.
 XX
 XX AAY71487;
 AC
 XX
 XX 12-OCT-2000 (first entry)
 DT
 XX
 XX Human MAGE-A10 nonapeptide-1.
 DE
 XX
 XX MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
 KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
 KW immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
 KW cancer; TNF; tumour necrosis factor; vaccine; cytostatic.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200032769-A2.
 PN
 XX
 XX 08-JUN-2000.
 PD
 XX
 XX 26-NOV-1999; 99WO-IB002018.
 PF
 XX
 XX 27-NOV-1998; 98GB-00026143.
 PR
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA

XX Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
XX WPI; 2000-412317/35.
XX Novel polypeptides expressed in tumor cells useful for treating cancers
PT have an ability to complex with a major histocompatibility complex
PT molecule and comprises a specific unbroken amino acid sequence.
XX Claim 8; Page 36; 80pp; English.
XX The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
CC decapeptide sequences, that function as tumour rejection antigens (TRAs).
CC These peptides are capable of forming a complex with major
CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
CC Antigen), that are recognised by T-lymphocytes and elicit an immune
CC response from cytolytic T-lymphocytes (CTL). They function as an immune
CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
CC therapy and diagnosis of tumours and are effective in controlling or
CC preventing tumour growth. The present peptide sequence is the human MAGE-
CC A10 nonapeptide-1, that corresponds to residues 254-262 of the MAGE-A10
CC protein. This peptide can serve as a tumour rejection antigen (TRA) and
CC in combination with adjuvants, can produce vaccines useful for treating a
CC variety of tumours that express MAGE-A10
XX
SQ Sequence 9 AA;
Query Match 2.4%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 254 GLYDGMGHEHL 262
DB 1 GLYDGMGHEHL 9
RESULT 7
AAY71491
ID AAY71491 standard; peptide; 9 AA.
AC AAY71491;
DT 12-OCT-2000 (first entry)
DE Human MAGE-A10 nonapeptide-2.
XX MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
KW immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
KW cancer; TNF; tumour necrosis factor; vaccine; cytostatic.
XX Homo sapiens.
OS
XX WO200032769-A2.
PN
XX 08-JUN-2000.
PD
XX 26-NOV-1999; 99WO-IB002018.
PF
XX 27-NOV-1998; 98GB-00026143.
PR
XX (LUDW-) LUDWIG INST CANCER RES.
PA
XX Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
PI WPI; 2000-412317/35.
DR
XX Novel polypeptides expressed in tumor cells useful for treating cancers
PT have an ability to complex with a major histocompatibility complex
PT molecule and comprises a specific unbroken amino acid sequence.
XX Claim 5; Page 36; 80pp; English.

CC The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
CC decapeptide sequences, that function as tumour rejection antigens (TRAs).
CC These peptides are capable of forming a complex with major
CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
CC Antigen), that are recognised by T-lymphocytes and elicit an immune
CC response from cytolytic T-lymphocytes (CTL). They function as an immune
CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
CC therapy and diagnosis of tumours and are effective in controlling or
CC preventing tumour growth. The present peptide sequence is the human MAGE-
CC A10 nonapeptide-2, that corresponds to residues 144-152 of the MAGE-A10
CC protein. This peptide can serve as a tumour rejection antigen (TRA) and
CC in combination with adjuvants, can produce vaccines useful for treating a
CC variety of tumours that express MAGE-A10
XX
SQ Sequence 9 AA;
Query Match 2.4%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 144 FLLFKYQMK 152
DB 1 FLLFKYQMK 9
RESULT 8
AAY71492
ID AAY71492 standard; peptide; 9 AA.
XX
AC AAY71492;
DT 12-OCT-2000 (first entry)
DE Human MAGE-A10 nonapeptide-3.
XX MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
KW immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
KW cancer; TNF; tumour necrosis factor; vaccine; cytostatic.
XX Homo sapiens.
OS
XX WO200032769-A2.
PN
XX 08-JUN-2000.
PD
XX 26-NOV-1999; 99WO-IB002018.
PF
XX 27-NOV-1998; 98GB-00026143.
PR
XX (LUDW-) LUDWIG INST CANCER RES.
PA
XX Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
PI WPI; 2000-412317/35.
DR
XX Novel polypeptides expressed in tumor cells useful for treating cancers
PT have an ability to complex with a major histocompatibility complex
PT molecule and comprises a specific unbroken amino acid sequence.
XX Claim 5; Page 36; 80pp; English.
XX The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
CC decapeptide sequences, that function as tumour rejection antigens (TRAs).
CC These peptides are capable of forming a complex with major
CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
CC Antigen), that are recognised by T-lymphocytes and elicit an immune
CC response from cytolytic T-lymphocytes (CTL). They function as an immune
CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
CC therapy and diagnosis of tumours and are effective in controlling or
CC preventing tumour growth. The present peptide sequence is the human MAGE-
CC A10 nonapeptide-3, that corresponds to residues 235-243 of the MAGE-A10
CC protein. This peptide can serve as a tumour rejection antigen (TRA) and

CC in combination with adjuvants, can produce vaccines useful for treating a
CC variety of tumours that express MAGE-A10
XX
SQ Sequence 9 AA;

Query Match 2.4%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 FIEGYCTPE 243
Db 1 FIEGYCTPE 9
|||||

RESULT 9
AAY92269
ID AAY92269 standard; peptide; 9 AA.

XX
AC AAY92269;

XX 10-AUG-2000 (first entry)

XX MAGE-A1 antigenic peptide epitope (residues 258-266).

XX MAGE-A1; antigen; epitope; cytotoxic T lymphocyte; CTL; complex; HLA;
KW human leukocyte antigen.

XX Homo sapiens.

XX WO200020445-A2.

XX 13-APR-2000.

XX 15-SEP-1999; 99WO-IB001664.

XX 02-OCT-1998; 98US-00165863.

XX 09-APR-1999; 99US-00289350.

XX (CHAU/) CHAUX P.

XX (LUIT/) LUITEN R.

XX (DEMO/) DEMOTTE N.

XX (DUFF/) DUFFOUR M.

XX (LURQ/) LURQUIN C.

XX (TRAV/) TRAVERSARI C.

XX (STRO/) STROOBANT V.

XX (COR/) CORNELIS G R.

XX (BOON/) BOON-FALLEUR T.

XX (VBRU/) VAN DER BRUGGEN P.

XX (SCHU/) SCHULTZ E.

XX (WARN/) WARNIER G.

XX Chaux P, Luiten R, Demotte N, Duffour M, Lurquin C, Traversari C;

XX Stroobant V, Cornelis GK, Boon-Falleur T, Van Der Bruggen P;

XX Schultz E, Warnier G;

XX WPI; 2000-303739/26.

XX Isolation of cytotoxic T-lymphocytes clones by successive steps of

PT stimulation and testing of lymphocytes with antigen presenting cells

PT which present antigens derived from different expression systems.

XX Claim 10; Page 26; 99pp; English.

CC specific for the complexes, peptides or cells which present the complexes
CC on the cell surface are useful for treating pathological conditions
CC characterized by abnormal expression of the complexes

XX Sequence 9 AA;

Query Match 2.4%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 DPARYEFLLW 298
Db 1 DPARYEFLLW 9
|||||

RESULT 10

AAB31307

ID AAB31307 standard; peptide; 9 AA.

XX
AC AAB31307;

XX 20-APR-2001 (first entry)

XX Exemplary antigen characteristic of tumours and derived from MAGE-A1.

XX MAGE-A1; HLA; human leukocyte antigen; CD4+ T lymphocyte; cancer;

KW MAGE-A1 HLA class II-binding protein; vaccine.

XX Homo sapiens.

XX WO200078806-A1.

XX 28-DEC-2000.

XX 14-JUN-2000; 2000WO-US016287.

XX 18-JUN-1999; 99US-00336091.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Van Snick J, Lethe B, Chaux P, Boon-Falleur T, Van Der Bruggen P;

XX WPI; 2001-102698/11.

XX Novel MAGE-A1 human leukocyte antigen class II peptides which bind to and
PT are presented to the class II molecules, useful for inducing immune
PT response and treating cancers characterized by expression of MAGE-A1.

XX Disclosure; Page 31; 78pp; English.

XX AAB31302-59 represent exemplary antigens which are characteristic of
CC tumours. They can be used to enhance the immune response of vaccines
CC comprising peptides derived from human MAGE-A1 HLA (human leukocyte
CC antigen) class II-binding protein. Peptides derived from the MAGE-A1 HLA
CC binding protein stimulate the activity and proliferation of CD4+ T
CC lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic
CC agent for diagnosing a disorder characterized by expression of MAGE-A1.
CC The protein is used for treating a disorder characterized by expression
CC of MAGE-A1 such as cancers e.g. melanoma, squamous cell carcinoma,
CC colorectal carcinomas, osteosarcomas, and lymphocytic leukemias. Peptides
CC derived from the MAGE-A1 HLA binding protein are useful in the production
CC of anti-tumour vaccines

XX Sequence 9 AA;

Query Match 2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 DPARYEFLLW 298
Db 1 DPARYEFLLW 9
|||||

```

RESULT 11
AAB31323
ID AAB31323 standard; peptide; 9 AA.
XX
AC AAB31323;
XX
DT 20-APR-2001 (first entry)
XX
DE Exemplary antigen characteristic of tumours and derived from MAGE-A10.
XX
KW MAGE-A1; HLA; human leukocyte antigen; CD4+ T lymphocyte; cancer;
KW MAGE-A1 HLA class II-binding protein; vaccine.
XX
OS Homo sapiens.
XX
PN WO200078806-A1.
XX
PD 28-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016287.
XX
PR 18-JUN-1999; 99US-00336091.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Van Snick J, Lethe B, Chaux P, Boon-Falleur T, Van Der Bruggen P;
XX
DR WPI; 2001-102698/11.
XX
PT Novel MAGE-A1 human leukocyte antigen class II peptides which bind to and
PT are presented to the class II molecules, useful for inducing immune
PT response and treating cancers characterized by expression of MAGE-A1.
XX
PS Disclosure; Page 32; 78pp; English.
XX
CC AAB31302-59 represent exemplary antigens which are characteristic of
CC tumours. They can be used to enhance the immune response of vaccines
CC comprising peptides derived from human MAGE-A1 HLA (human leukocyte
CC antigen) class II-binding protein. Peptides derived from the MAGE-A1 HLA
CC binding protein stimulate the activity and proliferation of CD4+ T
CC lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic
CC agent for diagnosing a disorder characterized by expression of MAGE-A1.
CC The protein is used for treating a disorder characterized by expression
CC of MAGE-A1 such as cancers e.g. melanoma, squamous cell carcinomas,
CC colorectal carcinomas, osteosarcomas, and lymphocytic leukemias. Peptides
CC derived from the MAGE-A1 HLA binding protein are useful in the production
CC of anti-tumour vaccines
XX
SQ Sequence 9 AA;

Query Match 2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 GLYDGMHEHL 262
DB 1 GLYDGMHEHL 9
|||||
RESULT 12
AAO17088
ID AAO17088 standard; peptide; 9 AA.
XX
AC AAO17088;
XX
DT 06-JUN-2002 (first entry)
XX
DE Human mage-A10 protein antigen SEQ ID NO: 8.
XX
KW Cryopreserved mature dendritic cell; antigen; vaccine; cytostatic;
KW virucide; cancer; hepatitis B virus.
XX

```

```

OS Homo sapiens.
XX
PN WO200216560-A1.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-EP009790.
XX
PR 24-AUG-2000; 2000DE-01041515.
XX
PA (SCHU/) SCHULER G.
XX
PI Schuler G, Schuler-Thurner B;
XX
DR WPI; 2002-292062/33.
XX
PT Preparation of cryopreserved, mature dendritic cells, useful in vaccines,
PT comprises culturing immature cells on medium containing cocktail of
PT maturation factors, then freezing.
XX
PS Disclosure; Fig 28; 87pp; German.
XX
CC The present invention relates to a method for the preparation of ready-
CC for-use, cryopreserved, mature dendritic cells comprising growing
CC immature dendritic cells in a culture medium that includes a 'maturation
CC cocktail' of one or more maturation stimuli and freezing the resulting
CC matured cells in a freezing medium that does not contain heterologous
CC serum. When loaded with antigens, the dendritic cells can be used as
CC vaccines, e.g. against tumours and hepatitis B virus. The present
CC sequence is an antigen described in the invention
XX
SQ Sequence 9 AA;

Query Match 2.4%; Score 9; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 GLYDGMHEHL 262
DB 1 GLYDGMHEHL 9
|||||
RESULT 13
AAB31265
ID AAB31265 standard; peptide; 9 AA.
XX
AC AAB31265;
XX
DT 24-FEB-2003 (first entry)
XX
DE Human mageA peptide #5.
XX
KW Human; T-lymphocyte; vaccine; viral infection; gene therapy; cancer.
XX
OS Homo sapiens.
XX
PN WO200272627-A2.
XX
PD 19-SEP-2002.
XX
PF 11-MAR-2002; 2002WO-EP002666.
XX
PR 09-MAR-2001; 2001US-0274250P.
XX
PR 14-MAY-2001; 2001US-0290353P.
XX
PR 18-MAY-2001; 2001US-0291610P.
XX
PA (CALL-) CALLISTOGEN AG.
XX
PI Wrede P, Walden P, Eichler-Wertens M, Filter M;
XX
DR WPI; 2002-759836/82.
XX
PT Providing, identifying or optimizing peptides for inducing cytotoxic T-

```

PT lymphocytes and for treating cancer, comprises selecting conserved
PT regions in antigenic proteins and identifying CD8+ T-cell epitopes in the
PT protein.

XX PS Disclosure; Page 10; 32pp; English.

XX CC The invention relates to a method for providing, identifying or/and
CC optimising peptides which induce cytotoxic T-lymphocytes and to the uses
CC of the obtained peptides for vaccination. The method is useful for
CC providing, identifying and/or optimising peptides that are useful in
CC manufacturing a pharmaceutical composition for the induction of cytotoxic
CC T-lymphocytes, and for the prevention, treatment or diagnosis of cancer
CC or viral infections. The invention is also used in gene therapy. The
CC present sequence is human mageA peptide used to illustrate the method of
CC the invention

XX SQ Sequence 9 AA;

Query Match 2.4%; Score 9; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 LVQFLLEFKY 149

Db 1 LVQFLLEFKY 9

RESULT 14

AAE31269
ID AAE31269 standard; peptide; 9 AA.

XX AC AAE31269;

XX DT 24-FEB-2003 (first entry)

XX DE Human mageA peptide #9.

XX KW Human; T-lymphocyte; vaccine; viral infection; gene therapy; cancer.

XX OS Homo sapiens.

XX FN WO200272627-A2.

XX PD 19-SEP-2002.

XX PF 11-MAR-2002; 2002WO-EP002666.

XX PR 09-MAR-2001; 2001US-0274250P.

XX PR 14-MAY-2001; 2001US-0290353P.

XX PR 18-MAY-2001; 2001US-0291610P.

XX PA (CALL-) CALLISTOGEN AG.

XX PI Wrede P, Walden P, Eichler-Mertens M, Filter M;

XX DR WPI; 2002-759836/82.

XX PT Providing, identifying or optimizing peptides for inducing cytotoxic T-
PT lymphocytes and for treating cancer, comprises selecting conserved
PT regions in antigenic proteins and identifying CD8+ T-cell epitopes in the
PT protein.

XX PS Disclosure; Page 10; 32pp; English.

XX CC The invention relates to a method for providing, identifying or/and
CC optimising peptides which induce cytotoxic T-lymphocytes and to the uses
CC of the obtained peptides for vaccination. The method is useful for
CC providing, identifying and/or optimising peptides that are useful in
CC manufacturing a pharmaceutical composition for the induction of cytotoxic
CC T-lymphocytes, and for the prevention, treatment or diagnosis of cancer
CC or viral infections. The invention is also used in gene therapy. The
CC present sequence is human mageA peptide used to illustrate the method of
CC the invention

XX SQ Sequence 9 AA;

Query Match 2.4%; Score 9; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 KLLTQDWVQ 277

Db 1 KLLTQDWVQ 9

RESULT 15

AAE31261
ID AAE31261 standard; peptide; 9 AA.

XX AC AAE31261;

XX DT 24-FEB-2003 (first entry)

XX DE Human mageA peptide #1.

XX KW Human; T-lymphocyte; vaccine; viral infection; gene therapy; cancer.

XX OS Homo sapiens.

XX FN WO200272627-A2.

XX PD 19-SEP-2002.

XX PF 11-MAR-2002; 2002WO-EP002666.

XX PR 09-MAR-2001; 2001US-0274250P.

XX PR 14-MAY-2001; 2001US-0290353P.

XX PR 18-MAY-2001; 2001US-0291610P.

XX PA (CALL-) CALLISTOGEN AG.

XX PI Wrede P, Walden P, Eichler-Mertens M, Filter M;

XX DR WPI; 2002-759836/82.

XX PT Providing, identifying or optimizing peptides for inducing cytotoxic T-
PT lymphocytes and for treating cancer, comprises selecting conserved
PT regions in antigenic proteins and identifying CD8+ T-cell epitopes in the
PT protein.

XX PS Disclosure; Page 10; 32pp; English.

XX CC The invention relates to a method for providing, identifying or/and
CC optimising peptides which induce cytotoxic T-lymphocytes and to the uses
CC of the obtained peptides for vaccination. The method is useful for
CC providing, identifying and/or optimising peptides that are useful in
CC manufacturing a pharmaceutical composition for the induction of cytotoxic
CC T-lymphocytes, and for the prevention, treatment or diagnosis of cancer
CC or viral infections. The invention is also used in gene therapy. The
CC present sequence is human mageA peptide used to illustrate the method of
CC the invention

XX SQ Sequence 9 AA;

Query Match 2.4%; Score 9; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AVEEDASS 41

Db 1 AVEEDASS 9

Search completed: March 17, 2006, 22:48:47
Job time : 186 secs

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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:49:28 ; Search time 47 Seconds
(without alignments)
15.832 Million cell updates/sec

Title: US-09-856-812B-57
Perfect score: 9
Sequence: 1 CIGLSYDGL 9

Scoring table: COLIGO-->
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/1aa/6_COMB.pep.*
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4: /cgn2_6/prodata/1/1aa/PCUS_COMB.pep.*
5: /cgn2_6/prodata/1/1aa/RS_COMB.pep.*
6: /cgn2_6/prodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	100.0	9	1	US-08-217-188A-31
2	9	100.0	9	1	US-08-217-186-3
3	9	100.0	9	1	US-08-261-160A-3
4	9	100.0	9	1	US-08-687-226-31
5	9	100.0	9	1	US-08-290-381A-3
6	9	100.0	9	2	US-08-667-725B-31
7	9	100.0	9	2	US-09-007-748-31
8	9	100.0	9	2	US-09-533-499B-3
9	9	100.0	10	1	US-08-217-188A-32
10	9	100.0	10	1	US-08-687-226-32
11	9	100.0	10	2	US-08-667-725B-32
12	9	100.0	10	2	US-09-007-748-32
13	9	100.0	11	1	US-08-217-188A-57
14	9	100.0	11	1	US-08-687-226-57
15	9	100.0	11	2	US-08-667-725B-57
16	9	100.0	11	2	US-09-007-748-57
17	9	100.0	309	1	US-08-465-167A-24
18	9	100.0	309	1	US-08-993-118-10
19	9	100.0	309	2	US-08-845-528C-10
20	9	100.0	309	2	US-08-627-820-24
21	9	100.0	309	2	US-09-066-281B-10
22	9	100.0	309	2	US-09-468-433C-10
23	9	100.0	309	2	US-09-392-714-29
24	9	100.0	309	2	US-09-949-016-6574
25	9	100.0	314	1	US-08-928-615-2
26	9	100.0	314	2	US-09-166-448-2
27	9	100.0	314	2	US-09-348-933-2

28	9	100.0	314	2	US-09-697-884-2	Sequence 2, Appli
29	9	100.0	314	2	US-09-392-714-30	Sequence 30, Appli
30	9	100.0	314	2	US-09-396-315-2	Sequence 2, Appli
31	9	100.0	314	2	US-09-849-602-29	Sequence 29, Appli
32	9	100.0	355	2	US-09-949-016-8559	Sequence 8559, Ap
33	6	66.7	8	2	US-08-159-339A-1182	Sequence 1182, Ap
34	6	66.7	9	1	US-08-186-266-17	Sequence 17, Appli
35	6	66.7	9	1	US-08-186-266-18	Sequence 18, Appli
36	6	66.7	9	1	US-08-159-339A-1214	Sequence 1214, Ap
37	6	66.7	10	1	US-08-186-266-20	Sequence 20, Appli
38	6	66.7	172	2	US-09-489-039A-12246	Sequence 12246, A
39	6	66.7	187	2	US-09-242-890-1	Sequence 1, Appli
40	6	66.7	193	2	US-09-540-236-2160	Sequence 2160, Ap
41	6	66.7	200	2	US-09-242-890-10	Sequence 2, Appli
42	6	66.7	224	2	US-09-229-583A-2	Sequence 11, Appli
43	6	66.7	224	2	US-09-242-890-11	Sequence 2, Appli
44	6	66.7	224	2	US-10-187-904-2	Sequence 2, Appli
45	6	66.7	314	2	US-09-692-401-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-217-188A-31
; Sequence 31, Application US/08217188A
; Patent No. 5554724
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelia J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Failleu, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,188A
; FILING DATE: 24-MARCH-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5554724man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-217-188A-31

Query Match 100.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CIGLSYDGL 9

|||||

✓

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; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 9 amino acid residues
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-687-226-31

Query Match      100.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CLGLSYDGL 9
DB      1 CLGLSYDGL 9

RESULT 5
US-08-290-381A-3
; Sequence 3, Application US/08290381A
; Patent No. 5851523
; GENERAL INFORMATION:
; APPLICANT: Townsend, Alan; Bastin, Judy;
; APPLICANT: Boon-Palleur, Thierry; van der Bruggen, Pierre;
; APPLICANT: Coullie, Pierre; Gajewski, Thomas;
; TITLE OF INVENTION: ISOLATED, PEPTIDES DERIVED FROM MAGE
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS WHICH COMPLEX WITH
; TITLE OF INVENTION: HLA-A2 MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,381A
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/261,160
; FILING DATE: 17-JUNE-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/217,186
; FILING DATE: 24-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5851523man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5327.2
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 9 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-290-381A-3

Query Match      100.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CLGLSYDGL 9
DB      1 CLGLSYDGL 9

RESULT 6
US-08-667-725B-31
; Sequence 31, Application US/08667725B
; Patent No. 6063900
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Palleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,725B
; FILING DATE: 21 June 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6063900man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340.1 DIV (081585)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 9 amino acid residues
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-667-725B-31

Query Match      100.0%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CLGLSYDGL 9
DB      1 CLGLSYDGL 9

RESULT 7
US-09-007-748-31
; Sequence 31, Application US/09007748
; Patent No. 6147187
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Palleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
```

; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,748
; FILING DATE: 15 January 1998
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6147187man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340.2 DIV (081572)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-007-748-31

Query Match 100.0%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9
DB 1 CLGLSYDGL 9

RESULT 8
US-09-533-499B-3
; Sequence 3, Application US/09533499B
; Patent No. 6682731
; GENERAL INFORMATION:
; APPLICANT: Townsend, Alan; Bastin, Judy; Boon-Falleur, Thierry; van der
; Bruggen, Pierre; Coulie, Pierre; Gajewski, Thomas; Melief,
; Cornelis J.M.; Visseren, M.W.; Kast, W.M.
; TITLE OF INVENTION: ISOLATED PEPTIDES DERIVED FROM MAGE TUMOR
; REJECTION ANTIGEN PRECURSORS WHICH COMPLEX WITH
; HLA-A2 MOLECULES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/533,499B
; FILING DATE: 23-Mar-2000
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/722,115
; FILING DATE: February 6, 1997
; APPLICATION NUMBER: 08/290,381
; FILING DATE: 15-August-1994
; APPLICATION NUMBER: 08/261,160
; FILING DATE: 17-June-1994
; APPLICATION NUMBER: 08/217,186
; FILING DATE: 24-March-1994
; APPLICATION NUMBER: 08/217,188

; FILING DATE: 24-March-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6682731man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5327.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-533-499B-3

Query Match 100.0%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9
DB 1 CLGLSYDGL 9

RESULT 9
US-08-217-188A-32
; Sequence 32, Application US/08217188A
; Patent No. 5554724
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,188A
; FILING DATE: 24-MARCH-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5554724man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-217-188A-32

Query Match 100.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0006;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,748
; FILING DATE: 15 January 1998
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6147187man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340.2 DIV (081572)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-007-748-31

Query Match 100.0%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9
DB 1 CLGLSYDGL 9

RESULT 8
US-09-533-499B-3
; Sequence 3, Application US/09533499B
; Patent No. 6682731
; GENERAL INFORMATION:
; APPLICANT: Townsend, Alan; Bastin, Judy; Boon-Falleur, Thierry; van der
; Bruggen, Pierre; Coulie, Pierre; Gajewski, Thomas; Melief,
; Cornelis J.M.; Visseren, M.W.; Kast, W.M.
; TITLE OF INVENTION: ISOLATED PEPTIDES DERIVED FROM MAGE TUMOR
; REJECTION ANTIGEN PRECURSORS WHICH COMPLEX WITH
; HLA-A2 MOLECULES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/533,499B
; FILING DATE: 23-Mar-2000
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/722,115
; FILING DATE: February 6, 1997
; APPLICATION NUMBER: 08/290,381
; FILING DATE: 15-August-1994
; APPLICATION NUMBER: 08/261,160
; FILING DATE: 17-June-1994
; APPLICATION NUMBER: 08/217,186
; FILING DATE: 24-March-1994
; APPLICATION NUMBER: 08/217,188


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QY      1  CLGLSYDGL 9
Db      1  CLGLSYDGL 9

RESULT 10
US-08-687-226-32
; Sequence 32, Application US/08687226
; Patent No. 5686068
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.; Visseren, M. W.;
; APPLICANT: van der Burg, Spoerd; van der Bruggen, Pierre;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Derived From
; TITLE OF INVENTION: MAGE-2, Cytolytic T Cells Specific To Complexes Of
; TITLE OF INVENTION: Peptides And HLA-A2 Molecules, And Uses Thereof
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,226
; FILING DATE: 25-JULY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5686068man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5447
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-687-226-32

Query Match      100.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0006;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CLGLSYDGL 9
Db      1  CLGLSYDGL 9

RESULT 11
US-08-667-725B-32
; Sequence 32, Application US/0866725B
; Patent No. 6063900
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
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; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,725B
; FILING DATE: 21 June 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6063900man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340.1 DIV (081585)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-667-725B-32

Query Match      100.0%; Score 9; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0006;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CLGLSYDGL 9
Db      1  CLGLSYDGL 9

RESULT 12
US-09-007-748-32
; Sequence 32, Application US/09007748
; Patent No. 6147187
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,748
; FILING DATE: 15 January 1998
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6147187man D.
; REGISTRATION NUMBER: 30,946
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REFERENCE/DOCKET NUMBER: LUD 5340.2 DIV (081572)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-007-748-32

Query Match 100.0%; Score 9; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00066;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9

Db 1 CLGLSYDGL 9

RESULT 13

US-08-217-188A-57

Sequence 57, Application US/08217188A

Patent No 5554724

GENERAL INFORMATION:

APPLICANT: Melief, Cornelis J. M.

APPLICANT: Visseren, M. J. W.

APPLICANT: Kast, W. M.

APPLICANT: van der Bruggen, Pierre

APPLICANT: Boon-Falleur, Thierry

TITLE OF INVENTION: Isolated Tumor Rejection Antigen

TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/217,188A

FILING DATE: 24-MARCH-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5554724man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5340

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acid residues

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-217-188A-57

Query Match 100.0%; Score 9; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00066;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9

Db 3 CLGLSYDGL 11

RESULT 14

US-08-687-226-57

Sequence 57, Application US/08687226

Patent No. 5686068

GENERAL INFORMATION:

APPLICANT: Melief, Cornelis J. M.; Visseren, M. W.;

APPLICANT: van der Burg, Sjoerd; van der Bruggen, Pierre;

APPLICANT: Boon-Falleur, Thierry

TITLE OF INVENTION: Isolated Peptides Derived From

TITLE OF INVENTION: MAGE-2, Cytolytic T Cells Specific To Complexes Of

TITLE OF INVENTION: Peptides And HLA-A2 Molecules, And Uses Thereof

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/687,226

FILING DATE: 25-JULY-1996

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/217,188

FILING DATE: 24-MARCH-1994

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5686068man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5447

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acid residues

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-687-226-57

Query Match

Best Local Similarity 100.0%; Score 9; DB 1; Length 11;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9

Db 3 CLGLSYDGL 11

RESULT 15

US-08-667-725B-57

Sequence 57, Application US/08667725B

Patent No. 6063900

GENERAL INFORMATION:

APPLICANT: Melief, Cornelis J. M.

APPLICANT: Kast, W. M.

APPLICANT: van der Bruggen, Pierre

APPLICANT: Boon-Falleur, Thierry

TITLE OF INVENTION: Isolated Tumor Rejection Antigen

TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fulbright & Jaworski LLP

STREET: 666 Fifth Avenue

CITY: New York City

Mon Mar 20 09:16:49 2006

STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,725B
FILING DATE: 21 June 1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6063900man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5340.1 DIV (081585)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-667-725B-57

Query Match 100.0%; Score 9; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||
Db 3 CLGLSYDGL 11

Search completed: March 17, 2006, 23:50:45
Job time : 48 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 17, 2006, 22:53:00 ; Search time 45 Seconds
(without alignments)
677.941 Million cell updates/sec

Title: US-09-856-812B-1
Perfect score: 369
Sequence: 1 MPRAKRCQRCPEEDLOSQ.....DTTAMASASSATGSFSYPE 369

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Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 111694

Minimum DB seq length: 0

Maximum-DB-seq-length: 9

Post-processing: Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/6 COMB.pap.*
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4: /cgn2_6/ptodata/1/iaa/pCTUS COMB.pap.*
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6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	2.4	9	2	US-09-165-863-42
2	9	2.4	9	2	US-09-289-350-42
3	9	2.4	9	2	US-09-533-499B-18
4	9	2.4	9	2	US-09-533-499B-19
5	9	2.4	9	2	US-09-533-499B-20
6	9	2.4	9	2	US-09-806-769-42
7	9	2.4	9	2	US-09-865-548A-39
8	8	2.2	9	1	US-08-465-167A-35
9	8	2.2	9	1	US-08-465-167A-38
10	8	2.2	9	2	US-08-159-339A-37
11	8	2.2	9	2	US-08-159-339A-98
12	7	1.9	9	1	US-08-217-188A-47
13	7	1.9	9	1	US-08-195-186A-4
14	7	1.9	9	1	US-08-217-186-6
15	7	1.9	9	1	US-08-261-160A-6
16	7	1.9	9	1	US-08-687-226-47
17	7	1.9	9	1	US-08-106-981-11
18	7	1.9	9	1	US-08-465-167A-5
19	7	1.9	9	1	US-08-787-547-50
20	7	1.9	9	1	US-08-787-547-52
21	7	1.9	9	1	US-08-498-461-9
22	7	1.9	9	1	US-08-290-381A-6
23	7	1.9	9	1	US-08-902-516-22
24	7	1.9	9	1	US-08-902-516-24
25	7	1.9	9	1	US-09-036-582-2
26	7	1.9	9	1	US-09-036-582-4
27	7	1.9	9	2	US-08-880-963-19

Sequence 47, Appl
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Sequence 9, Appl
Sequence 47, Appl
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Sequence 30, Appl
Sequence 35, Appl
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Sequence 19, Appl
Sequence 19, Appl
Sequence 46, Appl
Sequence 5, Appl
Sequence 7, Appl
Sequence 19, Appl
Sequence 4, Appl

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29 7 1.9 9 2 US-08-785-831-47
30 7 1.9 9 2 US-09-064-964-9
31 7 1.9 9 2 US-09-007-748-47
32 7 1.9 9 2 US-09-183-931-28
33 7 1.9 9 2 US-09-183-931-30
34 7 1.9 9 2 US-09-183-931-35
35 7 1.9 9 2 US-09-183-931-38
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37 7 1.9 9 2 US-09-183-706-7
38 7 1.9 9 2 US-09-162-934-2
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41 7 1.9 9 2 US-09-166-448-48
42 7 1.9 9 2 US-09-567-995-5
43 7 1.9 9 2 US-09-567-995-7
44 7 1.9 9 2 US-09-099-543C-19
45 7 1.9 9 2 US-08-292-492D-4

ALIGNMENTS

RESULT 1
US-09-165-863-42
; Sequence 42, Application US/09165863
; Patent No. 6407063
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Duffour, Marie-Therese
; APPLICANT: Demotte, Nathalie
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Cornelis, Guy
; APPLICANT: Stroobant, Vincent
; APPLICANT: Lurquin, Christophe
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Chau, Pascal
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; FILE REFERENCE: 11727
; CURRENT APPLICATION NUMBER: US/09/165,863
; CURRENT FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 42
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human MAGE-A1 peptide
US-09-165-863-42

Query Match 2.4%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 DPARYEFLW 298
Db 1 DPARYEFLW 9
|||||||

RESULT 2
US-09-289-350-42
; Sequence 42, Application US/09289350
; Patent No. 6531451
; GENERAL INFORMATION:
; APPLICANT: Chau, Pascal
; APPLICANT: Luiten, Rosalie
; APPLICANT: Demotte, Nathalie
; APPLICANT: Duffour, Marie-Therese
; APPLICANT: Lurquin, Christophe
; APPLICANT: Traversari, Catia
; APPLICANT: Stroobant, Vincent
; APPLICANT: Cornelis, Guy R.
; APPLICANT: Boon-Falleur, Thierry

```
; APPLICANT: Van Der Bruggen, Pierre
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; FILE REFERENCE: 117272
; CURRENT APPLICATION NUMBER: US/09/289,350
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/165,863
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 42
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human MAGE-A1 peptide
US-09-289-350-42

Query Match          2.4%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      290 DPARYEFLLW 298
      |||||
Db      1 DPARYEFLLW 9

RESULT 3
US-09-533-499B-18
; Sequence 18, Application US/09533499B
; Patent No. 6682731
; GENERAL INFORMATION:
; APPLICANT: Townsend, Alan; Bastin, Judy; Boon-Palleur, Thierry; van der
; Bruggen, Pierre; Coullie, Pierre; Gajewski, Thomas; Melief,
; Cornelis J.M.; Visseren, M.W.; Kast, W.M.
; TITLE OF INVENTION: ISOLATED PEPTIDES DERIVED FROM MAGE TUMOR
; REJECTION ANTIGEN PRECURSORS WHICH COMPLEX WITH
; HLA-A2 MOLECULES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/533,499B
; FILING DATE: 23-Mar-2000
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/722,115
; FILING DATE: February 6, 1997
; APPLICATION NUMBER: 08/290,381
; FILING DATE: 15-August-1994
; APPLICATION NUMBER: 08/261,160
; FILING DATE: 17-June-1994
; APPLICATION NUMBER: 08/217,186
; FILING DATE: 24-March-1994
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-March-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6682731man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5327.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-533-499B-19
Query Match          2.4%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      290 DPARYEFLLW 298
      |||||
Db      1 DPARYEFLLW 9

RESULT 4
US-09-533-499B-19
; Sequence 19, Application US/09533499B
; Patent No. 6682731
; GENERAL INFORMATION:
; APPLICANT: Townsend, Alan; Bastin, Judy; Boon-Palleur, Thierry; van der
; Bruggen, Pierre; Coullie, Pierre; Gajewski, Thomas; Melief,
; Cornelis J.M.; Visseren, M.W.; Kast, W.M.
; TITLE OF INVENTION: ISOLATED PEPTIDES DERIVED FROM MAGE TUMOR
; REJECTION ANTIGEN PRECURSORS WHICH COMPLEX WITH
; HLA-A2 MOLECULES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/533,499B
; FILING DATE: 23-Mar-2000
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/722,115
; FILING DATE: February 6, 1997
; APPLICATION NUMBER: 08/290,381
; FILING DATE: 15-August-1994
; APPLICATION NUMBER: 08/261,160
; FILING DATE: 17-June-1994
; APPLICATION NUMBER: 08/217,186
; FILING DATE: 24-March-1994
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-March-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6682731man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5327.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-533-499B-19
Query Match          2.4%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
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; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-533-499B-18

Query Match          2.4%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      144 FLLPKYQMK 152
      |||||
Db      1 FLLPKYQMK 9

RESULT 4
US-09-533-499B-19
; Sequence 19, Application US/09533499B
; Patent No. 6682731
; GENERAL INFORMATION:
; APPLICANT: Townsend, Alan; Bastin, Judy; Boon-Palleur, Thierry; van der
; Bruggen, Pierre; Coullie, Pierre; Gajewski, Thomas; Melief,
; Cornelis J.M.; Visseren, M.W.; Kast, W.M.
; TITLE OF INVENTION: ISOLATED PEPTIDES DERIVED FROM MAGE TUMOR
; REJECTION ANTIGEN PRECURSORS WHICH COMPLEX WITH
; HLA-A2 MOLECULES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/533,499B
; FILING DATE: 23-Mar-2000
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/722,115
; FILING DATE: February 6, 1997
; APPLICATION NUMBER: 08/290,381
; FILING DATE: 15-August-1994
; APPLICATION NUMBER: 08/261,160
; FILING DATE: 17-June-1994
; APPLICATION NUMBER: 08/217,186
; FILING DATE: 24-March-1994
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-March-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6682731man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5327.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-533-499B-19
Query Match          2.4%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
```

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 FIEGYCTPE 243
|||||

Db 1 FIEGYCTPE 9

RESULT 5
US-09-533-499B-20
; Sequence 20, Application US/09533499B
; Patent No. 6682731
; GENERAL INFORMATION:
; APPLICANT: Townsend, Alan; Bastin, Judy; Boon-Palleur, Thierry; van der
; Bruggen, Pierre; Coulie, Pierre; Gajewski, Thomas; Meliet,
; Cornelis J.M.; Visseren, M.W.; Kast, W.M.
; TITLE OF INVENTION: ISOLATED PEPTIDES DERIVED FROM MAGE TUMOR
; REJECTION ANTIGEN PRECURSORS WHICH COMPLEX WITH
; HLA-A2 MOLECULES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/533,499B
; FILING DATE: 23-Mar-2000
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/722,115
; FILING DATE: February 6, 1997
; APPLICATION NUMBER: 08/290,381
; FILING DATE: 15-August-1994
; APPLICATION NUMBER: 08/261,160
; FILING DATE: 17-June-1994
; APPLICATION NUMBER: 08/217,186
; FILING DATE: 24-March-1994
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-March-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6682731man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5327.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 20: A
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-533-499B-20

Query Match 2.4%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GLEGAQAPL 32
|||||

Db 1 GLEGAQAPL 9

RESULT 6
US-09-806-769-42

; Sequence 42, Application US/09806769
; Patent No. 6710172
; GENERAL INFORMATION:
; APPLICANT: Chau, Pascal
; APPLICANT: Luiten, Rosalie
; APPLICANT: Demotte, Nathalie
; APPLICANT: Deffour, Marie-Therese
; APPLICANT: Lurquin, Christophe
; APPLICANT: Traversari, Catia
; APPLICANT: Stroobant, Vincent
; APPLICANT: Cornelis, Guy R.
; APPLICANT: Boon-Palleur, Thierry
; APPLICANT: Van Der Bruggen, Pierre
; APPLICANT: Schultz, Erwin
; APPLICANT: Warnier, Guy
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; FILE REFERENCE: 117272y
; CURRENT APPLICATION NUMBER: US/09/806,769
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 09/165,863
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 09/289,350
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/806,769
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human MAGE-A1 peptide
US-09-806-769-42

Query Match 2.4%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 DPARYEFLW 298
|||||

Db 1 DPARYEFLW 9

RESULT 7
US-09-865-548A-39
; Sequence 39, Application US/09865548A
; Patent No. 6867283
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECUL
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-39

Query Match 2.4%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 GLYDGMHL 262
Db 1 GLYDGMHL 9

RESULT 8
US-08-465-167A-35
; Sequence 35, Application US/08465167A
; Patent No. 5750395
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Sette, Alessandro D.
; APPLICANT: Sidney, John C.
; TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,167A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/103,623
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-60-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-465-167A-35
Query Match 2.2%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 289 SDPARVEF 296
Db 2 SDPARVEF 9

RESULT 9
US-08-465-167A-38
; Sequence 38, Application US/08465167A
; Patent No. 5750395
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Sette, Alessandro D.
; APPLICANT: Sidney, John C.
; TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,167A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/103,623
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-60-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-465-167A-38
Query Match 2.2%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 295 EFLMGFRA 302
Db 1 EFLMGFRA 8

RESULT 10
US-08-159-339A-97
; Sequence 97, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Eteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-Seq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-0050300S
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:

INFORMATION FOR SEQ ID NO: 97:

SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-97

Query Match 2.2%; Score 8; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 LESVIKYN 168
|||||
Db 2 LESVIKYN 9

RESULT 11
US-08-159-339A-98
Sequence 98, Application US/08159339A
Patent No. 6037135

GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Eteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Us88
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993

ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-0050300S
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-98

Query Match 2.2%; Score 8; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 LVFGIDVK 192
|||||
Db 2 LVFGIDVK 9

RESULT 12
US-08-217-188A-47
Sequence 47, Application US/08217188A
Patent No. 5554724

GENERAL INFORMATION:
APPLICANT: Melief, Cornelis J. M.
APPLICANT: Visseren, M. J. W.
APPLICANT: Kast, W. M.
APPLICANT: van der Bruggen, Pierre
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Tumor Rejection Antigen
TITLE OF INVENTION: Precursor Mage-2 Derived Peptides, and Uses Thereof
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSER: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,188A
FILING DATE: 24-MARCH-1994
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5554724man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5340
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-217-188A-47

Query Match 1.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 FLWGPRA 302
|||||
Db 1 FLWGPRA 7

```
RESULT 13
US-08-195-186A-4
; Sequence 4, Application US/08195186A
; Patent No. 558995
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: METHOD FOR IDENTIFYING INDIVIDUALS
; TITLE OF INVENTION: SUFFERING FROM A CELLULAR ABNORMALITY SOME OF WHOSE
; TITLE OF INVENTION: ABNORMAL CELLS PRESENT COMPLEXES OF HLA-C-CLONE
; TITLE OF INVENTION: 10/MAGE-1 DERIVED PEPTIDES, AND METHODS FOR TREATING
; TITLE OF INVENTION: SAID INDIVIDUALS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,186A
; FILING DATE: 14-FEB-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/008,446
; FILING DATE: 22-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 558995man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5361
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 838-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
US-08-195-186A-4
Query Match 1.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPKRL 270
DB 3 YGEPKRL 9

RESULT 14
US-08-217-186-6
; Sequence 6, Application US/08217186
; Patent No. 5585461
; GENERAL INFORMATION:
; APPLICANT: Townsend, Alan; Bastin, Judy;
; APPLICANT: Boon-Falleur, Thierry; van der Bruggen, Pierre;
; APPLICANT: Coullie, Pierre
; TITLE OF INVENTION: ISOLATED, MAGE-3 DERIVED PEPTIDES
; TITLE OF INVENTION: WHICH COMPLEX WITH HLA-A2 MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
```

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,186
; FILING DATE: 24-MARCH-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5585461man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 327
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; TOPOLOGY: MOLECULE TYPE: protein
US-08-217-186-6
Query Match 1.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 FLWGPR 302
DB 1 FLWGPR 7

RESULT 15
US-08-261-160A-6
; Sequence 6, Application US/08261160A
; Patent No. 5591430
; GENERAL INFORMATION:
; APPLICANT: Townsend, Alan; Bastin, Judy;
; APPLICANT: Boon-Falleur, Thierry; van der Bruggen, Pierre;
; APPLICANT: Coullie, Pierre; Gajewski, Thomas;
; TITLE OF INVENTION: ISOLATED, MAGE-3 DERIVED PEPTIDES
; TITLE OF INVENTION: WHICH COMPLEX WITH HLA-A2 MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,160A
; FILING DATE: 17-JUNE-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/217,186
; FILING DATE: 24-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5591430man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5327.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
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;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-261-160A-6

Query Match      1.9%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. NO. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      296 FLWGPRA 302
      |||||
Db      1 FLWGPRA 7

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Search completed: March 17, 2006, 22:54:16
Job time : 46 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 18, 2006, 00:20:21 ; Search time 47 Seconds
(without alignments)
15.832 Million cell updates/sec

Title: US-09-856-812b-1_COPY_254_262

Perfect score: 9

Sequence: 1 GLYDGMHL 9

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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4: /cgn2_6/ptodata/1/1aa/pCTUS COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	100.0	9	2	US-09-865-548A-39
2	9	100.0	369	1	US-08-773-870-4
3	6	66.7	398	1	US-08-599-171A-29
4	6	66.7	398	1	US-08-646-590B-29
5	6	66.7	398	2	US-09-069-226-29
6	6	66.7	398	2	US-09-412-184-29
7	6	66.7	471	2	US-10-254-763A-13
8	5	55.6	10	2	US-08-403-459-15
9	5	55.6	30	1	US-08-140-137A-41
10	5	55.6	36	2	US-08-216-592A-13
11	5	55.6	44	1	US-08-140-137A-48
12	5	55.6	81	2	US-09-732-210-273
13	5	55.6	81	2	US-09-732-210-1549
14	5	55.6	82	2	US-09-732-210-1551
15	5	55.6	102	2	US-10-004-381-9
16	5	55.6	123	2	US-09-107-532A-6258
17	5	55.6	125	2	US-09-489-039A-13934
18	5	55.6	134	2	US-09-489-039A-12144
19	5	55.6	152	2	US-09-270-767-47623
20	5	55.6	158	2	US-09-502-540-15971
21	5	55.6	180	1	US-08-049-473-31
22	5	55.6	180	1	US-08-312-648-31
23	5	55.6	180	4	PCT-US94-04190-31
24	5	55.6	192	2	US-09-949-016-9891
25	5	55.6	199	1	US-08-849-376-4
26	5	55.6	199	4	PCT-US95-16450-4
27	5	55.6	213	2	US-09-771-161A-109

28	5	55.6	226	1	US-08-836-620A-7	Sequence 7, Appli
29	5	55.6	227	6	524657-9	Patent No. 524657
30	5	55.6	227	6	5433945-9	Patent No. 5433945
31	5	55.6	228	2	US-09-249-645-2	Sequence 2, Appli
32	5	55.6	228	2	US-09-844-132B-2	Sequence 2, Appli
33	5	55.6	228	6	5223610-9	Patent No. 5223610
34	5	55.6	229	2	US-09-249-645-1	Sequence 1, Appli
35	5	55.6	229	2	US-09-844-132B-1	Sequence 1, Appli
36	5	55.6	230	2	US-09-949-016-7366	Sequence 7366, Ap
37	5	55.6	233	2	US-09-608-088-4	Sequence 4, Appli
38	5	55.6	233	2	US-09-711-288-4	Sequence 2, Appli
39	5	55.6	235	2	US-09-885-827-2	Sequence 4, Appli
40	5	55.6	237	1	US-08-970-133-5	Sequence 5, Appli
41	5	55.6	237	2	US-09-294-545-5	Sequence 5, Appli
42	5	55.6	243	1	US-08-836-620A-8	Sequence 8, Appli
43	5	55.6	243	1	US-08-836-620A-9	Sequence 9, Appli
44	5	55.6	243	1	US-08-836-620A-10	Sequence 10, Appli
45	5	55.6	249	2	US-09-248-796A-22159	Sequence 22159, A

ALIGNMENTS

RESULT 1

US-09-865-548A-39

; Sequence 39, Application US/09865548A

; Patent No. 6867283

; GENERAL INFORMATION:

; APPLICANT: Barnea, Rilon

; APPLICANT: Beer, Ilan

; APPLICANT: Ziv, Tamar

; APPLICANT: Admon, Arle

; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECUL

; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES

; FILE REFERENCE: 01/22080

; CURRENT APPLICATION NUMBER: US/09/865,548A

; PRIORITY FILING DATE: 2001-05-16

; PRIOR APPLICATION NUMBER: US 60/290,958

; PRIOR FILING DATE: 2001-05-16

; NUMBER OF SEQ ID NOS: 204

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 39

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthetic peptide

US-09-865-548A-39

Query Match 100.0%; Score 9; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 4.6e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMHL 9

|||||||

Db 1 GLYDGMHL 9

RESULT 2

US-08-773-870-4

; Sequence 4, Application US/08773870

; Patent No. 5912143

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Goli, Surya K.

; TITLE OF INVENTION: NOVEL HUMAN MAGE-LIKE PROTEIN

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

Qy 3 YDGMH 8
Db 211 YDGMH 216

RESULT 5
US-09-069-226-29
; Sequence 29, Application US/09069226
; Patent No. 6013509
; GENERAL INFORMATION:
; APPLICANT: WARREN, Patrick V.
; TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESS: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,226
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/599,171
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HERRON, CHARLES J.
; REGISTRATION NUMBER: 28,019
; REFERENCE/DOCKET NUMBER: 331400-38
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-069-226-29

Query Match 66.7%; Score 6; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YDGMH 8
Db 211 YDGMH 216

RESULT 6
US-09-412-184-29
; Sequence 29, Application US/09412184
; Patent No. 6268188
; GENERAL INFORMATION:
; APPLICANT: Warren, Patrick V.
; APPLICANT: Swanson, Ronald V.
; TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/412,184
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,590
; FILING DATE: 08-May-1996
; APPLICATION NUMBER: 08/599,171
; FILING DATE: 09-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/01094
; FILING DATE: 21-January-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09010/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-412-184-29

Query Match 66.7%; Score 6; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YDGMH 8
Db 211 YDGMH 216

RESULT 7
US-10-254-763A-13
; Sequence 13, Application US/10254763A
; Patent No. 6946268
; GENERAL INFORMATION:
; APPLICANT: TAKAGI, HIROSHI
; APPLICANT: WADA, MASARU
; APPLICANT: NAKAMORI, SHIGERU
; TITLE OF INVENTION: L-Cysteine-Producing Bacterium and Method for Producing L-Cystein.
; FILE REFERENCE: 228254US0
; CURRENT APPLICATION NUMBER: US/10/254,763A
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: JP 2001-302008
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-254-763A-13

Query Match 66.7%; Score 6; DB 2; Length 471;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGM 6
Db 321 GLYDGM 326

RESULT 8
US-08-403-459-15
; Sequence 15, Application US/08403459
; Patent No. 6514942
; GENERAL INFORMATION:
; APPLICANT: Ioannides, Constantin G.
; APPLICANT: Fisk, Bryan A.
; APPLICANT: Ioannides, Maria G.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING
; T-LYMPHOCYTES
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,459
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSC:390/KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-403-459-15

Query Match 55.6%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GMEHL 9
DB 3 GMEHL 7

RESULT 9
US-08-140-137A-41
; Sequence 41, Application US/08140137A
; Patent No. 5817617
; GENERAL INFORMATION:
; APPLICANT: TUOMANEN, ELAINE
; APPLICANT: MASURE, H. R.
; TITLE OF INVENTION: ANALOGS OF ENDOTHELIAL LEUKOCYTE
; ADHESION MOLECULE (ELAM)
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/140,137A
; FILING DATE: 27-MAY-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-140-137A-41

Query Match 55.6%; Score 5; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDG 5
DB 25 GLYDG 29

RESULT 10
US-08-216-592A-13
; Sequence 13, Application US/08216592A
; Patent No. 6635429
; GENERAL INFORMATION:
; APPLICANT: LEID, MARK
; APPLICANT: KASTNER, PHILIPPE
; APPLICANT: CHAMON, PIERRE
; TITLE OF INVENTION: NOVEL HETERODIMERIC STEROID RECEPTOR
; PROTEINS, GENES ENCODING SAME, AND USAGE THEREOF
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue NW Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/216,592A
; FILING DATE: 23-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/825,667
; FILING DATE: 24-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDSTEIN, JORGE A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 1383.0060002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-216-592A-13

Query Match 55.6%; Score 5; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GMEHL 9
Db 25 GMEHL 29

RESULT 11
US-08-140-137A-48
Sequence 48, Application US/08140137A
Patent No. 5817617
GENERAL INFORMATION:
APPLICANT: TUOMANEN, ELAINE
APPLICANT: MASURE, H. R.
TITLE OF INVENTION: ANALOGS OF ENDOTHELIAL LEUKOCYTE
ADHESION MOLECULE (ELAM)
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/140,137A
FILING DATE: 27-MAY-1994
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-096
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684

TELEX: 133521
INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: S3 peptide sequence
US-08-140-137A-48

Query Match 55.6%; Score 5; DB 1; Length 44;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDG 5
Db 38 GLYDG 42

RESULT 12
US-09-732-210-273
Sequence 273, Application US/09732210
Patent No. 6573361
GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Mittanck, Cindy A.

APPLICANT: Seale, Jeffrey W.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 273
LENGTH: 81
TYPE: PRT
ORGANISM: Zea mays
US-09-732-210-273

Query Match 55.6%; Score 5; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDG 5
Db 43 GLYDG 47

RESULT 13
US-09-732-210-1549
Sequence 1549, Application US/09732210
Patent No. 6573361
GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Mittanck, Cindy A.
APPLICANT: Seale, Jeffrey W.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 1549
LENGTH: 81
TYPE: PRT
ORGANISM: Zea mays
US-09-732-210-1549

Query Match 55.6%; Score 5; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDG 5
Db 43 GLYDG 47

RESULT 14
US-09-732-210-1551
Sequence 1551, Application US/09732210
Patent No. 6573361
GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Mittanck, Cindy A.
APPLICANT: Seale, Jeffrey W.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)B
CURRENT APPLICATION NUMBER: US/09/732,210

; CURRENT FILING DATE: 2000-12-07
 ; PRIOR APPLICATION NUMBER: US 60/169,513
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: US 60/169,340
 ; PRIOR FILING DATE: 1999-12-07
 ; NUMBER OF SEQ ID NOS: 1753
 ; SEQ ID NO 1551
 ; LENGTH: 82
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; US-09-732-210-1551

Query Match 55.6%; Score 5; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDG 5
 Db 43 GLYDG 47

RESULT 15
 US-10-004-381-9
 ; Sequence 9, Application US/10004381
 ; Patent No. 6841359
 ; GENERAL INFORMATION:
 ; APPLICANT: SZOSTAK, JACK W.
 ; APPLICANT: WILSON, DAVID S.
 ; APPLICANT: KEEPE, ANTHONY D.
 ; TITLE OF INVENTION: STREPTAVIDIN-BINDING PEPTIDES AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: 00786/388002
 ; CURRENT APPLICATION NUMBER: US/10/004,381
 ; CURRENT FILING DATE: 2001-10-31
 ; PRIOR APPLICATION NUMBER: US 60/244,541
 ; PRIOR FILING DATE: 2000-10-31
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 9
 ; LENGTH: 102
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: selected peptide
 US-10-004-381-9

Query Match 55.6%; Score 5; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDG 5
 Db 10 GLYDG 14

Search completed: March 18, 2006, 00:21:36
 Job time : 48 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 22:37:09 ; Search time 41 Seconds
(without alignments)
865.951 Million cell updates/sec

Title: US-09-856-812B-1
Perfect score: 369
Sequence: 1 MPRAPKRCMPEDLQSQS.....DTTAMASASSATGTSFSYPE 369
Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues
Word size : 0
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	369	100.0	369	I38659	melanoma antigen M
2	29	7.9	315	I38668	melanoma antigen M
3	26	7.0	317	I38661	melanoma antigen M
4	17	4.6	314	JC2360	melanoma antigen M
5	17	4.6	314	I68889	melanoma antigen M
6	17	4.6	314	I54519	melanoma antigen M
7	17	4.6	314	JC2361	melanoma antigen M
8	14	3.8	280	JC2358	melanoma antigen M
9	12	3.3	319	I38660	melanoma antigen M
10	12	3.3	1006	JC5526	kinase-defective E
11	11	3.0	491	T52398	hypothetical prote
12	11	3.0	639	T46577	arylsulfatase (EC
13	10	2.7	132	T49536	hypothetical prote
14	10	2.7	154	S55017	hypothetical prote
15	10	2.7	181	T46017	hypothetical prote
16	10	2.7	211	D96507	hypothetical prote
17	10	2.7	230	D86352	protein T26F17.14
18	10	2.7	234	I38667	hypothetical prote
19	10	2.7	244	T51481	hypothetical prote
20	10	2.7	255	WJHU4B	homeotic protein H
21	10	2.7	279	T01924	hypothetical prote
22	10	2.7	291	T08189	hypothetical prote
23	10	2.7	317	T39869	probable lysophosp
24	10	2.7	344	T40167	hypothetical prote
25	10	2.7	347	I38008	melanoma antigen M
26	10	2.7	354	T49806	hypothetical prote
27	10	2.7	360	T45649	hypothetical prote
28	10	2.7	364	I48188	gene NX6.1 protei
29	10	2.7	372	E85170	hypothetical prote

30	10	2.7	383	2	T38443	hypothetical prote
31	10	2.7	383	2	T38442	hypothetical prote
32	10	2.7	440	2	G96600	protein F14J16.24
33	10	2.7	460	2	H96536	hypothetical prote
34	10	2.7	464	2	T51090	plastid division p
35	10	2.7	484	2	JE0341	R-SNAD protein, Sm
36	10	2.7	512	2	S41292	glucose-1-phosphat
37	10	2.7	524	2	S33640	homeotic protein s
38	10	2.7	537	2	B33485	spore coat protein
39	10	2.7	542	2	T06728	pectate lyase (EC
40	10	2.7	586	2	C30411	synapsin Iia - rat
41	10	2.7	614	2	A32608	thyroid hormone re
42	10	2.7	633	2	T04179	hypothetical prote
43	10	2.7	669	2	JC5662	hepatoma-derived g
44	10	2.7	693	2	S64904	probable membrane
45	10	2.7	707	2	S60588	drebrin A - rat

ALIGNMENTS

RESULT 1

I38659
melanoma antigen MAGE-10 - human
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C:Accession: I38659
R:De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; B oon, T.
Immunogenetics 40, 360-369, 1994
A:Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fa
A:Reference number: I38659; MUID:95012457; PMID:7927540
A:Accession: I38659
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: UNIPROT:P43363; UNIPARC:UPI00000000C57; EMBL:U10685; NID:g533510; PI
C:Genetics:
A:Gene: GDB:MAGEA10; MAGE10
A:Cross-references: GDB:331126
A:Map position: Xq28-Xq28
A:Introns: #status absent
C:Superfamily: tumor associated protein MAGE

Query Match	100.0%	Score 369;	DB 2;	Length 369;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 369;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MPRAPKRCMPEDLQSQSETQGLEGAQAPLAVEDASSSTSTSSSPSSPSSSSSSSS 60		
Db	1	MPRAPKRCMPEDLQSQSETQGLEGAQAPLAVEDASSSTSTSSSPSSPSSSSSSSS 60		
QY	61	SSCYPLIPSTPREVSADDETPNPQSAQIACSSPSVVASLPDQSDGSSSKKESPSSTL 120		
Db	61	SSCYPLIPSTPREVSADDETPNPQSAQIACSSPSVVASLPDQSDGSSSKKESPSSTL 120		
QY	121	QVLPSESLPRSEIDEKVTDLVQFLFKYQKMEPTTKAILESVKNYEDHPFLFSEAS 180		
Db	121	QVLPSESLPRSEIDEKVTDLVQFLFKYQKMEPTTKAILESVKNYEDHPFLFSEAS 180		
QY	181	ECMLLVFGIDVKVEPTGHSFVLVTSGLTYDGMGLSDVQSMKPTGILLIILSIIFIEGYC 240		
Db	181	ECMLLVFGIDVKVEPTGHSFVLVTSGLTYDGMGLSDVQSMKPTGILLIILSIIFIEGYC 240		
QY	241	TPEEVIWALNMGLYDGMHLYGEPKLLTQDVQENLYEYRQVPGSDPARYEFLWGP 300		
Db	241	TPEEVIWALNMGLYDGMHLYGEPKLLTQDVQENLYEYRQVPGSDPARYEFLWGP 300		
QY	301	RAHAIRKMSLLKFLAKVNGSDPRFFPLWYEALKDEBERAQDRIATTDTTTAMASASS 360		
Db	301	RAHAIRKMSLLKFLAKVNGSDPRFFPLWYEALKDEBERAQDRIATTDTTTAMASASS 360		
QY	361	ATGGSFSYPE 369		

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Db      361 ATGTSFSYPE 369
|||||
RESULT 2
138668
melanoma antigen MAGE-9 - human
C:Species: Homo sapiens (man)
C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C:Accession: I38668
R:De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Bz
con, T.
Immunogenetics 40, 360-369, 1994
A:Title: Structure, chromosomal localization, and expression of the MAGE fam
A:Reference number: I38659; MUID:95012457; PMID:7927540
A:Accession: I38668
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-315 <RES>
A:Cross-references: UNIPROT:P43362; UNIPARC:UPI000012EB2B; EMBL:U10694; NID:G533527; PID
C:Genetics:
A:Gene: GDB:MAGEA9; MAGE9
A:Cross-references: GDB:331125
A:Map position: Xp21.3-xp21.3
A:Introns: #status absent
C:Superfamily: tumor associated protein MAGE

Query Match      7.9%; Score 29; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 3e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      264 YGEPKLLTQDWQVQENYLEYRQVPGSDPA 292
|||||
DB      238 YGEPKLLTQDWQVQENYLEYRQVPGSDPA 266
|||||

RESULT 3
138661
melanoma antigen MAGE-4 - human
N:Alternate names: MAGE 41 protein; melanoma antigen MAGE-X2
C:Species: Homo sapiens (man)
C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C:Accession: I38661; I38662; PH1297; PH1298; JC2359; G01446
R:De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Bz
con, T.
Immunogenetics 40, 360-369, 1994
A:Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fam
A:Reference number: I38659; MUID:95012457; PMID:7927540
A:Accession: I38661
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-317 <DEP1>
A:Cross-references: UNIPROT:P43358; UNIPARC:UPI000013EA1P; EMBL:U10687; NID:G533514; PID
A:Experimental source: antigen MAGE-4a
A:Accession: I38662
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-172,'T',174-317 <DEP2>
A:Cross-references: UNIPARC:UPI00000104C; EMBL:U10688; NID:G533516; PIDN:AAA68872.1; PI
A:Experimental source: antigen MAGE-4b
R:Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,
J. Exp. Med. 176, 1453-1457, 1992
A:Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic
A:Reference number: PH1294; MUID:93018875; PMID:1402688
A:Accession: PH1297
A:Molecule type: DNA
A:Residues: 169-177 <TRAI>
A:Cross-references: UNIPARC:UPI000014A1B6
A:Experimental source: antigen MAGE-4
A:Accession: PH1298
A:Molecule type: DNA
A:Residues: 169-172,'T',174-177 <TRA2>
A:Cross-references: UNIPARC:UPI0000042626

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A:Experimental source: antigen MAGE-41
R:Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
Biochem. Biophys. Res. Commun. 202, 549-555, 1994
A:Title: Cloning and analysis of MAGE-1-related genes.
A:Reference number: JC2358; MUID:94311935; PMID:8037761
A:Accession: JC2359
A:Molecule type: mRNA
A:Residues: 1-172,'T',174-306,'Q',308-317 <DIN>
A:Cross-references: UNIPARC:UPI000016AOC1; EMBL:U10340; NID:G499123; PIDN:AAA19007.1; PI
A:Experimental source: melanoma cell line DM150
C:Genetics:
A:Gene: GDB:MAGEA4; MAGE4; MAGE-X2
A:Cross-references: GDB:331119
A:Map position: Xq28-Xq28
A:Introns: #status absent
C:Superfamily: tumor associated protein MAGE
F:169-177/Region: HLA-A1 binding #status predicted

Query Match      7.0%; Score 26; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.6e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      264 YGEPKLLTQDWQVQENYLEYRQVPGS 289
|||||
DB      240 YGEPKLLTQDWQVQENYLEYRQVPGS 265
|||||

RESULT 4
JC2360
melanoma antigen MAGE-6 - human
N:Alternate names: tumor-associated antigen, MAGE-3b
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: JC2360; PH1301; I38665; G01445
R:Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
Biochem. Biophys. Res. Commun. 202, 549-555, 1994
A:Title: Cloning and analysis of MAGE-1-related genes.
A:Reference number: JC2358; MUID:94311935; PMID:8037761
A:Accession: JC2360
A:Molecule type: mRNA
A:Residues: 1-314 <DIN>
A:Cross-references: UNIPROT:P43360; UNIPARC:UPI000000D9B0
A:Experimental source: melanoma cell line DM150
R:Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,
J. Exp. Med. 176, 1453-1457, 1992
A:Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic
A:Reference number: PH1294; MUID:93018875; PMID:1402688
A:Accession: PH1301
A:Molecule type: DNA
A:Residues: 168-176 <TRA>
A:Cross-references: UNIPARC:UPI0000042625
R:De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Bz
con, T.
Immunogenetics 40, 360-369, 1994
A:Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fam
A:Reference number: I38659; MUID:95012457; PMID:7927540
A:Accession: I38665
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-314 <RES>
A:Cross-references: UNIPARC:UPI000000D9B0; EMBL:U10691; NID:G533522; PIDN:AAA68875.1; P
R:Fenton, R.G.
submitted to the EMBL Data Library, June 1994
A:Reference number: G01426
A:Accession: G01445
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-314 <PEN>
A:Cross-references: UNIPARC:UPI000000D9B0; EMBL:U10339; NID:G499121; PIDN:AAA19006.1; P
C:Genetics:
A:Gene: GDB:MAGEA6; MAGE6
A:Map position: Xq28-Xq28

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A;Introns: #status absent
 C;Superfamily: tumor associated protein MAGE
 F;168-176/Region: HLA-A1 binding #status predicted

Query Match 4.6%; Score 17; DB 2; Length 314;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 VOENYLEYRQVPGSDPA 292
 Db 251 VOENYLEYRQVPGSDPA 267

RESULT 5
 I68889
 melanoma antigen MAGE-2 - human
 C;Species: Homo sapiens (man)
 C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
 C;Accession: I68889; PH1294
 R;De Smet, C.; Lurquin, C.; van der Bruggen, P.; De Plaen, E.; Brasseur, F.; Boon, T.
 Immunogenetics 39, 121-129, 1994
 A;Title: Sequence and expression pattern of the human MAGE2 gene.
 A;Reference number: I54519; MUID:94102805; PMID:8276455
 A;Accession: I68889
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-314 <RES>
 A;Cross-references: UNIPROT:P43356; UNIPARC:UPI000012EB28; GB:L18920; NID:g436180; PIDN:
 R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,
 J. Exp. Med. 176, 1453-1457, 1992
 A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic
 A;Reference number: PH1294; MUID:93018875; PMID:1402688
 A;Accession: PH1294
 A;Molecule type: DNA
 A;Residues: 168-176 <TRA>
 A;Cross-references: UNIPARC:UPI000004262C
 C;Genetics:
 A;Gene: GDB:MAGEA2; MAGE2
 A;Cross-references: GDB:273684
 A;Map position: Xq28-Xq28
 C;Superfamily: tumor associated protein MAGE

Query Match 4.6%; Score 17; DB 2; Length 314;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 VOENYLEYRQVPGSDPA 292
 Db 251 VOENYLEYRQVPGSDPA 267

RESULT 6
 I54519
 melanoma antigen MAGE-12 - human
 N;Alternate names: MAGE 21 protein
 C;Species: Homo sapiens (man)
 C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
 C;Accession: I54519; JC2362; PH1295
 R;De Smet, C.; Lurquin, C.; van der Bruggen, P.; De Plaen, E.; Brasseur, F.; Boon, T.
 Immunogenetics 39, 121-129, 1994
 A;Title: Sequence and expression pattern of the human MAGE2 gene.
 A;Reference number: I54519; MUID:94102805; PMID:8276455
 A;Accession: I54519
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-314 <DES>
 A;Cross-references: UNIPROT:P43365; UNIPARC:UPI0000039F48; GB:L18877; NID:g499345; PIDN:
 R;Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
 Biochem. Biophys. Res. Commun. 202, 549-555, 1994
 A;Title: Cloning and analysis of MAGE-1-related genes.
 A;Reference number: JC2358; MUID:94311935; PMID:8037761
 A;Accession: JC2362
 A;Molecule type: mRNA

A;Residues: 1-9,'S',11-186,'D',188-299,'S',301-314 <DIN>
 A;Cross-references: UNIPARC:UPI0000178981
 A;Experimental source: melanoma cell line DM150; MAGE-12f
 R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,
 J. Exp. Med. 176, 1453-1457, 1992
 A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic.
 A;Reference number: PH1294; MUID:93018875; PMID:1402688
 A;Accession: PH1295
 A;Molecule type: DNA
 A;Residues: 168-176 <TRA>
 A;Cross-references: UNIPARC:UPI0000039F49
 A;Experimental source: MAGE-21
 C;Genetics:
 A;Gene: GDB:MAGEA12; MAGE12; MAGE-12f
 A;Cross-references: GDB:331129
 A;Map position: Xq28-Xq28
 C;Superfamily: tumor associated protein MAGE
 F;168-176/Region: HLA-A1 binding #status predicted

Query Match 4.6%; Score 17; DB 2; Length 314;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 VOENYLEYRQVPGSDPA 292
 Db 251 VOENYLEYRQVPGSDPA 267

RESULT 7
 JC2361
 melanoma antigen MAGE-3 - human
 N;Alternate names: MAGE 3 protein
 C;Species: Homo sapiens (man)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C;Accession: JC2361; PH1296; I38438
 R;Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
 Biochem. Biophys. Res. Commun. 202, 549-555, 1994
 A;Title: Cloning and analysis of MAGE-1-related genes.
 A;Reference number: JC2358; MUID:94311935; PMID:8037761
 A;Accession: JC2361
 A;Molecule type: mRNA
 A;Residues: 1-314 <DIN>
 A;Cross-references: UNIPROT:P43357; UNIPARC:UPI0000062194
 A;Experimental source: melanoma cell line DM150
 R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,
 J. Exp. Med. 176, 1453-1457, 1992
 A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic.
 A;Reference number: PH1294; MUID:93018875; PMID:1402688
 A;Accession: PH1296
 A;Molecule type: DNA
 A;Residues: 168-176 <TRA>
 A;Cross-references: UNIPARC:UPI000002F152
 R;Gaugler, B.; Van den Eynde, B.; van der Bruggen, P.; Romero, P.; Gaforio, J.J.; De Pl,
 J. Exp. Med. 179, 921-930, 1994
 A;Title: Human gene MAGE-3 codes for an antigen recognized on a melanoma by autologous
 A;Reference number: I38438; MUID:94157413; PMID:8113684
 A;Accession: I38438
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-314 <RES>
 A;Cross-references: UNIPARC:UPI0000062194; EMBL:U03735; NID:g468925; PIDN:AAA17446.1; P
 C;Genetics:
 A;Gene: MAGE-3
 C;Superfamily: tumor associated protein MAGE
 F;168-176/Region: HLA-A1 binding #status predicted

Query Match 4.6%; Score 17; DB 2; Length 314;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 VOENYLEYRQVPGSDPA 292
 Db 251 VOENYLEYRQVPGSDPA 267

A:Accession: JC5526
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1006 <MAT>
A:Cross-references: UNIPROT:O15197; UNIPARC:UPI000012A088; DDBJ:DB83492; NID:G2281007; P1
C:Comment: This protein is highly homologous to Eph-family receptor tyrosine kinase, but
C:Genetics:
A:Gene: hep
A:Map position: 7q33-35
C:Superfamily: SAM homology
C:Keywords: ATP
F:1-16/Domain: signal sequence #status predicted <SIG>
F:353-456/Domain: fibronectin type III repeat homology <FN3A>
F:472-556/Domain: fibronectin type III repeat homology <FN3B>
F:578-603/Domain: transmembrane #status predicted <TM>
F:653-907/Domain: protein kinase homology <KIN>
F:661-669/Region: protein kinase ATP-binding motif

Query Match 3.3%; Score 12; DB 2; Length 1006;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 SPPSSSSSSSSSS 62
Db 148 SPPSSSSSSSSSS 159
|||||

RESULT 11
T52398
hypothetical protein MMB12.17 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 31-Dec-2004
C:Accession: T52398
R:Kaneko, T.; Kato, T.; Sato, S.; Nakamura, Y.; Asamizu, E.; Tabata, S.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z26062
A:Accession: T52398
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-491 <KAN>
A:Cross-references: UNIPROT:Q9LUM6; UNIPARC:UPI00000AC290; EMBL:AF000417; PIDN:BAB02555
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 3
A:Introns: 234/2
C:Superfamily: Hypothetical protein

Query Match 3.0%; Score 11; DB 2; Length 491;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 FPPSSSSSSSSSS 62
Db 18 FPPSSSSSSSSSS 28
|||||

RESULT 12
T46577
arylsulfatase (EC 3.1.6.1) [validated] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004
C:Accession: T46577
R:Baker, D.L.; Paietta, J.V.
submitted to the EMBL Data Library, February 1997
A:Description: Molecular characterization of the arylsulfatase gene of Neurospora crassa
A:Reference number: Z23090
A:Accession: T46577
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-639 <BAK>
A:Cross-references: UNIPROT:O43113; UNIPARC:UPI000006B2E2; EMBL:U89492; PIDN:AAC02716.1
A:Experimental source: strain wild type 74-OR23-1A
C:Genetics:

A:Accession: JC2358
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1006 <MAT>
A:Cross-references: UNIPROT:O15197; UNIPARC:UPI000012A088; DDBJ:DB83492; NID:G2281007; P1
C:Comment: This protein is highly homologous to Eph-family receptor tyrosine kinase, but
C:Genetics:
A:Gene: hep
A:Map position: 7q33-35
C:Superfamily: SAM homology
C:Keywords: ATP
F:1-16/Domain: signal sequence #status predicted <SIG>
F:353-456/Domain: fibronectin type III repeat homology <FN3A>
F:472-556/Domain: fibronectin type III repeat homology <FN3B>
F:578-603/Domain: transmembrane #status predicted <TM>
F:653-907/Domain: protein kinase homology <KIN>
F:661-669/Region: protein kinase ATP-binding motif

Query Match 3.8%; Score 14; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 SDPARYEFLWGPRA 302
Db 257 SDPARYEFLWGPRA 270
|||||

RESULT 9
I38660
melanoma antigen Mage-11 - human
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1997 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C:Accession: I38660
R:De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Biondini, T.
Immunogenetics 40, 360-369, 1994
A:Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fam
A:Reference number: I38659; MUID:95012457; PMID:7927540
A:Accession: I38660
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-319 <RES>
A:Cross-references: UNIPROT:P43364; UNIPARC:UPI0000000C62; EMBL:U10686; NID:G533512; PID
C:Genetics:
A:Gene: GDB:MAGE11; MAGE11
A:Cross-references: GDB:I331128
A:Map position: Xq28-Xq28
A:Introns: #status absent
C:Superfamily: tumor associated protein MAGE

Query Match 3.3%; Score 12; DB 2; Length 319;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 YEFLWGPRAHAE 305
Db 272 YEFLWGPRAHAE 283
|||||

RESULT 10
JC5526
kinase-defective Eph-family receptor protein precursor - human
C:Species: Homo sapiens (man)
C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 31-Dec-2004
C:Accession: JC5526
R:Matsuoka, H.; Iwata, N.; Ito, M.; Shimoyama, M.; Nagata, A.; Chihara, K.; Takai, S.; M
Biochem. Biophys. Res. Commun. 235, 487-492, 1997
A:Title: Expression of a kinase-defective Eph-like receptor in the normal human brain.
A:Reference number: JC5526; MUID:97350806; PMID:9207182

A:Gene: ars-1

A:Map position: 7

A:Introns: 115/1; 518/3

C:Function:

A:Description: EC 3.1.1.6.1 [validated, MUID:89384589]

A:Note: genes are expressed under conditions of sulfur limitation and are under coordination

C:Superfamily: arylsulfatase, plant type

C:Keywords: sulfuric ester hydrolase

Query Match 3.0%; Score 11; DB 2; Length 639;

Best Local Similarity 100.0%; Pred. No. 0.026; 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 PSSSSSSSSSS 62

DB 239 PSSSSSSSSSS 249

RESULT 13

T49536

hypothetical protein B21J21.150 [imported] - Neurospora crassa

C:Species: Neurospora crassa

C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

C:Accession: T49536

R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,

submitted to the Protein Sequence Database, May 2000

A:Reference number: Z25022

A:Accession: T49536

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-132 <SCH>

A:Cross-references: UNIPARC:UPI000017B475; EMBL:AL355929; GSPDB:GN00116; NCSP:B21J21.150

A:Experimental source: BAC clone B21J21; strain OR74A

C:Genetics:

A:Gene: NCSP:B21J21.150

A:Map position: 6

Query Match

Best Local Similarity 2.7%; Score 10; DB 2; Length 132;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 PSSSSSSSSSS 62

DB 20 PSSSSSSSSSS 29

RESULT 14

S55017

hypothetical protein 2 - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 16-Feb-1997

C:Accession: S55017

R:Bergstrom, D.E.; Merli, C.A.; Cygan, J.A.; Shelby, R.; Blackman, R.K.

Genetics 139, 1331-1346, 1995

A:Title: Regulatory autonomy and molecular characterization of the Drosophila out at fir

A:Reference number: S55016; MUID:95286060; PMID:7768442

A:Accession: S55017

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-154 <BER>

A:Cross-references: UNIPARC:UPI000017B2A2; EMBL:L31349

C:Genetics:

A:Gene: FlyBase:oa1

A:Cross-references: FlyBase:FBgn0011818

Query Match

Best Local Similarity 2.7%; Score 10; DB 2; Length 154;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 PSSSSSSSSSS 62

DB 138 PSSSSSSSSSS 147

RESULT 15

T46017

hypothetical protein T10K17.160 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C:Accession: T46017

R:Benes, V.; Wurmbach, E.; Drzonek, H.; Ansoerge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.

submitted to the Protein Sequence Database, January 2000

A:Reference number: Z23019

A:Accession: T46017

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-181 <BEN>

A:Cross-references: UNIPROT:Q9M2Q3; UNIPARC:UPI00000A0B13; EMBL:AL132977

A:Experimental source: cultivar Columbia; BAC clone T10K17

C:Genetics:

A:Map position: 3

A:Note: T10K17.160

Query Match

Best Local Similarity 2.7%; Score 10; DB 2; Length 181;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 PSSSSSSSSSS 62

DB 8 PSSSSSSSSSS 17

Search completed: March 17, 2006, 22:41:28

Job time : 45 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:34:23 ; Search time 28.3333 Seconds
(without alignments)
26.262 Million cell updates/sec

Title: US-09-856-812B-48

Perfect score: 47

Sequence: 1 FLLFKYQMK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/1aa/5 COMB pep.*
- 2: /cgn2_6/ptodata/1/1aa/6 COMB pep.*
- 3: /cgn2_6/ptodata/1/1aa/H COMB pep.*
- 4: /cgn2_6/ptodata/1/1aa/PCITUS COMB pep.*
- 5: /cgn2_6/ptodata/1/1aa/RE COMB pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	9	2	US-09-533-499B-18
2	47	100.0	369	1	US-08-773-870-4
3	40	85.1	312	2	US-09-949-016-9310
4	37	78.7	1142	1	US-08-993-118-7
5	37	78.7	1142	2	US-08-845-528C-7
6	37	78.7	1142	2	US-09-061-709-2
7	37	78.7	1142	2	US-09-066-281B-7
8	37	78.7	1142	2	US-09-899-651-2
9	37	78.7	1142	2	US-09-468-433C-7
10	37	78.7	1142	2	US-09-392-714-26
11	37	78.7	1142	2	US-09-270-437D-2
12	36	76.6	275	2	US-09-468-433C-24
13	35	74.5	67	2	US-09-270-767-44621
14	35	74.5	346	2	US-09-468-433C-22
15	33	70.2	81	2	US-09-270-767-35366
16	33	70.2	81	2	US-09-270-767-50583
17	32	68.1	39	2	US-09-270-767-42032
18	32	68.1	214	2	US-09-270-767-56828
19	32	68.1	503	2	US-09-270-767-41594
20	31	66.0	72	2	US-09-621-976-7160
21	31	66.0	170	2	US-09-270-767-43206
22	31	66.0	251	1	US-08-933-750C-44
23	31	66.0	251	2	US-09-234-613-44
24	31	66.0	251	2	US-09-991-181-6
25	31	66.0	251	2	US-09-990-444-6
26	31	66.0	251	2	US-09-997-333-6
27	31	66.0	251	2	US-09-992-598-6

28	31	66.0	279	2	US-09-673-395A-300	Sequence 300, Appl
29	31	66.0	390	2	US-09-248-796A-16838	Sequence 16838, A
30	31	66.0	484	2	US-09-583-110-3997	Sequence 3997, Ap
31	31	66.0	484	2	US-09-107-433-4661	Sequence 4661, Ap
32	30	63.8	78	2	US-09-248-796A-21996	Sequence 21996, A
33	30	63.8	96	2	US-09-902-540-10587	Sequence 10587, A
34	30	63.8	176	2	US-09-270-767-40762	Sequence 40762, A
35	30	63.8	176	2	US-09-270-767-55978	Sequence 55978, A
36	30	63.8	240	2	US-09-248-796A-24008	Sequence 24008, A
37	30	63.8	295	2	US-09-107-532A-6252	Sequence 6252, A
38	30	63.8	324	2	US-09-489-039A-13042	Sequence 13042, A
39	30	63.8	380	1	US-08-773-870-5	Sequence 5, Appli
40	30	63.8	477	2	US-09-876-221-2	Sequence 2, Appli
41	30	63.8	563	2	US-09-248-796A-20006	Sequence 20006, A
42	30	63.8	638	2	US-09-270-767-46019	Sequence 46019, A
43	30	63.8	756	2	US-09-711-164-426	Sequence 426, App
44	29	61.7	41	2	US-09-270-767-39123	Sequence 39123, A
45	29	61.7	41	2	US-09-270-767-54340	Sequence 54340, A

ALIGNMENTS

RESULT 1

US-09-533-499B-18

; Sequence 18, Application US/09533499B

; Patent No. 6682731

; GENERAL INFORMATION:

; APPLICANT: Townsend, Alan; Bastin, Judy; Boon-Palleur, Thierry; van der
; Bruggen, Pierre; Coulie, Pierre; Gajewski, Thomas; Melief,
; Cornelis J.M.; Visseren, M.W.; Kast, W.M.

; TITLE OF INVENTION: ISOLATED PEPTIDES DERIVED FROM MAGE TUMOR
; REJECTION ANTIGEN PRECURSORS WHICH COMPLEX WITH
; HLA-A2 MOLECULES

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Fulbright & Jaworski LLP

; STREET: 666 Fifth Avenue

; CITY: New York City

; STATE: New York

; COUNTRY: USA

; ZIP: 10103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/533,499B

; FILING DATE: 23-Mar-2000

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/722,115

; FILING DATE: February 6, 1997

; APPLICATION NUMBER: 08/290,381

; FILING DATE: 15-August-1994

; APPLICATION NUMBER: 08/261,160

; FILING DATE: 17-June-1994

; APPLICATION NUMBER: 08/217,186

; FILING DATE: 24-March-1994

; APPLICATION NUMBER: 08/217,188

; FILING DATE: 24-March-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, No. 6682731man D.

; REGISTRATION NUMBER: 30,946

; REFERENCE/DOCKET NUMBER: LUD 5327.3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 318-3168

; TELEFAX: (212) 318-3400

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-533-499B-18

Query Match      100.0%; Score 47; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
   |||||
Db 1 FLLFKYQMK 9

RESULT 2
US-08-773-870-4
; Sequence 4, Application US/08773870
; Patent No. 5912143
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MAGE-LIKE PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/773,870
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0179 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 533511
US-08-773-870-4

Query Match      100.0%; Score 47; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
   |||||
Db 144 FLLFKYQMK 152

RESULT 3
US-09-949-016-9310
; Sequence 9310, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9310
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9310

Query Match      85.1%; Score 40; DB 2; Length 312;
Best Local Similarity 77.8%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
   |||||
Db 85 FLLFKYQMK 93

RESULT 4
US-08-993-118-7
; Sequence 7, Application US/08993118
; Patent No. 5997872
; GENERAL INFORMATION:
; APPLICANT: LUCAS, Sophie;
; APPLICANT: BOON-PALLEUR, Thierry
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR
; TITLE OF INVENTION: REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,118
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,528
; FILING DATE: April 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary Anne Schofield
; REGISTRATION NUMBER: 36,669
; REFERENCE/DOCKET NUMBER: LUD 5455
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1142
; TYPE: amino acids
```

; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
US-08-993-118-7

Query Match 78.7%; Score 37; DB 1; Length 1142;
Best Local Similarity 77.8%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
||| |||:
Db 918 FLLKXQVK 926

RESULT 5
US-08-845-528C-7
; Sequence 7, Application US/08845528C
; Patent No. 6027924
; GENERAL INFORMATION:
; APPLICANT: LUCAS, Sophie;
; APPLICANT: DE SMET, Charles;
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR
; TITLE OF INVENTION: REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,528C
; FILING DATE: April 25, 1997
; CLASSIFICATION: 4335
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary Anne Schofield
; REGISTRATION NUMBER: 36,669
; REFERENCE/DOCKET NUMBER: LUD 5455
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1142
; TYPE: amino acids
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
US-08-845-528C-7

Query Match 78.7%; Score 37; DB 2; Length 1142;
Best Local Similarity 77.8%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
||| |||:
Db 918 FLLKXQVK 926

RESULT 6
US-09-061-709-2
; Sequence 2, Application US/09061709B
; Patent No. 6297364
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam

; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
; TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
; FILE REFERENCE: LUD 5538
; CURRENT APPLICATION NUMBER: US/09/061,709B
; CURRENT FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 1142
; TYPES: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-061-709-2

Query Match 78.7%; Score 37; DB 2; Length 1142;
Best Local Similarity 77.8%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
||| |||:
Db 918 FLLKXQVK 926

RESULT 7
US-09-066-281B-7
; Sequence 7, Application US/09066281B
; Patent No. 6475783
; GENERAL INFORMATION:
; APPLICANT: LUCAS, Sophie; DE SMET, Charles; BOON-FALLEUR, Thierry
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING
; TITLE OF INVENTION: FOR TUMOR REJECTION ANTIGEN PRECURSOR MAGE-C1 AND MAGE-C2
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Fulbright & Jaworski L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/066,281B
; FILING DATE: April 24, 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/845,528
; FILING DATE: April 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary Anne Schofield
; REGISTRATION NUMBER: 36,669
; REFERENCE/DOCKET NUMBER: LUD 5455.2 US - JEL/MAS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3100
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1142
; TYPE: amino acids
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
US-09-066-281B-7

Query Match 78.7%; Score 37; DB 2; Length 1142;
Best Local Similarity 77.8%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY      1 FLLFKYQMK 9
Db      918 FLLKYQVK 926

RESULT 8
US-09-899-651-2
; Sequence 2, Application US/09899651
; Patent No. 6576756
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseeng
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer
; TITLE OF INVENTION: Associated
; TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
; FILE REFERENCE: LUD 5538
; CURRENT APPLICATION NUMBER: US/09/899,651
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/061,709
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-899-651-2

Query Match      78.7%; Score 37; DB 2; Length 1142;
Best Local Similarity 77.8%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLLFKYQMK 9
Db      918 FLLKYQVK 926

RESULT 9
US-09-468-433C-7
; Sequence 7, Application US/09468433C
; Patent No. 6680191
; GENERAL INFORMATION:
; APPLICANT: LUCAS, Sophie; BOON-FALLEUR, Thierry
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING FOR
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS OF MEMBERS OF THE MAGE-C AN
; TITLE OF INVENTION: MAGE-B FAMILIES AND USES THEREOF
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Fulbright & Jaworecki L.L.P.
; STREET: 801 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/468,433C
; FILING DATE: December 17, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/066,281
; FILING DATE: April 24, 1998
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 08/845,528
; FILING DATE: April 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary Anne Schofield
; REGISTRATION NUMBER: 36,669
; REFERENCE/DOCKET NUMBER: LUD 5611 JEL/MAS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 662-0200
; TELEFAX: (202) 662-4643
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1142
; TYPE: amino acids
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; US-09-468-433C-7

Query Match      78.7%; Score 37; DB 2; Length 1142;
Best Local Similarity 77.8%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY      1 FLLFKYQMK 9
Db      918 FLLKYQVK 926
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RESULT 10
US-09-392-714-26
; Sequence 26, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tseeng
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-392-714-26
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Query Match      78.7%; Score 37; DB 2; Length 1142;
Best Local Similarity 77.8%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY      1 FLLFKYQMK 9
Db      918 FLLKYQVK 926
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RESULT 11
US-09-270-437D-2
; Sequence 2, Application US/09270437D
; Patent No. 6830924
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseeng
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antig
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;
; TITLE OF INVENTION: Antigens Per Se, And Uses Thereof
; FILE REFERENCE: LUD 5538.1
; CURRENT APPLICATION NUMBER: US/09/270,437D
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/061,709
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 2
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-270-437D-2

Query Match 78.7%; Score 37; DB 2; Length 1142;
Best Local Similarity 77.8%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
|||:|:
DB 918 FLLKYQVK 926

RESULT 12
US-09-468-433C-24
; Sequence 24, Application US/09468433C
; Patent No. 6680191
; GENERAL INFORMATION:
; APPLICANT: LUCAS, Sophie; BOON-FALLEUR, Thierry
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING FOR
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS OF MEMBERS OF THE MAGE-C AN
; TITLE OF INVENTION: MAGE-B FAMILIES AND USES THEREOF
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 801 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/468,433C
FILING DATE: December 17, 1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/066,281
FILING DATE: April 24, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/845,528
FILING DATE: April 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5611 JEL/MAS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 662-0200
TELEFAX: (202) 662-4643
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 275
TYPE: amino acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear

US-09-468-433C-24
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Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
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DB 50 FLLYKFKMK 58
RESULT 13
US-09-270-767-44621
; Sequence 44621, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44621
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-44621

Query Match 74.5%; Score 35; DB 2; Length 67;
Best Local Similarity 66.7%; Pred. No. 8.8;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
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DB 20 FLLFKYSLE 28

RESULT 14
US-09-468-433C-22
; Sequence 22, Application US/09468433C
; Patent No. 6680191
; GENERAL INFORMATION:
; APPLICANT: LUCAS, Sophie; BOON-FALLEUR, Thierry
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING FOR
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS OF MEMBERS OF THE MAGE-C AN
; TITLE OF INVENTION: MAGE-B FAMILIES AND USES THEREOF
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 801 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/468,433C
FILING DATE: December 17, 1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/066,281
FILING DATE: April 24, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/845,528
FILING DATE: April 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5611 JEL/MAS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 662-0200

TELEFAX: (202) 662-4643
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 346
 TYPE: amino acid
 STRANDEDNESS: single-stranded
 TOPOLOGY: linear
 US-09-468-433C-22

Query Match 74.5%; Score 35; DB 2; Length 346;
 Best Local Similarity 77.8%; Pred. NO. 45;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
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 Db 168 FLLFKYQTK 176

RESULT 15
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 ; Sequence 35366, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 35366
 ; LENGTH: 81
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-09-270-767-35366

Query Match 70.2%; Score 33; DB 2; Length 81;
 Best Local Similarity 66.7%; Pred. No. 26;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
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 Db 72 FLLFKYQMK 80

Search completed: March 17, 2006, 23:36:19
 Job time : 31.3333 secs

GenCore version 5.1.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Word size: 1
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=6 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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3: /cgn2_6/prodata/1/1aa/H COMB.pcp.*
4: /cgn2_6/prodata/1/1aa/ECTUS COMB.pcp.*
5: /cgn2_6/prodata/1/1aa/RE COMB.pcp.*
6: /cgn2_6/prodata/1/1aa/baCkfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	12	6.2	313	2	US-09-270-767-37193
3	12	6.2	313	2	US-09-270-767-52410
4	12	6.2	1024	2	US-09-949-016-7276
5	11	5.6	242	2	US-09-902-540-13477
6	11	5.6	249	2	US-09-248-796A-27128
7	10	5.1	20	2	US-09-736-457-1856
8	10	5.1	20	2	US-10-017-754-1856
9	10	5.1	34	2	US-08-857-636-73
10	10	5.1	59	2	US-09-513-999C-6477
11	10	5.1	120	2	US-10-101-464A-641

12	10	5.1	129	2	US-08-968-686-2	Sequence 2, Appl1
13	10	5.1	146	2	US-09-621-976-4320	Sequence 4920, Ap
14	10	5.1	154	2	US-09-248-796A-19284	Sequence 19284, A
15	10	5.1	161	4	PCT-US95-05741-11	Sequence 11, Appl
16	10	5.1	167	2	US-09-248-796A-27833	Sequence 27833, A
17	10	5.1	200	2	US-09-702-705-324	Sequence 324, App
18	10	5.1	200	2	US-09-736-457-324	Sequence 324, App
19	10	5.1	200	2	US-09-614-124B-324	Sequence 324, App
20	10	5.1	200	2	US-09-671-325-324	Sequence 324, App
21	10	5.1	200	2	US-09-589-184-324	Sequence 324, App
22	10	5.1	200	2	US-09-658-824-324	Sequence 324, App
23	10	5.1	200	2	US-10-017-754-324	Sequence 324, App
24	10	5.1	200	2	US-09-651-563-324	Sequence 324, App
25	10	5.1	200	2	US-09-519-642-324	Sequence 324, App
26	10	5.1	209	2	US-09-248-796A-26412	Sequence 26412, A
27	10	5.1	220	2	US-10-101-464A-628	Sequence 628, App
28	10	5.1	223	2	US-09-009-816-4	Sequence 4, Appl1
29	10	5.1	226	2	US-09-163-285-4	Sequence 4, Appl1
30	10	5.1	245	2	US-09-248-796A-19051	Sequence 19051, A
31	10	5.1	248	2	US-09-163-285-2	Sequence 2, Appl1
32	10	5.1	255	2	US-09-270-767-38028	Sequence 38028, A
33	10	5.1	255	2	US-09-270-767-53245	Sequence 53245, A
34	10	5.1	255	2	US-09-949-016-6882	Sequence 6882, Ap
35	10	5.1	258	2	US-09-508-849-1	Sequence 1, Appl1
36	10	5.1	258	2	US-10-104-047-3034	Sequence 3034, Ap
37	10	5.1	265	2	US-08-968-686-10	Sequence 10, Appl
38	10	5.1	268	2	US-08-968-686-6	Sequence 6, Appl1
39	10	5.1	277	2	US-09-508-849-2	Sequence 2, Appl1
40	10	5.1	281	1	US-08-810-453-2	Sequence 2, Appl1
41	10	5.1	281	2	US-08-815-190A-2	Sequence 2, Appl1
42	10	5.1	281	2	US-09-290-640-25	Sequence 25, Appl
43	10	5.1	281	2	US-09-479-524-3	Sequence 3, Appl1
44	10	5.1	281	2	US-08-339-214-8	Sequence 8, Appl1
45	10	5.1	281	2	US-08-339-214-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-08-773-870-4
; Sequence 4, Application US/08773870
; Patent No. 5912143
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN WAGE-LIKE PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/773,870
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCES/DOCKET NUMBER: PF-0179 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166

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; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 533511
;
US-08-773-870-4
Alignment Scores:
Pred. No.: 9,896-174 Length: 369
Score: 195.00 Matches: 195
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0
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QY 61 GAGACACAGGGCTCGAGGGTCACAGAGTCCCTCGCTGTCGAGGAGGATGTTTCATCA 120
DB 21 GluThrGlnGlyLeuGluGlyAlaGlnAlaProLeuAlaValGluGluAspAlaSerSer 40
QY 121 TCACATCCACAGCTCCTCTTTTCCATCTCTTTCCCTCCCTCCCTCTCTCTCTCTCC 180
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QY 181 TCCTCTGCTATCTCTAATACCAAGCACCCAGAGAGGTTTCTGCTGATGATGAGACA 240
DB 61 SerSerCysTyProLeuIleProSerThrProGluGluValSerAlaAspAspGluThr 80
QY 241 CCAATCTCTCCAGAGTGTCTAGATAGCTGTCTCTCCCTCCGCTCGTGTGCTTCCCTT 300
DB 81 ProAsnProProGlnSerAlaGlnIleAlaCysSerSerProSerValValAlaSerLeu 100
QY 301 CCATTAGATCAATCTCATGAGGGCTCCAGCAGCAAAAGGAGAGAGTCCCAAGCACCTA 360
DB 101 ProLeuAspGlnSerAspGluGlySerSerSerGlnGlySerProSerThrLeu 120
QY 361 CAGGTCTGCACACAGTGAAGTCTTTACCCAGAGTGCAGATAGATGAAAGGTGACTGAT 420
DB 121 GlnValLeuProAspSerGluSerLeuProArgSerGluIleAspGluIleValThrAsp 140
QY 421 TTGGTGCAGTTTCTGCTTCAAGTATCAATGAAGAGCGGATCACAAGGCAGAAATA 480
DB 141 LeuValGlnPheLeuLeuPheLysTyGlnMetLysGluProIleThrLysAlaGluIle 160
QY 481 CTGAGAGTGTCAATAAATATGAGACCACTTCCCTTTGTTGTTTGTAGTGAAGCTCC 540
DB 161 LeuGluSerValIleLysAsnTyGlnAspHisPheProLeuLeuPheSerGluAlaSer 180
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DB 181 GluCysMetLeuLeuValPheGlyIleAspValLysGluValAsp 195
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RESULT 2
US-09-270-767-37193
; Sequence 37193, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
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QY 151 TCTTTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 186
DB 31 SerPheProSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 42
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RESULT 3
US-09-270-767-52410
; Sequence 52410, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52410
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-52410
Alignment Scores:
Pred. No.: 0,00832 Length: 313
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 6.2% Indels: 0
DB: 2 Gaps: 0
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QY 151 TCTTTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 186
DB 31 SerPheProSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 42
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RESULT 4
US-09-949-016-7276
; Sequence 7276, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
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US-09-856-812B-7_COPY_334_918 (1-585) x US-09-736-457-1856 (1-20)

QY 188 CAGGAGGAGGAGGAGGAGGAGGAGGAG 159
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Db 11 GInGluGluGluGluGluGluGlu 20

RESULT 8
US-10-017-754-1856
; Sequence 1856, Application US/10017754
; Patent No. 6858204
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.

APPLICANT: Retter, Marc W.
APPLICANT: Marnerakis, Margarita
APPLICANT: Carter, Garrick
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.478C18
CURRENT APPLICATION NUMBER: US/10/017,754
CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SOFTWARE: PastSeq for Windows Version 4.0
SEQ ID NO 1856
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-017-754-1856

Alignment Scores:
Pred. No.: 0.777 Length: 20
Score: 10.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 5.1% Indels: 0
DB: 2 Gaps: 0

US-09-856-812B-7_COPY_334_918 (1-585) x US-10-017-754-1856 (1-20)

QY 188 CAGGAGGAGGAGGAGGAGGAGGAG 159
DB 11 GlnGluGluGluGluGluGluGluGlu 20

RESULT 9
US-08-857-636-73
Sequence 73, Application US/08857636
Patent No. 6552181
GENERAL INFORMATION:
APPLICANT: Dean, Michael Carlton
APPLICANT: Hahn, Heidi Eve
APPLICANT: Wickling, Carol
APPLICANT: Christiansen, Jeffrey
APPLICANT: Zaphiropoulos, Peter G.
APPLICANT: Gallani, Mae R.
APPLICANT: Shanley, Susan Mary
APPLICANT: Chidambaram, Abirami
APPLICANT: Vorechovsky, Igor
APPLICANT: Holmberg-Lindstrom, Erika
APPLICANT: Udden, Anne Birgitte
APPLICANT: Gillies, Susan Alana
APPLICANT: Negus, Kylie
APPLICANT: Smyth, Ian Mcleod
APPLICANT: Pressman, Carol Leah
APPLICANT: Leffell, David J.
APPLICANT: Gerrard, Bernard
APPLICANT: Goldstein, Alisa Miriam
APPLICANT: Wainwright, Brandon
APPLICANT: Toftgard, Rune Carl-Magnus
APPLICANT: Chenevix-Trench, Georgia
APPLICANT: Bale, Allen E.
TITLE OF INVENTION: A Basal Cell Carcinoma Tumor Suppressor Gene
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
STREET: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/857,636
FILING DATE: 16-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,906
FILING DATE: 17-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P00011
FILING DATE: 21-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P00363
FILING DATE: 07-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,765
FILING DATE: 14-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-278200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-857-636-73

Alignment Scores:
Pred. No.: 0.742 Length: 34
Score: 10.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 5.1% Indels: 0
DB: 2 Gaps: 0

US-09-856-812B-7_COPY_334_918 (1-585) x US-08-857-636-73 (1-34)

QY 187 AGGAGGAGGAGGAGGAGGAGGAGG 158
DB 6 ArgArgArgArgArgArgArgArg 15

RESULT 10
US-09-513-999C-6477
Sequence 6477, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 6477
LENGTH: 59
TYPE: PRT
ORGANISM: Homo sapiens
US-09-513-999C-6477

Alignment Scores:
Pred. No.: 0.708 Length: 59

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,686
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Pochopien, Donald J.
; REGISTRATION NUMBER: 32,167
; REFERENCE/DOCKET NUMBER: 1361.003/11964US03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-654-5360
; TELEFAX: 510-655-3542
; TELEX: 1
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-968-686-2

Alignment Scores:
Pred. No.: 0.662 Length: 129
Score: 10.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 5.1% Indels: 0
DB: 2 Gaps: 0

US-09-856-812B-7_COPY_334_918 (1-585) x US-08-968-686-2 (1-129)

Qy 158 CCTCTCTCTCTCTCTCTCTCTCTCTCTCT 187
Db 50 ProProProLeuProProProProPro 59

RESULT 13
US-09-621-976-4920
; Sequence 4920, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4920
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 3
; OTHER INFORMATION: Xaa = Ala, Asp, Glu, Gly, Val
; US-09-621-976-4920

Alignment Scores:
Pred. No.: 0.655 Length: 146
Score: 10.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 5.1% Indels: 0
DB: 2 Gaps: 0

US-09-856-812B-7_COPY_334_918 (1-585) x US-09-621-976-4920 (1-146)

Qy 185 GAGGAGGAGGAGGAGGAGGAGGAGGAGGA 156
Db 156 GAGGAGGAGGAGGAGGAGGAGGAGGAGGA 156

```

Db 85 GluGluGluGluGluGluGluGluGluGlu 94

RESULT 14

US-09-248-796A-19284

; Sequence 19284, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 19284

; LENGTH: 154

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-19284

Alignment Scores:

Pred. No.:	0.652	Length:	154
Score:	10.00	Matches:	10
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.1%	Indels:	0
DB:	2	Gaps:	0

US-09-856-812B-7_COPY_334_918 (1-585) x US-09-248-796A-19284 (1-154)

QY 188 CAGGAGGAGGAGGAGGAGGAGGAGGAG 159

Db 23 GluGluGluGluGluGluGluGluGluGlu 32

RESULT 15

PCT-US95-05741-11

; Sequence 11, Application PC/TUS9505741

; GENERAL INFORMATION:

; APPLICANT: Weintraub, Harold

; APPLICANT: Lee, Jacqueline E.

; APPLICANT: Tapscott, Stephen J.

; APPLICANT: Hollenberg, Stanley M.

; TITLE OF INVENTION: Neurogenic Differentiation (NeuroD) Gene

; TITLE OF INVENTION: and Protein

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Christensen O'Connor Johnson Kindness

; STREET: 1420 Fifth Avenue, Suite 2800

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101-2347

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/05741

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Broderick, Thomas F.

; REGISTRATION NUMBER: 31,332

; REFERENCE/DOCKET NUMBER: FHCR-1-8504

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-682-8100

; TELEFAX: 206-225-0709

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 161 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US95-05741-11

Alignment Scores:

Pred. No.:	0.65	Length:	161
Score:	10.00	Matches:	10
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	5.1%	Indels:	0
DB:	4	Gaps:	0

US-09-856-812B-7_COPY_334_918 (1-585) x PCT-US95-05741-11 (1-161)

QY 185 GAGGAGGAGGAGGAGGAGGAGGAGGGA 156

Db 38 GluGluGluGluGluGluGluGluGluGly 47

Search completed: March 18, 2006, 00:07:43

Job time : 37 secs

GenCore version 5.1.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 17, 2006, 23:59:14 ; Search time 7.1 Seconds
(without alignments)
1585.544 Million cell updates/sec

Title: US-09-856-812B-7_COPY_334_918
Perfect score: 195
Sequence: 1 atgcctcgagctccaaagc.....ttgatgtaaaaggaagtggat 585

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Word size: 1

Total number of hits satisfying chosen parameters: 565918

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
-MODEL=frame+n2p.model -DEV=xlp
-O=/abs/ABSSWEB spool/US09856812/runat.17032006.150558.5495/app_query.fasta_1
-DB=PIR-QPMT-fastan SUPFIX=n2p_olig.tpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pro
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs802p
-USER=US09856812 @CN 1.1.63 @runat.17032006.150558.5495 -NCPU=6 -ICPU=3
-NO WMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DSLOP=6 -DELEXT=7

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	195	100.0	369	I38659	melanoma antigen M
2	12	6.2	759	S25330	SC11 protein - yea
3	12	6.2	1006	JC5526	kinase-defective E
4	11	5.6	491	T52398	hypothetical prote
5	11	5.6	639	T46577	arylsulfatase (EC
6	11	5.6	819	S40400	protein kinase SWE
7	11	5.6	845	D96799	hypothetical prote
8	10	5.1	103	T47718	hypothetical prote
9	10	5.1	132	T49536	hypothetical prote
10	10	5.1	136	T29282	hypothetical prote
11	10	5.1	150	C86224	hypothetical prote
12	10	5.1	154	S55017	hypothetical prote
13	10	5.1	155	C86206	hypothetical prote
14	10	5.1	162	C85356	glycine-rich prote

C 15	10	5.1	166	2	T10463	glycine-rich prote
C 16	10	5.1	169	1	S38331	glycine-rich RNA-b
C 17	10	5.1	181	2	T46017	hypothetical prote
C 18	10	5.1	196	2	T29343	hypothetical prote
C 19	10	5.1	211	2	D96507	hypothetical prote
C 20	10	5.1	214	1	KNNT28	glycine-rich prote
C 21	10	5.1	227	1	S68150	eosinophil major b
C 22	10	5.1	230	2	D86352	protein T26F17.14
C 23	10	5.1	239	2	S49193	GCR 101 protein -
C 24	10	5.1	244	2	T51481	hypothetical prote
C 25	10	5.1	255	1	WJHU48	homeotic protein H
C 26	10	5.1	259	2	I50727	sensory organ home
C 27	10	5.1	271	2	S34666	glycine-rich prote
C 28	10	5.1	279	2	T01924	hypothetical prote
C 29	10	5.1	281	2	I38707	Fas ligand - human
C 30	10	5.1	291	2	T08189	hypothetical prote
C 31	10	5.1	299	2	T02515	cytoskeletal prote
C 32	10	5.1	302	2	C84470	hypothetical prote
C 33	10	5.1	314	2	T16300	hypothetical prote
C 34	10	5.1	317	2	T39869	probable lysosomop
C 35	10	5.1	321	2	A38712	fibrillarin [valid
C 36	10	5.1	329	2	S07577	legumin storage pr
C 37	10	5.1	335	2	S07576	legumin storage pr
C 38	10	5.1	344	2	T40167	hypothetical prote
C 39	10	5.1	351	2	F96597	hypothetical prote
C 40	10	5.1	354	2	T49806	hypothetical prote
C 41	10	5.1	359	2	T13478	hypothetical prote
C 42	10	5.1	360	2	T45649	hypothetical prote
C 43	10	5.1	364	2	I48188	gene NKx6.1 protei
C 44	10	5.1	372	2	E85170	hypothetical prote
C 45	10	5.1	373	2	S40777	heterogeneous ribo

ALIGNMENTS

RESULT 1
I38659
melanoma antigen MAGE-10 - human
C:Species: Homo sapiens (man)
C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C:Accession: I38659
R:De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; B
oon, T.
Immunogenetics 40, 360-369, 1994
A:Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fa.
A:Reference number: I38659; MUID:95012457; PMID:7927540
A:Accession: I38659
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: UNIPROT:P43363; UNIPARC:UPI00000000C57; EMBL:U10685; NID:9533510; PI
C:Genetics:
A:Gene: GDB:MAGEA10; MAGE10
A:Cross-references: GDB:331126
A:Map position: Xq28-Xq28
A:Introns: #status absent
C:Superfamily: tumor associated protein MAGE

Alignment Scores:				
Pred. No.:	5.96e-169	Length:	369	
Score:	195.00	Matches:	195	
Percent Similarity:	100.0%	Conservative:	0	
Best Local Similarity:	100.0%	Mismatches:	0	
Query Match:	100.0%	Indels:	0	
DB:	2	Gaps:	0	

US-09-856-812B-7_COPY_334_918 (1-585) x I38659 (1-369)

QY	1	ATGCGCTCCAGCTCCAAAGCGTCAGCGCTGCATGCTGGAAGAGATCTTCAATCCCAAGT	60
Db	1	MetProArgAlaProlyArgGlnArgCysMetProGluGluAspLeuGlnSerGlnSer	20
QY	61	GAGACACAGGGCGCTCAGGGTGCACAGGGTCCCTGGCTGTGTGGAGGAGGATGCTTCATCA	120

A;Cross-references: UNIPROT:O80490; UNIPARC:UPI00000AA4AB; GB:AE005172; NID:g3249112; PI
C;Genetics:
A;Map position: 1

Alignment Scores:
Pred. No.: 1-25 Length: 150
Score: 10.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 5.1% Indels: 0
DB: 2 Gaps: 0

US-09-856-812B-7_COPY_334_918 (1-585) x C86224 (1-150)

QY 186 GGAGGAGGAGGAGGAGGAGGAGGAGG 157
Db 69 GlyGlyGlyGlyGlyGlyGlyGlyGlyGly 78

RESULT 12
S55017
hypothetical protein 2 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 16-Feb-1997
C;Accession: S55017
R;Bergstrom, D.E.; Meril, C.A.; Cygan, J.A.; Shelby, R.; Blackman, R.K.
Genetics 139, 1331-1346, 1995
A;Title: Regulatory autonomy and molecular characterization of the Drosophila out at fix
A;Reference number: S55016; MUID:95286060; PMID:7768442
A;Accession: S55017
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-154 <BER>
A;Cross-references: UNIPARC:UPI000017BEA2; EMBL:L31349
C;Genetics:
A;Gene: FlyBase:oaf
A;Cross-references: FlyBase:FBgn0011818

Alignment Scores:
Pred. No.: 1-24 Length: 154
Score: 10.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 5.1% Indels: 0
DB: 2 Gaps: 0

US-09-856-812B-7_COPY_334_918 (1-585) x S55017 (1-154)

QY 157 CCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 186
Db 138 ProSerSerSerSerSerSerSerSerSer 147

RESULT 13
C86206
hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C86206
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C86206
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-155 <STO>
A;Cross-references: UNIPROT:Q9LMK6; UNIPARC:UPI00000A913C; GB:AE005172; NID:g8954033; PI

C;Genetics:
A;Map position: 1

Alignment Scores:
Pred. No.: 1-24 Length: 155
Score: 10.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 5.1% Indels: 0
DB: 2 Gaps: 0

US-09-856-812B-7_COPY_334_918 (1-585) x C86206 (1-155)

QY 186 GGAGGAGGAGGAGGAGGAGGAGGAGGAGG 157
Db 68 GlyGlyGlyGlyGlyGlyGlyGlyGlyGly 77

RESULT 14
C85356
glycine-rich protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: C85356
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spr
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: C85356
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-162 <STO>
A;Cross-references: UNIPROT:Q9M0B4; UNIPARC:UPI00000AC155; GB:NC_001268; NID:g7269947;
C;Genetics:
A;Gene: AT4g30460
A;Map position: 4
A;Superfamily: glycine-rich cell wall structural protein 1

Alignment Scores:
Pred. No.: 1-23 Length: 162
Score: 10.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 5.1% Indels: 0
DB: 2 Gaps: 0

US-09-856-812B-7_COPY_334_918 (1-585) x C85356 (1-162)

QY 186 GGAGGAGGAGGAGGAGGAGGAGGAGGAGG 157
Db 130 GlyGlyGlyGlyGlyGlyGlyGlyGlyGly 139

RESULT 15
T10463
glycine-rich protein 1a - white mustard
C;Species: Sinapis alba (white mustard)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10463
R;Heintzen, C.; Melzer, S.; Fischer, R.; Kappeler, S.; Apel, K.; Staiger, D.
Plant J. 5, 799-813, 1994
A;Title: A light- and temperature-entrained circadian clock controls expression of tran
A;Reference number: Z17029; MUID:94332156; PMID:8054987
A;Accession: T10463
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-166 <HEI>
A;Cross-references: UNIPROT:P49310; UNIPARC:UPI000012BAPF; EMBL:L31374; NID:g496232; PI
C;Superfamily: glycine-rich RNA-binding protein; ribonucleoprotein repeat homology
F;3-76/Domain: ribonucleoprotein repeat homology <RRM>

Alignment Scores:
Pred. No.: 1-22 Length: 166
Score: 10.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0
Query Match: 5.1% Indels: 0
DB: 2 Gaps: 0

US-09-856-812B-7_COPY_334_918 (1-585) x T10463 (1-166)

Qy 186 GGAGGAGGAGGAGGAGGAGGAGGAGGAGG 157

Db 91 GlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100

Search completed: March 18, 2006, 00:06:30
Job time : 40.5 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 17, 2006, 22:41:39 ; Search time 163 Seconds
(without alignments)
945.884 Million cell updates/sec

Title: US-09-856-812B-1
Perfect score: 369
Sequence: 1 MPRAPKRCMPEDLQSQS.....DTTMASSSSATGFSFSYPE 369

Scoring table: <OLIGO>

Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database : Published Applications AA.Main:*
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5: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/prodata1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	369	100.0	369	4	US-10-036-542-84
2	369	100.0	369	4	US-10-188-832-149
3	369	100.0	369	5	US-10-558-884-4
4	369	100.0	369	5	US-10-756-149-4721
5	362	98.1	383	4	US-10-029-386-32058
6	29	7.9	82	4	US-10-029-386-32967
7	29	7.9	151	4	US-10-029-386-33360
8	29	7.9	315	4	US-10-093-766-40
9	29	7.9	315	4	US-10-157-031-54
10	29	7.9	315	4	US-10-295-027-366
11	29	7.9	315	5	US-10-473-127-1079
12	29	7.9	315	5	US-10-473-127-1082
13	29	7.9	315	5	US-10-473-127-1087
14	29	7.9	315	5	US-10-473-127-1091
15	29	7.9	315	5	US-10-473-127-1120
16	29	7.9	315	5	US-10-473-127-1122
17	29	7.9	315	5	US-10-482-029-168
18	29	7.9	315	5	US-10-756-149-4729
19	28	7.6	28	4	US-10-261-208-4
20	26	7.0	317	4	US-10-157-031-52
21	26	7.0	317	4	US-10-218-095-2
22	26	7.0	317	5	US-10-482-029-148
23	26	7.0	317	5	US-10-756-149-4740
24	17	4.6	30	4	US-10-296-734-1314
25	17	4.6	105	4	US-10-029-386-31281
26	17	4.6	155	4	US-10-029-386-32994
27	17	4.6	221	3	US-09-784-199-4

28	17	4.6	221	5	US-10-473-127-1098	Sequence 1098, Ap
29	17	4.6	292	3	US-09-864-761-38124	Sequence 38124, A
30	17	4.6	299	4	US-10-146-473-75	Sequence 75, Appl
31	17	4.6	314	3	US-09-766-889A-55	Sequence 55, Appl
32	17	4.6	314	3	US-09-784-199-2	Sequence 2, Appl
33	17	4.6	314	3	US-09-860-840-2	Sequence 2, Appl
34	17	4.6	314	3	US-09-849-602-29	Sequence 29, Appl
35	17	4.6	314	4	US-10-146-473-53	Sequence 53, Appl
36	17	4.6	314	4	US-10-177-390-20	Sequence 20, Appl
37	17	4.6	314	4	US-10-170-832-2	Sequence 2, Appl
38	17	4.6	314	4	US-10-117-937-72	Sequence 72, Appl
39	17	4.6	314	4	US-10-117-937-73	Sequence 73, Appl
40	17	4.6	314	4	US-10-149-135-2439	Sequence 2439, Ap
41	17	4.6	314	4	US-10-149-135-2440	Sequence 2440, Ap
42	17	4.6	314	4	US-10-296-734-829	Sequence 829, App
43	17	4.6	314	4	US-10-444-683-2	Sequence 2, Appl
44	17	4.6	314	4	US-10-444-683-44	Sequence 44, Appl
45	17	4.6	314	4	US-10-657-022-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1

US-10-036-542-84
; Sequence 84, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: PA002P1
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/1144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-036-542-84

Query Match		100.0%	Score 369;	DB 4;	Length 369;
Best Local Similarity		100.0%	Pred. No. 0;		
Matches 369;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MPRAPKRCMPEDLQSQSQTQGLEGAQAPLAVEDASSSTSTSSFPSSSSSSSS	60		
DB	1	MPRAPKRCMPEDLQSQSQTQGLEGAQAPLAVEDASSSTSTSSFPSSSSSSSS	60		
QY	61	SSCYPLIPSTPREVSADDETPNPQSAQIACSSPSVVASLPLDQSDGSSSQKEESPSTL	120		
DB	61	SSCYPLIPSTPREVSADDETPNPQSAQIACSSPSVVASLPLDQSDGSSSQKEESPSTL	120		
QY	121	QVLPDSESLPREIDEKVTDLVQFLFKYQMKEPITKAEILSESVKNYEDHPLELSEAS	180		
DB	121	QVLPDSESLPREIDEKVTDLVQFLFKYQMKEPITKAEILSESVKNYEDHPLELSEAS	180		
QY	181	ECWLLVFGIDVKEVDPTGHSFVLVTSGLTYDQMLSDVQSMPTGLILILSIFIEGYC	240		
DB	181	ECWLLVFGIDVKEVDPTGHSFVLVTSGLTYDQMLSDVQSMPTGLILILSIFIEGYC	240		

QY 241 TPEEVIWEALNMGLYDGMHLYGPRKLLTQDWQENYLVYQVPGSDPARYEFLWGP 300
DB 241 TPEEVIWEALNMGLYDGMHLYGPRKLLTQDWQENYLVYQVPGSDPARYEFLWGP 300
QY 301 RAHAERIKMSLLKFLAKVNGSDPRSFPPLWYEEALKDDEERAQDRIATTTDDTTAMASASS 360
DB 301 RAHAERIKMSLLKFLAKVNGSDPRSFPPLWYEEALKDDEERAQDRIATTTDDTTAMASASS 360
QY 361 ATGSFSYPE 369
DB 361 ATGSFSYPE 369
RESULT 2
US-10-188-832-149
; Sequence 149, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Bos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 149
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-149

Query Match 100.0%; Score 369; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPKRCMPEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSFPSSPSSSSSS 60
DB 1 MPRAPKRCMPEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSFPSSPSSSSSS 60
QY 61 SSCYPLIPSTPEVVSADDETPNPQSAQIACSSPSVVASLPDQSDGSSSQKEESPSTL 120
DB 61 SSCYPLIPSTPEVVSADDETPNPQSAQIACSSPSVVASLPDQSDGSSSQKEESPSTL 120
QY 121 QVLPDSESLPRSEIDKVTDLVQFLFKYQMKPEPITKAEILESVIKNYEDHFPFLFSEAS 180
DB 121 QVLPDSESLPRSEIDKVTDLVQFLFKYQMKPEPITKAEILESVIKNYEDHFPFLFSEAS 180
QY 181 ECLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMQLSDVQSMPTGILLILILSIFIEGYC 240
DB 181 ECLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMQLSDVQSMPTGILLILILSIFIEGYC 240
QY 241 TPEEVIWEALNMGLYDGMHLYGPRKLLTQDWQENYLVYQVPGSDPARYEFLWGP 300
DB 241 TPEEVIWEALNMGLYDGMHLYGPRKLLTQDWQENYLVYQVPGSDPARYEFLWGP 300
QY 301 RAHAERIKMSLLKFLAKVNGSDPRSFPPLWYEEALKDDEERAQDRIATTTDDTTAMASASS 360
DB 301 RAHAERIKMSLLKFLAKVNGSDPRSFPPLWYEEALKDDEERAQDRIATTTDDTTAMASASS 360

QY 361 ATGSFSYPE 369
DB 361 ATGSFSYPE 369
RESULT 3
US-10-658-884-4
; Sequence 4, Application US/10658884
; Publication No. US20050019304A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MAGE-LIKE PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/10/658,884
; APPLICATION NUMBER: US/10/658,884
; FILING DATE: 09-Sep-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/773,870
; FILING DATE: 27-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0179 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 369 amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 533511
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-658-884-4

Query Match 100.0%; Score 369; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPKRCMPEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSFPSSPSSSSSS 60
DB 1 MPRAPKRCMPEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSFPSSPSSSSSS 60
QY 61 SSCYPLIPSTPEVVSADDETPNPQSAQIACSSPSVVASLPDQSDGSSSQKEESPSTL 120
DB 61 SSCYPLIPSTPEVVSADDETPNPQSAQIACSSPSVVASLPDQSDGSSSQKEESPSTL 120
QY 121 QVLPDSESLPRSEIDKVTDLVQFLFKYQMKPEPITKAEILESVIKNYEDHFPFLFSEAS 180
DB 121 QVLPDSESLPRSEIDKVTDLVQFLFKYQMKPEPITKAEILESVIKNYEDHFPFLFSEAS 180
QY 181 ECLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMQLSDVQSMPTGILLILILSIFIEGYC 240
DB 181 ECLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMQLSDVQSMPTGILLILILSIFIEGYC 240

QY 241 TPEEVIWEALNMGLYDGMHEHLYGEPKLLTQDWQENYLEYRQVPGSDPARYEFLWGP 300
Db 241 TPEEVIWEALNMGLYDGMHEHLYGEPKLLTQDWQENYLEYRQVPGSDPARYEFLWGP 300
QY 301 RAHAERKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEBRAQDRIATDDTTAMASASS 360
Db 301 RAHAERKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEBRAQDRIATDDTTAMASASS 360
QY 361 ATGFSFSYPE 369
Db 361 ATGFSFSYPE 369

RESULT 4

US-10-756-149-4721
; Sequence 4721, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; FILE REFERENCE: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 4721
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-4721

Query Match 100.0%; Score 369; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPKRCMPPEEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSPPSPSSSSSS 60
Db 1 MPRAPKRCMPPEEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSPPSPSSSSSS 60
QY 61 SSCYPLIPSTPEVSADDETPNPQSAQIACSPSVVASLPDQSDGSSSQKEESPSTL 120
Db 61 SSCYPLIPSTPEVSADDETPNPQSAQIACSPSVVASLPDQSDGSSSQKEESPSTL 120
QY 121 QVLPSESLPRSEIDEKVTDLVQFLFKYQKEPITKAEILSVKNYEDHPPLFSEAS 180
Db 121 QVLPSESLPRSEIDEKVTDLVQFLFKYQKEPITKAEILSVKNYEDHPPLFSEAS 180
QY 181 ECVLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMVQSMPTGILILSIIFIEGYC 240
Db 181 ECVLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMVQSMPTGILILSIIFIEGYC 240
QY 241 TPEEVIWEALNMGLYDGMHEHLYGEPKLLTQDWQENYLEYRQVPGSDPARYEFLWGP 300
Db 241 TPEEVIWEALNMGLYDGMHEHLYGEPKLLTQDWQENYLEYRQVPGSDPARYEFLWGP 300
QY 301 RAHAERKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEBRAQDRIATDDTTAMASASS 360
Db 301 RAHAERKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEBRAQDRIATDDTTAMASASS 360
QY 361 ATGFSFSYPE 369
Db 361 ATGFSFSYPE 369

RESULT 5

US-10-029-386-32058
; Sequence 32058, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEWICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32058
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AF134576.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
; OTHER INFORMATION: SWISSPROT HIT: P43363, EVALUATION 0.00e+00
US-10-029-386-32058

Query Match 98.1%; Score 362; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPKRCMPPEEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSPPSPSSSSSS 60
Db 22 MPRAPKRCMPPEEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSPPSPSSSSSS 81
QY 61 SSCYPLIPSTPEVSADDETPNPQSAQIACSPSVVASLPDQSDGSSSQKEESPSTL 120
Db 82 SSCYPLIPSTPEVSADDETPNPQSAQIACSPSVVASLPDQSDGSSSQKEESPSTL 141
QY 121 QVLPSESLPRSEIDEKVTDLVQFLFKYQKEPITKAEILSVKNYEDHPPLFSEAS 180
Db 142 QVLPSESLPRSEIDEKVTDLVQFLFKYQKEPITKAEILSVKNYEDHPPLFSEAS 201
QY 181 ECVLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMVQSMPTGILILSIIFIEGYC 240
Db 202 ECVLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMVQSMPTGILILSIIFIEGYC 261
QY 241 TPEEVIWEALNMGLYDGMHEHLYGEPKLLTQDWQENYLEYRQVPGSDPARYEFLWGP 300
Db 262 TPEEVIWEALNMGLYDGMHEHLYGEPKLLTQDWQENYLEYRQVPGSDPARYEFLWGP 321
QY 301 RAHAERKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEBRAQDRIATDDTTAMASASS 360
Db 322 RAHAERKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEBRAQDRIATDDTTAMASASS 381
QY 361 AT 362
Db 382 AT 383

RESULT 6

US-10-029-386-32967
; Sequence 32967, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEWICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32967

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; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO U69568.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.94
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.34
; OTHER INFORMATION: SWISSPROT HIT: P43362, EVALUATION 5.00e-45
US-10-029-386-32967

Query Match
Best Local Similarity 100.0%; Pred. No. 4.8e-18; Length 82;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPKLLTQDWQENYLEYRQVPGSDPA 292
Db 5 YGEPKLLTQDWQENYLEYRQVPGSDPA 33

RESULT 7
US-10-029-386-33360
; Sequence 33360, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33360
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO U66083.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.8
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.33
; OTHER INFORMATION: SWISSPROT HIT: P43362, EVALUATION 7.00e-79
; NAME/KEY: unsure
; LOCATION: 2
US-10-029-386-33360

Query Match
Best Local Similarity 100.0%; Pred. No. 8.3e-18; Length 151;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPKLLTQDWQENYLEYRQVPGSDPA 292
Db 74 YGEPKLLTQDWQENYLEYRQVPGSDPA 102

RESULT 8
US-10-093-766-40
; Sequence 40, Application US/10093766
; Publication No. US20030013099A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; APPLICANT: Karpf, Adam R.
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
; FILE REFERENCE: FA-0047 US
; CURRENT APPLICATION NUMBER: US/10/093,766
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PERL Program
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; SEQ ID NO 40
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030013099A1 2502336CD1
US-10-093-766-40

Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-17; Length 315;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPKLLTQDWQENYLEYRQVPGSDPA 292
Db 238 YGEPKLLTQDWQENYLEYRQVPGSDPA 266

RESULT 9
US-10-157-031-54
; Sequence 54, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Kravskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-54

Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-17; Length 315;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPKLLTQDWQENYLEYRQVPGSDPA 292
Db 238 YGEPKLLTQDWQENYLEYRQVPGSDPA 266

RESULT 10
US-10-295-027-366
; Sequence 366, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
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; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 366
; TYPE: PRT
; LENGTH: 315
; ORGANISM: Homo sapiens
; US-10-295-027-366

Query Match          7.9%; Score 29; DB 4; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPKLLTQDWQENYLEYRQVPGSDPA 292
    |||||
Db 238 YGEPKLLTQDWQENYLEYRQVPGSDPA 266

RESULT 11
US-10-473-127-1079
; Sequence 1079, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1079
; TYPE: PRT
; LENGTH: 315
; ORGANISM: Homo sapiens
; US-10-473-127-1079

Query Match          7.9%; Score 29; DB 5; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPKLLTQDWQENYLEYRQVPGSDPA 292
    |||||
Db 238 YGEPKLLTQDWQENYLEYRQVPGSDPA 266

RESULT 12
US-10-473-127-1082
; Sequence 1082, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1082
; TYPE: PRT
; LENGTH: 315
; ORGANISM: Homo sapiens
; US-10-473-127-1082

Query Match          7.9%; Score 29; DB 5; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPKLLTQDWQENYLEYRQVPGSDPA 292
    |||||
Db 238 YGEPKLLTQDWQENYLEYRQVPGSDPA 266

RESULT 13
US-10-473-127-1087
; Sequence 1087, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1087
; TYPE: PRT
; LENGTH: 315
; ORGANISM: Homo sapiens
; US-10-473-127-1087
```

Query Match 7.9%; Score 29; DB 5; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPKLLTQDWQENYLEYRQVPGSDPA 292
Db 238 YGEPKLLTQDWQENYLEYRQVPGSDPA 266

RESULT 14

US-10-473-127-1091
; Sequence 1091, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: ZYCOS Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1091
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1091

Query Match 7.9%; Score 29; DB 5; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPKLLTQDWQENYLEYRQVPGSDPA 292
Db 238 YGEPKLLTQDWQENYLEYRQVPGSDPA 266

RESULT 15

US-10-473-127-1120
; Sequence 1120, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: ZYCOS Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1120

; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1120

Query Match 7.9%; Score 29; DB 5; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPKLLTQDWQENYLEYRQVPGSDPA 292
Db 238 YGEPKLLTQDWQENYLEYRQVPGSDPA 266

Search completed: March 17, 2006, 22:45:08
Job time : 165 secs

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OM protein - protein search, using sw model

Run on: March 17, 2006, 22:21:28 ; Search time 182 Seconds
(without alignments)
21.728 Million cell updates/sec

Title: US-09-856-812B-42

Perfect score: 51

Sequence: 1 GLYDGMNHL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 401289

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	9	3	Aay71487 Human MAG
2	51	100.0	9	4	AAB31323 Exemplary
3	51	100.0	9	5	Aaol17088 Human mag
4	51	100.0	9	6	Ab119876 MHC bindi
5	51	100.0	9	8	Adg89586 Class I H
6	51	100.0	9	8	Adi119869 Human HLA
7	51	100.0	9	8	Adi19026 Human HLA
8	51	100.0	9	8	Adj58374 Peptide p
9	51	100.0	9	8	Adl26560 Melanoma
10	51	100.0	9	8	Adr69760 Novel hyb
11	51	100.0	9	9	Adx08536 Class I H
12	51	100.0	9	9	Aeb01337 Melanoma
13	41	80.4	9	3	Aay71488 Human MAG
14	34	66.7	6	5	ABG79151 Human MAG
15	32	62.7	9	2	AAY46134 Immunogen
16	31	60.8	9	2	AAY46090 Immunogen
17	28	54.9	9	2	AAY46489 Immunogen
18	28	54.9	9	2	AAY46037 Immunogen
19	28	54.9	9	2	AAY46435 Immunogen
20	28	54.9	9	4	AAG88669 HER2/NEU
21	28	54.9	9	4	AAG88319 HER2/NEU
22	28	54.9	9	6	ABJ19990 MHC bindi
23	28	54.9	9	8	ADP25980 Plasmodiu
24	28	54.9	9	9	ADW95463 Amino acid

25	27	52.9	9	7	ADe78951 Interleuk
26	27	52.9	9	7	ADe78688 Interleuk
27	27	52.9	9	7	ADe78950 Interleuk
28	27	52.9	9	8	ADH48474 HLA-A*02
29	27	52.9	9	8	ADz56682 Cytotoxic
30	26	51.0	6	5	ABg79016 Human MAG
31	26	51.0	8	7	ADb79001 Human ant
32	26	51.0	9	4	Aau26647 Human Leu
33	26	51.0	9	4	Aau26980 Human Leu
34	25	49.0	7	5	ABg77556 Targettin
35	25	49.0	8	2	AAR59204 Peptide f
36	25	49.0	8	2	AAR73323 Human TSH
37	25	49.0	8	2	AAR73322 Human TSH
38	25	49.0	8	2	ADC81364 Bovin TRF
39	25	49.0	9	7	ADK65307 Human NRP
40	25	49.0	9	7	ADK65261 Human NRP
41	24	47.1	6	8	ADO37836 Binding p
42	24	47.1	6	8	ADO28358 Capture s
43	24	47.1	6	8	ADR50535 6-mex pep
44	24	47.1	6	8	ADR596181 Tagged po
45	24	47.1	6	9	ADz46541 Antigenic

ALIGNMENTS

RESULT 1	
AAY71487	
ID	AAY71487 standard; peptide; 9 AA.
XX	
AC	AAY71487;
XX	
DT	12-OCT-2000 (first entry)
XX	
DE	Human MAGE-A10 nonapeptide-1.
XX	
KW	MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
KW	HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
KW	immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
KW	cancer; TNF; tumour necrosis factor; vaccine; cytostatic.
XX	
OS	Homo sapiens.
XX	
FN	WO200032769-A2.
XX	
PD	08-JUN-2000.
XX	
PF	26-NOV-1999; 99WO-IB002018.
XX	
PR	27-NOV-1998; 98GB-00026143.
PA	(LUDW-) LUDWIG INST CANCER RES.
XX	
PI	Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
XX	
DR	WPI; 2000-412317/35.
XX	
PT	Novel polypeptides expressed in tumor cells useful for treating cancers
PT	have an ability to complex with a major histocompatibility complex
PT	molecule and comprises a specific unbroken amino acid sequence.
XX	
XX	Claim 8; Page 36; 80pp; English.
XX	
CC	The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
CC	decapeptide sequences, that function as tumour rejection antigens (TRAS).
CC	These peptides are capable of forming a complex with major
CC	histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
CC	Antigen), that are recognised by T-lymphocytes and elicit an immune
CC	response from cytolytic T-lymphocytes (CTL). They function as an immune
CC	cancer stimulator. Tumour rejection antigens are useful in prophylaxis,
CC	therapy and diagnosis of tumours and are effective in controlling or
CC	preventing tumour growth. The present peptide sequence is the human MAGE-
CC	A10 nonapeptide-1, that corresponds to residues 254-262 of the MAGE-A10

CC protein. This peptide can serve as a tumour rejection antigen (TRA) and
CC in combination with adjuvants, can produce vaccines useful for treating a
CC variety of tumours that express MAGE-A10

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMGHEHL 9
DB 1 GLYDGMGHEHL 9

RESULT 2

AAB31323
ID AAB31323 standard; peptide; 9 AA.

XX AAB31323;

XX 20-APR-2001 (first entry)

XX Exemplary antigen characteristic of tumours and derived from MAGE-A10.

XX MAGE-A1; HLA; human leukocyte antigen; CD4+ T lymphocyte; cancer;
KW MAGE-A1 HLA class II-binding protein; vaccine.

XX Homo sapiens.

XX WO200078806-A1.

XX 28-DEC-2000.

XX 14-JUN-2000; 2000WO-US016287.

XX 18-JUN-1999; 99US-00336091.

XX (LUDW-) LUDWIG INST CANCER RES.

PI Van Snick J, Lethe B, Chaux P, Boon-Falleur T, Van Der Bruggen P;

XX WPI; 2001-102698/11.

XX Novel MAGE-A1 human leukocyte antigen class II peptides which bind to and
PT are presented to the class II molecules, useful for inducing immune
PT response and treating cancers characterized by expression of MAGE-A1.

XX Disclosure; Page 32; 78pp; English.

XX AAB31302-59 represent exemplary antigens which are characteristic of
CC tumours. They can be used to enhance the immune response of vaccines
CC comprising peptides derived from human MAGE-A1 HLA (human leukocyte
CC antigen) class II-binding protein. Peptides derived from the MAGE-A1 HLA
CC binding protein stimulate the activity and proliferation of CD4+ T
CC lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic
CC agent for diagnosing a disorder characterized by expression of MAGE-A1.
CC The protein is used for treating a disorder characterized by expression
CC of MAGE-A1 such as cancers e.g. melanoma, squamous cell carcinomas,
CC colorectal carcinomas, osteosarcomas, and lymphocytic leukemias. Peptides
CC derived from the MAGE-A1 HLA binding protein are useful in the production
CC of anti-tumour vaccines

XX Sequence 9 AA;

Query Match 100.0%; Score 51; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMGHEHL 9
DB 1 GLYDGMGHEHL 9

RESULT 3

AAO17088
ID AAO17088 standard; peptide; 9 AA.

XX AAO17088;

XX 06-JUN-2002 (first entry)

XX Human mage-A10 protein antigen SEQ ID NO: 8.

XX Cryopreserved mature dendritic cell; antigen; vaccine; cytostatic;
KW virucide; cancer; hepatitis B virus.

XX Homo sapiens.

XX WO200216560-A1.

XX 28-FEB-2002.

XX 24-AUG-2001; 2001WO-EP009790.

XX 24-AUG-2000; 2000DE-01041515.

XX (SCHU/) SCHULER G.

XX Schuler G, Schuler-Thurner B;

XX WPI; 2002-292062/33.

XX Preparation of cryopreserved, mature dendritic cells, useful in vaccines,
PT comprises culturing immature cells on medium containing cocktail of
PT maturation factors, then freezing.

XX Disclosure; Fig 28; 87pp; German.

XX The present invention relates to a method for the preparation of ready-
CC for-use, cryopreserved, mature dendritic cells comprising growing
CC immature dendritic cells in a culture medium that includes a 'maturation
CC cocktail' of one or more maturation stimuli and freezing the resulting
CC matured cells in a freezing medium that does not contain heterologous
CC serum. When loaded with antigens, the dendritic cells can be used as
CC vaccines, e.g. against tumours and hepatitis B virus. The present
CC sequence is an antigen described in the invention

XX Sequence 9 AA;

Query Match 100.0%; Score 51; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMGHEHL 9
DB 1 GLYDGMGHEHL 9

RESULT 4

ABU19876
ID ABU19876 standard; peptide; 9 AA.

XX ABU19876;

XX 10-APR-2003 (first entry)

XX MHC binding peptide SEQ ID No 39.

XX Antirheumatic; antiallergic; antiarthritic; nootropic; neuroprotective;
KW antinflammatory; major histocompatibility complex; MHC;
KW autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;
KW rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;
XX inflammation; gene therapy; MHC binding peptide.

XX Synthetic.

XX WO200294981-A2.
 XX 28-NOV-2002.
 XX 16-MAY-2002; 2002WO-IL000383.
 XX 16-MAY-2001; 2001US-0290958P.
 XX 29-MAY-2001; 2001US-00865548.
 XX (TECK) TECHNION RES & DEV FOUND LTD.
 XX Barnea E, Beer I, Ziv T, Admon A, Dassau L, Buchsbaum S;
 XX WPI; 2003-210043/20.
 XX Identifying peptides that are capable of binding to major
 XX histocompatibility complex (MHC) molecules of a particular haplotype by
 XX analyzing peptides bound to the soluble and secreted form of the MHC
 XX molecules of the particular haplotype.
 XX Example; Fig 5D; 238pp; English.
 XX The invention relates to a novel method for identifying peptides
 XX originating from a particular cell type, which are capable of binding to
 XX major histocompatibility complex (MHC) molecules of a particular
 XX haplotype. The method comprises analysing peptides bound to the soluble
 XX and secreted form of the MHC molecules of the particular haplotype. The
 XX method is useful for identifying peptides for treating an autoimmune
 XX disease, such as T or B cell and/or allergic disease or condition,
 XX rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,
 XX e.g. Alzheimer's disease, or diseases associated with inflammation. The
 XX sequences of the invention may be used in a gene therapy application.
 XX This sequence represents a peptide relating to the method for identifying
 XX MHC binding peptides of the invention
 XX Sequence 9 AA;
 Query Match 100.0%; Score 51; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLYDGMHEHL 9
 Db 1 GLYDGMHEHL 9
 RESULT 5
 ADG89586
 ID ADG89586 standard; peptide; 9 AA.
 AC ADG89586;
 DT 11-MAR-2004 (first entry)
 XX Class I HLA-restricted testis cancer antigen #21.
 DE metastatic cancer cell differentiation; mutated fibronectin;
 KW metastatic cancer; class I HLA-restricted; testis; cancer antigen.
 XX Unidentified.
 OS WO2003100027-A2.
 XX 04-DEC-2003.
 XX 28-MAY-2003; 2003WO-US016736.
 XX 28-MAY-2002; 2002US-0383530P.
 XX (BAYU) BAYLOR COLLEGE MEDICINE.
 XX Wang R;
 Query Match 100.0%; Score 51; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLYDGMHEHL 9
 Db 1 GLYDGMHEHL 9
 RESULT 6
 ADI19869
 ID ADI19869 standard; peptide; 9 AA.
 XX ADI19869;
 AC ADI19869;
 DT 22-APR-2004 (first entry)
 XX Human HLA-B18 binding MAGE-3 peptide #11.
 DE HLA; human leucocyte antigen; melanoma; lung cancer; head cancer;
 KW neck cancer; MAGE-3; human.
 XX Homo sapiens.
 OS US2003228325-A1.
 PN 11-DEC-2003.
 PD 05-JUN-2002; 2002US-00164078.
 PF 05-JUN-2002; 2002US-00164078.
 PR (BILS/) BILSBOROUGH J.
 PA (SCHU/) SCHULTZ E.
 PA (PANI/) PANICHELLI C.
 PA (BOON/) BOON-PALLEUR T.
 PA (BRUG/) BRUGEN P V D.
 XX Bilsborough J, Schultz E, Panichelli C, Boon-Falleur T;
 PI Bruggen PVD;
 PI WPI; 2004-042211/04.
 DR Treating subject with pathological condition having human leucocyte
 PT antigen-B18 molecules presented on cell surface by administering peptides
 PT to subject for generating immunologically active response against cells.
 XX Claim 22; SEQ ID NO 12; 15pp; English.
 XX The present invention relates to a peptide which binds HLA (human
 CC leucocyte antigen)-B18 to form T-cell epitope. The invention is useful
 CC for treating a pathological conditions such as melanoma, lung cancer and
 CC head and neck cancer. The present sequence is human HLA-B18 binding MAGE-
 CC 3 peptide.
 XX Sequence 9 AA;
 SQ

XX WPI; 2004-035134/03.
 XX Identifying a cell that differentiates into a metastatic cancer cell,
 PT useful for preventing metastatic cancer, comprises identifying a mutated
 PT fibronectin in the cell.
 XX Disclosure; SEQ ID NO 29; 137pp; English.
 XX The invention comprises a method for identifying a cell that will
 CC differentiate into a metastatic cancer cell. The method involves
 CC identifying a mutated fibronectin in the cell. The method of the
 CC invention is useful for preventing metastatic cancer. The present amino
 CC acid sequence represents a Class I HLA-restricted testis cancer antigen.
 XX Sequence 9 AA;
 Query Match 100.0%; Score 51; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLYDGMHEHL 9
 Db 1 GLYDGMHEHL 9
 RESULT 6
 ADI19869
 ID ADI19869 standard; peptide; 9 AA.
 XX ADI19869;
 AC ADI19869;
 DT 22-APR-2004 (first entry)
 XX Human HLA-B18 binding MAGE-3 peptide #11.
 DE HLA; human leucocyte antigen; melanoma; lung cancer; head cancer;
 KW neck cancer; MAGE-3; human.
 XX Homo sapiens.
 OS US2003228325-A1.
 PN 11-DEC-2003.
 PD 05-JUN-2002; 2002US-00164078.
 PF 05-JUN-2002; 2002US-00164078.
 PR (BILS/) BILSBOROUGH J.
 PA (SCHU/) SCHULTZ E.
 PA (PANI/) PANICHELLI C.
 PA (BOON/) BOON-PALLEUR T.
 PA (BRUG/) BRUGEN P V D.
 XX Bilsborough J, Schultz E, Panichelli C, Boon-Falleur T;
 PI Bruggen PVD;
 PI WPI; 2004-042211/04.
 DR Treating subject with pathological condition having human leucocyte
 PT antigen-B18 molecules presented on cell surface by administering peptides
 PT to subject for generating immunologically active response against cells.
 XX Claim 22; SEQ ID NO 12; 15pp; English.
 XX The present invention relates to a peptide which binds HLA (human
 CC leucocyte antigen)-B18 to form T-cell epitope. The invention is useful
 CC for treating a pathological conditions such as melanoma, lung cancer and
 CC head and neck cancer. The present sequence is human HLA-B18 binding MAGE-
 CC 3 peptide.
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 51; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMHL 9
| | | | |
DB 1 GLYDGMHL 9

RESULT 7
ADI19026
ID ADI19026 standard; peptide; 9 AA.
XX
AC ADI19026;
XX
DT 22-APR-2004 (first entry)
XX
XX Human HLA-Cw6 binding MAGE-1 peptide #11.
XX MHC; major histocompatibility; therapy; cancer; melanoma; HLA-Cw6; human;
KW MAGE-1; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003228308-A1.
XX
PD 11-DEC-2003.
XX
PF 05-JUN-2002; 2002US-00164121.
XX
PR 05-JUN-2002; 2002US-00164121.
XX
PA (ZHAN/) ZHANG Y.
PA (TRAV/) TRAVERSARI C.
PA (BOON/) BOON-FALLEUR T.
PA (BRUG/) BRUGGEN P V D.
XX
PI Zhang Y, Traversari C, Boon-Falleur T, Bruggen PVD;
XX
XX WPI; 2004-042210/04.
XX
XX Treating subject with pathological condition having human leukocyte
PT antigen-Cw6 molecules presented on cell surface by administering peptides
PT to subject for generating immunologically active response against cells.
XX
PS Example 7; SEQ ID NO 13; 15pp; English.
XX
CC The present invention relates to peptides which form immunologically
CC active complexes with MHC molecules. The invention is useful for treating
CC a subject with pathological condition such as cancer which is melanoma by
CC presenting HLA-Cw6 molecules on the cell surface. The present sequence is
CC human HLA-Cw6 binding MAGE-1 peptide.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMHL 9
| | | | |
DB 1 GLYDGMHL 9

RESULT 8
ADJ58374
ID ADJ58374 standard; peptide; 9 AA.
XX
AC ADJ58374;
XX
DT 06-MAY-2004 (first entry)
XX
XX (CYTO-) CYTOCURE LLC.

DE Peptide predicted to bind to HLA-A2 #34.
XX major histocompatibility complex; MHC; cytolytic T-cell; HLA-A2;
KW Cytostatic; cancer.
XX Synthetic.
XX WO2004011483-A2.
XX PD 05-FEB-2004.
XX PF 23-JUL-2003; 2003WO-US023306.
XX PR 31-JUL-2002; 2002US-0400076P.
XX (LUDW-) LUDWIG INST CANCER RES.
PA (TORR-) TORREY PINES INST MOLECULAR STUDIES.
XX Valmori D, Ayyoub M, Pinilla C;
XX WPI; 2004-143815/14.
XX New isolated SSX-2 and SSX-2-related peptides that bind to human
PT leukocyte antigen (HLA) molecules, useful for diagnosing or treating
PT cancer, particularly melanoma.
XX Example 8; SEQ ID NO 34; 20pp; English.
XX The present invention relates to an isolated peptide which binds to a
CC major histocompatibility complex (MHC) molecule to form a complex that is
CC recognized by a cytolytic T-cell which recognizes and lyses cells
CC presenting complexes of HLA-A2 molecules comprising a sequence of 9 amino
CC acids fully defined in the specification, with the proviso that the
CC peptide is not the peptide of S17 itself. Specifically claimed is an HLA-
CC binding peptide comprising a sequence of 9 amino acids fully defined in
CC the specification. The composition and methods are useful for diagnosing
CC or treating cancer, particularly melanoma. The present sequence
CC represents a peptide predicted to bind to HLA-A2.
XX Sequence 9 AA;
SQ

Query Match 100.0%; Score 51; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMHL 9
| | | | |
DB 1 GLYDGMHL 9

RESULT 9
ADL26560
ID ADL26560 standard; peptide; 9 AA.
XX
AC ADL26560;
XX
DT 03-JUN-2004 (first entry)
XX
DE Melanoma cell line MAGE gene encoded HLA-A2 peptide.
XX cytostatic; gene therapy; vaccine; cancer; immune response.
XX Homo sapiens.
XX WO2004019886-A2.
XX PD 11-MAR-2004.
XX PF 29-AUG-2003; 2003WO-US027125.
XX PR 29-AUG-2002; 2002US-0407492P.
XX (CYTO-) CYTOCURE LLC.

XX Durda PJ, Kurnick JT, Dunn IS;
XX WPI; 2004-239114/22.
XX Increasing an immune response against a tumor cell comprises
XX administering to a subject with a tumor an amount of IFN-beta receptor
XX agonist and tumor associated antigen (TAA).
XX
XX Example 7; Page 47; 80pp; English.
XX The present invention relates to a method of increasing an immune
XX response against a tumour cell, comprising administering to a subject
XX with a tumour an amount of IFN-beta receptor agonist and tumour
XX associated antigen (TAA). The method is useful for increasing an immune
XX response against a tumour cell. The present sequence is a peptide used in
XX the exemplification of the invention.
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 51; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLYDGMHEHL 9
DB 1 GLYDGMHEHL 9
RESULT 10
ADR69760
ID ADR69760 standard; peptide; 9 AA.
AC ADR69760;
XX 18-NOV-2004 (first entry)
XX
XX Novel hybrid antigen-related peptide #1340.
XX hybrid antigen; antigenic domain; infectious agent; tumour antigen;
XX binding domain; heat shock protein; antimicrobial; cytostatic; vaccine;
XX gene therapy; infectious disease; cancer.
XX Unidentified.
XX WO2004071457-A2.
XX 26-AUG-2004.
XX 13-FEB-2004; 2004WO-US004340.
XX 13-FEB-2003; 2003US-0447142P.
XX 11-APR-2003; 2003US-0462469P.
XX 18-APR-2003; 2003US-0463746P.
XX 16-SEP-2003; 2003US-0503417P.
XX 12-FEB-2004; 2004US-00776521.
XX (WOJA-) MOJAVE THERAPEUTICS INC.
XX
XX Fletchner J, Prince-Cohane K, Mehta S, Slusarewicz P, Andjelic S;
XX Barber B;
XX WPI; 2004-625768/60.
XX New hybrid antigens comprising an antigenic domain and improved heat
XX shock protein-binding domains, useful for preventing or treating
XX infectious diseases or cancer.
XX Example 11; Page 44; 56pp; English.
XX This invention relates to a novel hybrid antigen which comprises at least
XX one antigenic domain of an infectious agent or tumour antigen and a
XX binding domain that non-covalently binds to a heat shock protein. The

XX invention may be useful for the production of compounds with an
XX antimicrobial or cytostatic activity. In addition, the invention may
XX prove useful for the production of a vaccine or for gene therapy. The
XX composition and methods disclosed are useful for preventing or treating
XX infectious diseases or cancer. The present sequence is that of a peptide
XX which was used in the exemplification of the invention.
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 51; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLYDGMHEHL 9
DB 1 GLYDGMHEHL 9
RESULT 11
ADX08536
ID ADX08536 standard; peptide; 9 AA.
XX
XX AC ADX08536;
XX 21-APR-2005 (first entry)
XX
XX Class I HLA-restricted cancer/testis antigen peptide #21.
XX vaccine; infection; viral infections; virucide; bacterial infection;
XX antibacterial; yeast infection; fungicide; fungal infection;
XX protozoal infection; protozoicide; cancer; cytostatic; melanoma;
XX lung tumor; colon tumor; breast tumor; leukemia; autoimmune disease;
XX multiple sclerosis; neuroprotective; rheumatoid arthritis; antiarthritic;
XX antirheumatic; systemic lupus erythematosus; antiinflammatory;
XX dermatological; immunosuppressive.
XX Unidentified.
XX WO2005011730-A1.
XX 10-FEB-2005.
XX 30-JUL-2004; 2004WO-GB003285.
XX 01-AUG-2003; 2003GB-00018096.
XX (UNLO) QUEEN MARY & WESTFIELD COLLEGE.
XX Wang P, Li S;
XX WPI; 2005-152360/16.
XX New vaccine composition comprises inverted microsomes from animal cells
XX with an externally disposed peptide antigen and a protein of the Major
XX Histocompatibility Complex (MHC), useful for treating or preventing, e.g.
XX cancer.
XX Disclosure; Page 47; 83pp; English.
XX The invention comprises a vaccine composition that consists of isolated
XX inverted microsomes from an animal cell (or its membrane fragments), in
XX association with an externally disposed peptide antigen and a protein of
XX the MHC. The vaccine composition of the invention is useful for the
XX prophylaxis or treatment of: infection (e.g. viral, bacterial, yeast,
XX fungal or protozoal), cancer (e.g. melanoma, lung adenocarcinoma, colon
XX cancer, breast cancer or leukemia), autoimmune disease (e.g. multiple
XX sclerosis, rheumatoid arthritis or systemic lupus erythematosus). The
XX present amino acid sequence represents a class I HLA-restricted cancer
XX antigen which was found to be expressed by normal spermatocytes and/or
XX spermatogonia of testis.
XX Sequence 9 AA;
SQ

```

Query Match          100.0%; Score 51; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMHEHL 9
DB 1 GLYDGMHEHL 9

RESULT 12
ID AEB01337 standard; peptide; 9 AA.
XX
AC AEB01337;
XX
DT 25-AUG-2005 (first entry)
XX
DE Melanoma protein Mage 10 peptide, SEQ ID 11.
XX
KW Cytostatic; Vaccine; immunotherapy; tumor-associated antigen; cancer.
XX
OS Unidentified.
XX
PN WO2005053738-A1.
XX
PD 16-JUN-2005.
XX
PF 19-NOV-2004; 2004WO-BP014086.
XX
PR 21-NOV-2003; 2003US-0523632P.
XX
PA (INSP) INST PASTEUR.
PA (INRM) INERM INST NAT SANTE & RECH MEDICALE.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (CNRS) CENT NAT RECH SCI.
XX
PI Dadaglio G, Leclerc C, Ladant D, Van Den Eynde B, Morel S;
PI Bauche C;
XX
WPI; 2005-425294/43.
XX
Immunogenic composition useful for treating cancer comprises recombinant
PT protein or vector expressing the recombinant protein that has Bordetella
PT adenylate cyclase and peptide corresponding to tumor antigen.
XX
Example 5; SEQ ID NO 11; 56pp; English.
XX
The present invention relates to a novel immunogenic composition
CC comprising a recombinant protein or vector expressing the recombinant
CC protein, where the recombinant protein comprises Bordetella adenylate
CC cyclase (CyaA) (a), or its fragment, and a peptide (p) that corresponds
CC to a tumor antigen. The Bordetella CyaA is derived from B. pertussis, B.
CC paraptussis or B. bronchiseptica and the tumor antigen is an HLA*0201
CC epitope e.g. AEB01327 or AEB01330. The composition is useful in an
CC immunotherapy for inducing T cell response e.g. cytotoxic T lymphocytic
CC (CTL) response during treatment of cancer e.g. melanoma. The present
CC sequence was used to illustrate the invention.
XX
Sequence 9 AA;
XX
Query Match          100.0%; Score 51; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMHEHL 9
DB 1 GLYDGMHEHL 9

RESULT 13
AAY71488
ID AAY71488 standard; peptide; 9 AA.
XX

```

```

AC AAY71488;
XX
DT 12-OCT-2000 (first entry)
XX
DE Human MAGE-A8 nonapeptide-1.
XX
KW MAGE-A8; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
KW immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
KW cancer; TNF; tumour necrosis factor; vaccine; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200032769-A2.
XX
PD 08-JUN-2000.
XX
PF 26-NOV-1999; 99WO-IB002018.
XX
PR 27-NOV-1998; 98GB-00026143.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
XX
WPI; 2000-412317/35.
XX
Novel polypeptides expressed in tumor cells useful for treating cancers
PT have an ability to complex with a major histocompatibility complex
PT molecule and comprises a specific unbroken amino acid sequence.
XX
Claim 8; Page 36; 80pp; English.
XX
The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
CC decapeptide sequences, that function as tumour rejection antigens (TRA).
CC These peptides are capable of forming a complex with major
CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
CC Antigen), that are recognised by T-lymphocytes and elicit an immune
CC response from cytolytic T-lymphocytes (CTL). They function as an immune
CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
CC therapy and diagnosis of tumours and are effective in controlling or
CC preventing tumour growth. The present peptide sequence is the human MAGE-A8
CC nonapeptide-1, that corresponds to residues 232-240 of the MAGE-A8
CC protein. This peptide can serve as a tumour rejection antigen (TRA) and
CC in combination with adjuvants, can produce vaccines useful for treating a
CC variety of tumours that express MAGE-A8
XX
Sequence 9 AA;
XX
Query Match          80.4%; Score 41; DB 3; Length 9;
Best Local Similarity 87.5%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLYDGMHEH 8
DB 1 GLYDGMHEH 8

RESULT 14
ABG79151
ID ABG79151 standard; peptide; 6 AA.
XX
AC ABG79151;
XX
DT 15-NOV-2002 (first entry)
XX
KW Human MAGE-A10 class I HLA restricted testis cancer antigen peptide #1.
XX
Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;

```

KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
KW cytostatic; human.
XX
OS Homo sapiens.
OS Unidentified.
XX
XX WO200264057-A2.
XX
XX PD 22-AUG-2002.
XX
XX PF 15-FEB-2002; 2002WO-US005212.
XX
XX PF 15-FEB-2001; 2001US-0268687P.
XX
XX (BAYU) BAYLOR COLLEGE MEDICINE.
XX
XX PA Wang R;
XX
XX PI WPI; 2002-627577/67.
XX
XX DR Novel composition for treating a disease in an animal, comprises an
XX PT immune effector cell and cell penetrating peptide associated with an
XX PT antigen or antibody.
XX
XX PS Disclosure; Page 14; 61pp; English.
XX
XX CC The invention relates to a composition (I) comprising an immune effector
XX CC cell and a cell penetrating peptide (CPP) associated with an antigen or
XX CC antibody. Also included are (1) a vaccine comprising (I), CPP associated
XX CC with an antigen, and a pharmaceutically acceptable carrier and (2)
XX CC preparing a composition for a disease, by providing (I) and CPP
XX CC associated with an antigen for disease, and introducing the antigen-
XX CC associated CPP to (I), where antigen enters into the cell. The antigens
XX CC are, for example, tumour antigen derived epitopes recognised by tumour
XX CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
XX CC or II. The composition is useful for enhancing immunity in an animal to a
XX CC disease, by administering a mature dendritic cell comprising CPP
XX CC associated with an antigen to disease, to the animal, such that following
XX CC the administration, animal is protected from disease, where the animal
XX CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
XX CC disease (e.g. cancer, melanoma, thymoma, lymphoma, sarcoma, lung
XX CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
XX CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
XX CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
XX CC The animal is further subjected to a cancer treatment including surgery,
XX CC radiation, chemotherapy or gene therapy. The administration of (I),
XX CC preferably dendritic cell is prior to, subsequent to or concurrent with,
XX CC the cancer treatment. The present sequence is a tumour antigen derived
XX CC epitope for inclusion in the composition of the invention
XX
SQ Sequence 6 AA;
Query Match 66.7%; Score 34; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLYDGM 6
|||
Db 1 GLYDGM 6
RESULT 15
ID AAY46134
XX AAY46134 standard; peptide; 9 AA.
XX
XX AC AAY46134;
XX
XX DT 01-DEC-1999 (first entry)
XX
XX DE Immunogenic peptide having a human leukocyte antigen binding motif #745.
XX
XX KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW immune response; T cell activation; major histocompatibility complex;

KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX vaccine; immunisation.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX FN WO9945954-A1.
XX
XX PD 16-SEP-1999.
XX
XX PF 13-MAR-1998; 98WO-US005039.
XX
XX PF 13-MAR-1998; 98WO-US005039.
XX
XX PA (EPIM-) EPIMUNE INC.
XX
XX PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX WPI; 1999-551214/46.
XX
XX DR New immunogenic peptides with HLA binding motif, useful in treatment and
XX PT diagnosis of cancers and viral diseases.
XX
XX PS Claim 1; Page 58; 150pp; English.
XX
XX CC AAY45390 to AAY49214 represent specifically claimed immunogenic peptides
XX CC having a human major histocompatibility complex (MHC) Class I (also known
XX CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
XX CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
XX CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
XX CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
XX CC (CTLs) which destroy antigen-bearing cells are normally induced by an
XX CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
XX CC than the intact foreign antigen itself, and are particularly important in
XX CC tumour rejection and in fighting viral infections. The peptides are
XX CC therefore useful therapeutically to treat or prevent viral infections and
XX CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
XX CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
XX CC elicit an immune response in individuals susceptible or otherwise at risk
XX CC of viral infection or cancer, or used to treat chronic or acute
XX CC conditions. They are also useful diagnostically, and can be used to
XX CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
XX CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
XX CC patient. The polynucleotides encoding the immunogenic peptides are also
XX CC useful therapeutically and for immunisation as above
XX
SQ Sequence 9 AA;

Query Match 62.7%; Score 32; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 LYDGMH 8
: ||| ||
Db 3 VYDGRH 9

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Job time : 191 secs

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OM protein - protein search, using sw model

Run on: March 17, 2006, 22:28:58 ; Search time 47 Seconds
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15.832 Million cell updates/sec

Title: US-09-856-812B-42
Perfect score: 51
Sequence: 1 GLYDGMHL 9

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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 111694

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	9	2	US-09-865-548A-39
2	28	54.9	8	2	US-09-865-548A-155
3	25	49.0	8	1	US-08-571-985-22
4	25	49.0	8	1	US-09-116-766-22
5	24	47.1	8	1	US-08-178-570-45
6	24	47.1	8	1	US-08-446-206B-25
7	24	47.1	8	1	US-08-807-030-11
8	24	47.1	8	2	US-08-369-643-45
9	24	47.1	8	4	PCT-US95-00147-45
10	24	47.1	9	1	US-08-178-570-72
11	24	47.1	9	2	US-08-369-643-72
12	24	47.1	9	2	US-09-503-172A-3
13	24	47.1	9	2	US-08-403-459-19
14	24	47.1	9	2	US-09-462-453-14
15	24	47.1	9	2	US-09-865-548A-14
16	24	47.1	9	4	PCT-US95-00147-61
17	24	47.1	9	4	PCT-US95-00147-72
18	23	45.1	8	2	US-08-335-198-22
19	23	45.1	8	2	US-09-420-211-12
20	23	45.1	9	1	US-08-951-924A-3
21	22	43.1	6	1	US-07-718-577-20
22	22	43.1	6	2	US-09-198-092-4
23	22	43.1	8	2	US-08-477-928A-47
24	22	43.1	8	2	US-09-128-572-13
25	22	43.1	8	2	US-09-782-385A-13
26	22	43.1	9	1	US-08-186-266-11
27	22	43.1	9	2	US-09-593-870A-30

28	22	43.1	9	2	US-09-601-171-3	Sequence 3, Appli
29	22	43.1	9	4	PCT-US95-04975-6	Sequence 6, Appli
30	21	41.2	7	1	US-08-285-936-49	Sequence 49, Appl
31	21	41.2	7	1	US-08-487-860-49	Sequence 127, App
32	21	41.2	7	1	US-08-310-912A-127	Sequence 127, App
33	21	41.2	7	2	US-09-301-085-127	Sequence 127, App
34	21	41.2	7	4	PCT-US95-04589-127	Sequence 127, App
35	21	41.2	8	1	US-08-271-830-46	Sequence 46, Appl
36	21	41.2	8	1	US-08-571-985-12	Sequence 12, Appl
37	21	41.2	8	1	US-08-286-113C-1	Sequence 1, Appli
38	21	41.2	8	1	US-08-286-113C-2	Sequence 2, Appli
39	21	41.2	8	1	US-08-286-113C-3	Sequence 3, Appli
40	21	41.2	8	1	US-08-286-113C-4	Sequence 4, Appli
41	21	41.2	8	1	US-08-807-030-10	Sequence 10, Appl
42	21	41.2	8	1	US-09-116-766-12	Sequence 12, Appl
43	21	41.2	8	2	US-09-454-204A-22	Sequence 22, Appl
44	21	41.2	9	1	US-08-217-188A-31	Sequence 31, Appl
45	21	41.2	9	1	US-08-217-186-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-865-548A-39
; Sequence 39, Application US/09865548A
; Patent No. 6867283
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamir
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECUL
; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-39

Query Match 100.0%; Score 51; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHL 9
Db 1 GLYDGMHL 9

RESULT 2
US-09-865-548A-155
; Sequence 155, Application US/09865548A
; Patent No. 6867283
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamir
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECUL
; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958

;; PRIOR FILING DATE: 2001-05-16
;; NUMBER OF SEQ ID NOS: 204
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 155
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: synthetic peptide
US-09-865-548A-155

Query Match 54.9%; Score 28; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.6e+05;
Matches 5; Conservative 2; Mismatches 2; Indels 0;

Qy 1 GLYDGMHL 9
Db 1 GLYGLTWL 9

RESULT 3

US-08-571-985-22
; Sequence 22, Application US/08571985
; Patent No. 5783557
; GENERAL INFORMATION:
; APPLICANT: Burstein, Yigal
; APPLICANT: Trainin, Nathan
; APPLICANT: Rycus, Avigail
; TITLE OF INVENTION: THF-gamma2 Analogs and Pharmaceutical
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 5783557thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48334

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/571,985
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: IL 106214
FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 2163.00048
TELEPHONE: (810) 539-5050
TELEFAX: (810) 539-5055
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-571-985-22
Query Match 49.0%; Score 25; DB 1; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0;
Qy 2 LYDGMHL 9
Db 1 LEDGPKHL 8

US-08-571-985-22
Query Match 49.0%; Score 25; DB 1; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0;

Qy 2 LYDGMHL 9
Db 1 LEDGPKHL 8

RESULT 4

US-09-116-766-22
; Sequence 22, Application US/09116766
; Patent No. 596898
; GENERAL INFORMATION:
; APPLICANT: Burstein, Yigal
; APPLICANT: Trainin, Nathan
; APPLICANT: Rycus, Avigail
; TITLE OF INVENTION: THF-gamma2 Analogs and Pharmaceutical
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 596898thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,766
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 106214
FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2163.00050
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-09-116-766-22
Query Match 49.0%; Score 25; DB 1; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0;

Qy 2 LYDGMHL 9
Db 1 LEDGPKHL 8

RESULT 5

US-08-178-570-45
; Sequence 45, Application US/08178570
; Patent No. 5532187
; GENERAL INFORMATION:
; APPLICANT: Lewis C. Cantley
; APPLICANT: Zhou Song yang
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/178,570
FILING DATE: JANUARY 7, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-178-570-45

Query Match 47.1%; Score 24; DB 1; Length 8;
Best Local Similarity 42.9%; Pred. No. 4.6e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLYDGM 7
|.:|
Db 2 GIVEALE 8

RESULT 6
US-08-446-206B-25
; Sequence 25, Application US/08446206B
; Patent No. 5750647
; GENERAL INFORMATION:
; APPLICANT: Eyre, David R
; APPLICANT: Clemens, J Daniel
; APPLICANT: Ochs, Vincent W
; TITLE OF INVENTION: Synthetic Peptide Analogs of NTx
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson & Kindness PLLC
; STREET: 1420 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: WA 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelton, Dennis K
; REGISTRATION NUMBER: 26,997
; REFERENCE/DOCKET NUMBER: WROS18360
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206 682 8100
; TELEFAX: 206 224 0779
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
FEATURE:
LOCATION: 1
OTHER INFORMATION: Xaa is glutamine or pyrrolidone
US-08-446-206B-25

Query Match 47.1%; Score 24; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YDGM 6
| | | |
Db 2 YDGM 5

RESULT 7
US-08-807-030-11
; Sequence 11, Application US/08807030
; Patent No. 5817755
; GENERAL INFORMATION:
; APPLICANT: Eyre, David R.
; APPLICANT: Clemens, J. Daniel
; APPLICANT: Ochs, Vincent W.
; TITLE OF INVENTION: Synthetic Peptide Analogs of NTx
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen O'Connor Johnson & Kindness
; ADDRESSEE: PLLC
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/807,030
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446,206
; FILING DATE: 19-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelton, Dennis K.
; REGISTRATION NUMBER: 26,997
; REFERENCE/DOCKET NUMBER: WROS110387
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206 224 0718
; TELEFAX: 206 224 0779
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 1
; OTHER INFORMATION: Xaa is pyroglutamic acid
US-08-807-030-11

Query Match 47.1%; Score 24; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      3 YDGM 6
      ||||
Db      2 YDGM 5

RESULT 8
US-08-369-643-45
; Sequence 45, Application US/08369643A
; Patent No. 6004757
; GENERAL INFORMATION:
; APPLICANT: Cantley, Lewis C.
; APPLICANT: Songyang, Zhou
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; FILE REFERENCE: CNS-001CP
; CURRENT APPLICATION NUMBER: US/08/369,643A
; CURRENT FILING DATE: 1995-01-06
; EARLIER APPLICATION NUMBER: US 08/178,570
; EARLIER FILING DATE: 1994-01-07
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Enolase (Y43)
US-08-369-643-45

Query Match      47.1%; Score 24; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 4.6e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 GLYDGM 7
      ||:|:|
Db      2 GIYEAL 8

RESULT 9
PCT-US95-00147-45
; Sequence 45, Application PC/TUS9500147
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00147
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,570
; FILING DATE: JANUARY 7, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-004CPPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids

QY      3 YDGM 6
      ||||
Db      2 YDGM 5

RESULT 8
US-08-369-643-45
; Sequence 45, Application US/08369643A
; Patent No. 6004757
; GENERAL INFORMATION:
; APPLICANT: Cantley, Lewis C.
; APPLICANT: Songyang, Zhou
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; FILE REFERENCE: CNS-001CP
; CURRENT APPLICATION NUMBER: US/08/369,643A
; CURRENT FILING DATE: 1995-01-06
; EARLIER APPLICATION NUMBER: US 08/178,570
; EARLIER FILING DATE: 1994-01-07
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Enolase (Y43)
US-08-369-643-45

Query Match      47.1%; Score 24; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 4.6e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 GLYDGM 7
      ||:|:|
Db      2 GIYEAL 8

RESULT 9
PCT-US95-00147-45
; Sequence 45, Application PC/TUS9500147
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00147
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,570
; FILING DATE: JANUARY 7, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-004CPPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
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```
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US95-00147-45

Query Match      47.1%; Score 24; DB 4; Length 8;
Best Local Similarity 42.9%; Pred. No. 4.6e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 GLYDGM 7
      ||:|:|
Db      2 GIYEAL 8

RESULT 10
US-08-178-570-72
; Sequence 72, Application US/08178570
; Patent No. 5532167
; GENERAL INFORMATION:
; APPLICANT: Lewis C. Cantley
; APPLICANT: Zhou Song yang
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/178,570
; FILING DATE: JANUARY 7, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-178-570-72

Query Match      47.1%; Score 24; DB 1; Length 9;
Best Local Similarity 42.9%; Pred. No. 4.6e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 GLYDGM 7
      ||:|:|
Db      3 GIYEAL 9

RESULT 11
US-08-369-643-72
; Sequence 72, Application US/08369643A
; Patent No. 6004757
; GENERAL INFORMATION:
; APPLICANT: Cantley, Lewis C.
; APPLICANT: Songyang, Zhou
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
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; FILE REFERENCE: CNS-001CP
; CURRENT APPLICATION NUMBER: US/08/369,643A
; CURRENT FILING DATE: 1995-01-06
; EARLIER APPLICATION NUMBER: US 08/178,570
; EARLIER FILING DATE: 1994-01-07
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Human enolase
; OTHER INFORMATION: (Y43)
US-08-369-643-72

Query Match          47.1%; Score 24; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 4.6e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 GLYDGM 7
       |||:|
Db      3 GYEALE 9

RESULT 12
US-09-503-172A-3
; Sequence 3, Application US/09503172A
; Patent No. 6284510
; GENERAL INFORMATION:
; APPLICANT: ITO, Tetsuya
; APPLICANT: FUJITA, Koki
; APPLICANT: HARA, Kozo
; APPLICANT: TONOUZUKA, Takashi
; APPLICANT: SAKANO, Yoshiyuki
; TITLE OF INVENTION: BETA-FRUCTOFURANOSIDASE GENE
; FILE REFERENCE: 10749-0001-0
; CURRENT APPLICATION NUMBER: US/09/503,172A
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: JP 160416/1999
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Arthrobacter sp.
US-09-503-172A-3

Query Match          47.1%; Score 24; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GLYDGM 7
       |||||
Db      3 GLQDGPE 9

RESULT 13
US-08-403-459-19
; Sequence 19, Application US/08403459
; Patent No. 6514942
; GENERAL INFORMATION:
; APPLICANT: Ioannides, Constantin G.
; APPLICANT: Fisk, Bryan A.
; APPLICANT: Ioannides, Maria G.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING
; TITLE OF INVENTION: T-LYMPHOCYTES
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
```

```
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,459
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSC:390/KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-403-459-19

Query Match          47.1%; Score 24; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 GLYDGM 7
       |||||
Db      1 GLYQSCQ 7

RESULT 14
US-09-462-453-14
; Sequence 14, Application US/09462453
; Patent No. 6723695
; GENERAL INFORMATION:
; APPLICANT: BURROWS, SCOTT RENTON
; APPLICANT: KHANNA, RAJIV
; APPLICANT: SHERRITT, MARTINA ALISON
; TITLE OF INVENTION: CTL EPITOPES FROM BBV
; FILE REFERENCE: FBRC:010
; CURRENT APPLICATION NUMBER: US/09/462,453
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Epstein Barr Virus
US-09-462-453-14

Query Match          47.1%; Score 24; DB 2; Length 9;
Best Local Similarity 44.4%; Pred. No. 4.6e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 GLYDGM 9
       |||||
Db      1 GLYEERAHV 9

RESULT 15
US-09-865-548A-14
; Sequence 14, Application US/09865548A
; Patent No. 6867283
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
```

; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-14

Query Match 47.1%; Score 24; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLYDGM 6
|||:
Db 1 GLYPGL 6

Search completed: March 17, 2006, 22:30:16
Job time : 49 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 22:30:28 ; Search time 23 Seconds
(without alignments)
11.200 Million cell updates/sec

Title: US-09-856-812B-42
Perfect score: 51
Sequence: 1 GLYDGMHL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 37190

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_New:
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	9	6	US-10-994-204-11 Sequence 11, Appl
2	51	100.0	9	7	US-11-032-498-14 Sequence 14, Appl
3	25	49.0	7	7	US-11-047-383-36 Sequence 36, Appl
4	24	47.1	6	7	US-11-032-773-859 Sequence 859, Appl
5	23	45.1	6	7	US-11-047-383-31 Sequence 31, Appl
6	22	43.1	9	7	US-11-021-441-102 Sequence 102, Appl
7	22	43.1	9	7	US-11-041-893-66 Sequence 66, Appl
8	21	41.2	8	7	US-11-131-479-12 Sequence 12, Appl
9	21	41.2	9	7	US-11-045-024-2573 Sequence 2573, Ap
10	21	41.2	9	7	US-11-045-024-4952 Sequence 4952, Ap
11	21	41.2	9	7	US-11-045-024-8056 Sequence 8056, Ap
12	21	41.2	9	7	US-11-045-024-14230 Sequence 14230, A
13	21	41.2	9	7	US-11-074-373-52 Sequence 52, Appl
14	20	39.2	5	6	US-10-622-246-12 Sequence 12, Appl
15	20	39.2	5	6	US-10-622-246-30 Sequence 30, Appl
16	20	39.2	5	6	US-10-622-246-31 Sequence 31, Appl
17	20	39.2	5	6	US-10-622-246-32 Sequence 32, Appl
18	20	39.2	5	6	US-10-622-246-34 Sequence 34, Appl
19	20	39.2	5	6	US-10-622-246-35 Sequence 35, Appl
20	20	39.2	5	6	US-10-622-246-36 Sequence 36, Appl
21	20	39.2	5	6	US-10-622-246-112 Sequence 112, App
22	20	39.2	5	6	US-10-622-246-114 Sequence 114, App
23	20	39.2	5	6	US-10-622-246-158 Sequence 158, App
24	20	39.2	5	6	US-10-622-246-160 Sequence 160, App
25	20	39.2	5	6	US-10-622-246-161 Sequence 161, App

ALIGNMENTS

RESULT 1
US-10-994-204-11
; Sequence 11, Application US/10994204
; Publication No. US20050271679A1
; GENERAL INFORMATION:
; APPLICANT: DADAGLIO, GILLES
; APPLICANT: LECIERC, CLAUDE
; APPLICANT: LADANT, DANIEL
; APPLICANT: VAN DEN EYNDE, BENOIT
; APPLICANT: MOREL, SANDRA
; APPLICANT: BAUCHE, CECILE
; TITLE OF INVENTION: RECOMBINANT ADENYLATE CYCLASE TOXIN OF BORDETTELLA
; FILE REFERENCE: 03495.0327
; CURRENT APPLICATION NUMBER: US/10/994,204
; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: 60/523,632
; PRIOR FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-994-204-11
Query Match 100.0%; Score 51; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMHL 9
| | | | | | | |
DB 1 GLYDGMHL 9

RESULT 2
US-11-032-498-14
; Sequence 14, Application US/11032498
; Publication No. US20050249743A1
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Van der Bruggen, Pierre
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-A24 Molecule and Uses Thereof.
; FILE REFERENCE: LUD 5881
; CURRENT APPLICATION NUMBER: US/11/032,498

Sequence 163, App
Sequence 164, App
Sequence 166, App
Sequence 277, App
Sequence 279, App
Sequence 113, App
Sequence 159, App
Sequence 162, App
Sequence 165, App
Sequence 419, App
Sequence 901, App
Sequence 35, Appl
Sequence 1766, Ap
Sequence 5806, Ap
Sequence 10115, A
Sequence 12004, A
Sequence 129, App
Sequence 478, App
Sequence 110, App
Sequence 210, App

; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: US 60/535,751
; PRIOR FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MAGE-A10 peptide
US-11-032-498-14

Query Match 100.0%; Score 51; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGM 9
|||
DB 1 GLYDGM 9

RESULT 3

US-11-047-383-36
; Sequence 36, Application US/11047383
; Publication No. US20060003432A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; APPLICANT: BEATTIE, BRYAN
; APPLICANT: CLARKE, TERESA
; APPLICANT: KIMBER, MATTHEW
; TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM ENTEROCOCCUS FAECALIS
; FILE REFERENCE: IPT-318.01
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: PCT/CA03/01135
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: 60/400,435
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: 60/453,405
; PRIOR FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 36
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-047-383-36

Query Match 49.0%; Score 25; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLYDGM 6
|||
DB 2 GRDGL 7

RESULT 4

US-11-032-773-859
; Sequence 859, Application US/11032773
; Publication No. US20060018911A1
; GENERAL INFORMATION:
; APPLICANT: Ault-Riche, Dana
; APPLICANT: Levy, Ronald
; TITLE OF INVENTION: DESIGN OF THERAPEUTICS AND THERAPEUTICS
; FILE REFERENCE: 17102-013001 / 1762
; CURRENT APPLICATION NUMBER: US/11/032,773

; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/536,184
; PRIOR FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: 60/557,591
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 958
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 859
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-11-032-773-859

Query Match 47.1%; Score 24; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 DGM 8
|||
DB 2 DGM 6

RESULT 5

US-11-047-383-31
; Sequence 31, Application US/11047383
; Publication No. US20060003432A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; APPLICANT: BEATTIE, BRYAN
; APPLICANT: CLARKE, TERESA
; APPLICANT: KIMBER, MATTHEW
; TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM ENTEROCOCCUS FAECALIS
; FILE REFERENCE: IPT-318.01
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: PCT/CA03/01135
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: 60/400,435
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: 60/453,405
; PRIOR FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 31
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-047-383-31

Query Match 45.1%; Score 23; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLYDG 5
|||
DB 2 GRDGL 6

RESULT 6

US-11-021-441-102
; Sequence 102, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKI, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.

APPLICANT: COOK, David N.
TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
TITLE OF INVENTION: THEROF
FILE REFERENCE: 282172003900
CURRENT APPLICATION NUMBER: US/11/021,441
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: US 60/616,750
PRIOR FILING DATE: 2004-10-06
PRIOR APPLICATION NUMBER: US 60/615,287
PRIOR FILING DATE: 2004-10-01
PRIOR APPLICATION NUMBER: US 60/599,377
PRIOR FILING DATE: 2004-08-05
PRIOR APPLICATION NUMBER: PCT/US2004/23881
PRIOR FILING DATE: 2004-07-23
PRIOR APPLICATION NUMBER: US 10/883,599
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: US 60/556,744
PRIOR FILING DATE: 2004-03-26
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 102
LENGTH: 9
TYPE: PRT
ORGANISM: Listeria monocytogenes
US-11-021-441-102

Query Match 43.1%; Score 22; DB 7; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.3e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLYDGMHL 9
DB 1 GYKDGNEI 9

RESULT 7
US-11-041-893-66
Sequence 66, Application US/11041893
Publication No. US20060002941A1
GENERAL INFORMATION:
APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
ALTERING AGENTS AND METHODS OF USE
FILE REFERENCE: 100123.401
CURRENT APPLICATION NUMBER: US/11/041,893
CURRENT FILING DATE: 2005-01-24
PRIOR APPLICATION NUMBER: US 60/616,855
PRIOR FILING DATE: 2004-10-06
PRIOR APPLICATION NUMBER: US 60/538,713
PRIOR FILING DATE: 2004-01-23
NUMBER OF SEQ ID NOS: 295
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 66
LENGTH: 9
TYPE: PRT
ORGANISM: Listeria monocytogenes
US-11-041-893-66

Query Match 43.1%; Score 22; DB 7; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.3e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLYDGMHL 9
DB 1 GYKDGNEI 9

RESULT 8
US-11-131-479-12
Sequence 12, Application US/11131479
Publication No. US20060024670A1
GENERAL INFORMATION:

APPLICANT: Luke, Catherine J.
APPLICANT: Vilalta, Adrian
APPLICANT: Wloch, Mary K.
APPLICANT: Evans, Thomas G.
APPLICANT: Geall, Andrew J.
APPLICANT: Jimenez, Gretchen
TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
FILE REFERENCE: 1530.0640002/EJH/J-H
CURRENT APPLICATION NUMBER: US/11/131,479
CURRENT FILING DATE: 2005-05-18
PRIOR APPLICATION NUMBER: US 60/571,854
PRIOR FILING DATE: 2004-05-18
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn version 3.3
SEQ ID NO 12
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Linker Peptide
US-11-131-479-12

Query Match 41.2%; Score 21; DB 7; Length 8;
Best Local Similarity 42.9%; Pred. No. 1.3e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 YDGMHL 9
DB 1 FDRVHL 7

RESULT 9
US-11-045-024-2573
Sequence 2573, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Cheanut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Cellis, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2573
LENGTH: 9
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS

US-11-045-024-2573

Query Match 41.2%; Score 21; DB 7; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.3e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLYDGMHL 9
||| : :
DB 1 GLADQLIHM 9

RESULT 10

US-11-045-024-4952
; Sequence 4952, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4952
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4952

Query Match 41.2%; Score 21; DB 7; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.3e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLYDGMHL 9
||| : :
DB 1 GLADQLIHM 9

US-11-045-024-4952
; Sequence 4952, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4952
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4952

Query Match 41.2%; Score 21; DB 7; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.3e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLYDGMHL 9
||| : :
DB 1 GLADQLIHM 9

RESULT 11

US-11-045-024-8056
; Sequence 8056, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8056
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-8056

APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8056
LENGTH: 9
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-8056

Query Match 41.2%; Score 21; DB 7; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.3e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLYDGMHL 9
||| : :
DB 1 GLADQLIHM 9

RESULT 12

US-11-045-024-14230
; Sequence 14230, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14230
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-14230

Query Match 41.2%; Score 21; DB 7; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.3e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLYDGMHL 9
||| : :
DB 1 GLADQLIHM 9

US-11-045-024-14230
; Sequence 14230, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14230
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-14230

;
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14230
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-14230

Query Match 41.2%; Score 21; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YDGMH 8
|:|:
DB 3 YNGLIH 8

RESULT 13

US-11-074-373-52
; Sequence 52, Application US/11074373
; Publication No. US20060024302A1

GENERAL INFORMATION:

; APPLICANT: Achen et al.
; TITLE OF INVENTION: CHIMERIC ANTI-VEGF-D ANTIBODIES AND HUMANIZED ANTI-VEGF-D ANTIBOD
; FILE REFERENCE: 28967/39969A
; CURRENT APPLICATION NUMBER: US/11/074,373
; CURRENT FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus

US-11-074-373-52

Query Match 41.2%; Score 21; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YDGMH 8
|:|:
DB 4 YGGM DY 9

RESULT 14

US-10-622-246-12
; Sequence 12, Application US/10622246
; Publication No. US20060003926A1

GENERAL INFORMATION:

; APPLICANT: Rajopadhye, Milind
; APPLICANT: Edwards, D. Scott
; APPLICANT: Barrett, John A.
; APPLICANT: Carpenter, Jr., Alan P.
; APPLICANT: Harris, Thomas D.
; APPLICANT: Heminway, Stuart D.
; APPLICANT: Liu, Shuang
; APPLICANT: Prahlad, Singh R.
; TITLE OF INVENTION: PHARMACEUTICALS FOR THE IMAGING OF ANGIOGENIC DISORDERS
; FILE REFERENCE: BMS-2288

; CURRENT APPLICATION NUMBER: US/10/622,246
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 10/342,081
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 09/599,295
; PRIOR FILING DATE: 2000-06-21

;
; PRIOR APPLICATION NUMBER: US 09/281,474
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/080,150
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: US 60/112,715
; PRIOR FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(5)
; OTHER INFORMATION: cyclic amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (2)..(4)
; OTHER INFORMATION: D amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (3)..(3)
; OTHER INFORMATION: (N-[2-[[[5-[carbonyl]-2-pyridinyl]hydrazono]methyl]-benzenesulfo
; OTHER INFORMATION: ic acid]-3-aminopropyl)
US-10-622-246-12

Query Match 39.2%; Score 20; DB 6; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYDG 5
|:|:
DB 2 VYDG 5

RESULT 15

US-10-622-246-30
; Sequence 30, Application US/10622246
; Publication No. US20060003926A1

GENERAL INFORMATION:

; APPLICANT: Rajopadhye, Milind
; APPLICANT: Edwards, D. Scott
; APPLICANT: Barrett, John A.
; APPLICANT: Carpenter, Jr., Alan P.
; APPLICANT: Harris, Thomas D.
; APPLICANT: Heminway, Stuart D.
; APPLICANT: Liu, Shuang
; APPLICANT: Prahlad, Singh R.
; TITLE OF INVENTION: PHARMACEUTICALS FOR THE IMAGING OF ANGIOGENIC DISORDERS
; FILE REFERENCE: BMS-2288

; CURRENT APPLICATION NUMBER: US/10/622,246
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 10/342,081
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 09/599,295
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 09/281,474
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/080,150
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: US 60/112,715
; PRIOR FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct

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; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(5)
; OTHER INFORMATION: cyclic amino acid
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (2)..(4)
; OTHER INFORMATION: D amino acid
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (3)..(3)
; OTHER INFORMATION: (N-[2-[[[5-[carbonyl]-2-pyridinyl]hydrazono]methyl]-benzenesulfonyl]
; OTHER INFORMATION: ic acid]-3-aminopropyl)
US-10-622-246-30

Query Match      39.2%; Score 20; DB 6; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LYDG 5
       :|||
Db      2 VYDG 5

Search completed: March 17, 2006, 22:33:30
Job time : 24 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 22:25:13 ; Search time 37 Seconds
(without alignments)
23.404 Million cell updates/sec

Title: US-09-856-812b-42
Perfect score: 51
Sequence: 1 GLYDGMHL 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 791

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:
1: piri:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	37.3	9	2 S10784	enamelin i - bovin
2	18	35.3	9	2 E28854	fibrinopeptide B -
3	18	35.3	9	2 F28854	fibrinopeptide B -
4	18	35.3	9	2 PW0002	chlorophyll a/b-bi
5	18	35.3	9	2 A37027	macrophage chemota
6	17	33.3	7	2 A11483	aspartate transami
7	17	33.3	9	2 D28854	fibrinopeptide B -
8	17	33.3	9	2 PS0253	glycine cleavage s
9	16	31.4	8	2 A28719	thymic humoral fac
10	15	29.4	6	2 PC4392	whey glycoprotein
11	15	29.4	9	2 S70334	endosperm protein,
12	15	29.4	9	2 PT0225	Ig heavy chain CRD
13	15	29.4	9	2 A56029	N-methylpurine DNA
14	14	27.5	4	2 PT0240	Ig heavy chain CRD
15	14	27.5	6	2 JN0861	peptidyl-dipeptida
16	14	27.5	6	2 PT0589	T-cell receptor be
17	14	27.5	8	2 T14906	hypothetical prote
18	14	27.5	8	2 B33099	158K exoantigen -
19	14	27.5	8	2 PT0725	T-cell receptor be
20	14	27.5	8	2 XGHUEU	urine glycopeptide
21	13.5	26.5	8	2 E47393	neuropeptide calla
22	13	25.5	7	2 A12016	formylglycinamide
23	13	25.5	8	2 PA0032	protein QA300040 -
24	13	25.5	8	2 PNO043	phosphatidylethano
25	13	25.5	8	2 S11078	glucose-6-phosphat
26	13	25.5	8	2 PT0030	inulinase (EC 3.2.
27	13	25.5	8	2 E60588	sperm-activating p
28	13	25.5	8	2 G60588	
29	13	25.5	9	2 C24180	fibrinogen beta ch

30	13	25.5	9	2 PT0270	Ig heavy chain CRD
31	13	25.5	9	2 S36850	Ig heavy chain v r
32	13	25.5	9	2 PH0108	late G1-69 protein
33	13	25.5	9	2 B39841	dextranucrase (EC
34	12	23.5	4	2 A48360	gamma subunit of p
35	12	23.5	4	2 PT0271	Ig heavy chain CRD
36	12	23.5	5	2 B61445	Leu-enkephalin - b
37	12	23.5	5	2 A61445	Met-enkephalin - b
38	12	23.5	5	2 PT0699	T-cell receptor be
39	12	23.5	5	2 PT0703	T-cell receptor be
40	12	23.5	5	2 I40698	biotin B - Citroba
41	12	23.5	6	2 PT0519	T-cell receptor be
42	12	23.5	6	2 PT0604	T-cell receptor be
43	12	23.5	6	2 PT0657	T-cell receptor be
44	12	23.5	6	2 PT0720	T-cell receptor be
45	12	23.5	7	2 A60224	Met-enkephalin-Arg

ALIGNMENTS

RESULT 1

S10784
enamelin i - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C:Accession: S10784
R:Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A>Title: Tooth 'enamelin' identified mainly as serum proteins. Major 'enamelin' is also
A:Reference number: S10780; MUID:90336641; PMID:2379503
A:Accession: S10784
A:Molecule type: protein
A:Residues: 1-9 <STR>
A:CROSS-references: UNIPROT:O7M2M7; UNIPARC:UPI000017C506
C:Keywords: enamel; phosphoprotein

Query Match 37.3%; Score 19; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 YDG 5

DB 3 YDG 5

RESULT 2

E28854
fibrinopeptide B - hamadryas baboon
C:Species: Papio hamadryas (hamadryas baboon)
C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C:Accession: E28854
R:Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A>Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropit
A:Reference number: A91973; MUID:84161822; PMID:6423621
A:Accession: E28854
A:Molecule type: protein
A:Residues: 1-9 <NAK>

A:CROSS-references: UNIPROT:P19343; UNIPARC:UPI000012A780
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf

Query Match 35.3%; Score 18; DB 2; Length 9;

Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GLYDG 5

DB 4 GLFHG 8

RESULT 3

F28854

fibrinopeptide B - gelada baboon
C:Species: Theropithecus gelada (gelada baboon)
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C:Accession: F28854
R:Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A:Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus gelada)
A:Reference number: A91973; MUID:84161822; PMID:6423621
A:Accession: F28854
A:Molecule type: protein
A:Residues: 1-9 <NAK>
A:Cross-references: UNIPROT:P19342; UNIPARC:UPI000012A789
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 35.3%; Score 18; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLYDG 5
|||
Db 4 GLFGG 8

RESULT 4
PW0002
chlorophyll a/b-binding protein 31K - green alga (Dunaliella tertiolecta) (fragment)
N:Alternate names: photosystem II light-harvesting chlorophyll 31K protein
C:Species: Dunaliella tertiolecta
C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 24-Nov-1999
C:Accession: PW0002
R:LaRoche, J.; Bennett, J.; Falkowski, P.G.
Gene 95, 165-171, 1990
A:Title: Characterization of a cDNA encoding for the 28.5-kDa LHClI apoprotein from the green alga Dunaliella tertiolecta
A:Reference number: JW0040; MUID:91065528; PMID:2249775
A:Accession: PW0002
A:Molecule type: protein
A:Residues: 1-9 <LAR>
A:Cross-references: UNIPARC:UPI0000178176
C:Superfamily: chlorophyll a/b-binding protein
C:Keywords: chloroplast; grana; light-harvesting complex; membrane adhesion; membrane protein

Query Match 35.3%; Score 18; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YDGM 7
|||
Db 3 YDEMQ 7

RESULT 5
A37027
macrophage chemotactic factor - human (fragment)
N:Alternate names: T-cell hybridoma D6-18 protein
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 09-Jul-2004
C:Accession: A37027
R:Yoshizuka, N.; Yoshimura, M.; Tsuchiya, S.; Okamoto, K.; Kobayashi, Y.; Osawa, T.
Cell. Immunol. 123, 212-225, 1989
A:Title: Macrophage chemotactic factor (MCF) produced by a human T cell hybridoma clone.
A:Reference number: A37027; MUID:89376581; PMID:2505934
A:Accession: A37027
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <YOS>
A:Cross-references: UNIPROT:Q7M4S2; UNIPARC:UPI0000157D39

Query Match 35.3%; Score 18; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLYDGM 7
|||

Db 3 GRZDGE 9

RESULT 6
A11483
aspartate transaminase (EC 2.6.1.1), mitochondrial - sheep (fragment)
N:Alternate names: aspartate aminotransferase, mitochondrial
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 20-Aug-1999
C:Accession: A11483
R:Campos-Cavieles, M.; Milstein, C.P.
Biochem. J. 147, 275-281, 1975
A:Title: The sequences of the coenzyme-binding peptide in the cytoplasmic and the mitochondrial aspartate transaminase from sheep
A:Reference number: A11483; MUID:76039441; PMID:1180894
A:Accession: A11483
A:Molecule type: protein
A:Residues: 1-7 <CAM>
A:Cross-references: UNIPARC:UPI000017C59C
C:Experimental source: liver
C:Keywords: aminotransferase; mitochondrion; phosphoprotein; pyridoxal phosphate
P:2/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 33.3%; Score 17; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLY 3
|||
Db 5 GLY 7

RESULT 7
D28854
fibrinopeptide B - olive baboon
C:Species: Papio anubis, Papio hamadryas anubis (olive baboon)
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C:Accession: D28854
R:Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A:Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus gelada)
A:Reference number: A91973; MUID:84161822; PMID:6423621
A:Accession: D28854
A:Molecule type: protein
A:Residues: 1-9 <NAK>
A:Cross-references: UNIPROT:P19344; UNIPARC:UPI000012A77F
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 33.3%; Score 17; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLYDG 5
|||
Db 4 GLFRG 8

RESULT 8
PS0253
glycine cleavage system protein H - rice (strain Nihonbare) (fragment)
N:Alternate names: glycine decarboxylase complex H protein
C:Species: Oryza sativa (rice)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: PS0253
R:Tsugita, A.
submitted to JPIID, April 1993
A:Reference number: PS0206
A:Accession: PS0253
A:Molecule type: protein
A:Residues: 1-9 <TSU>
A:Cross-references: UNIPROT:Q7M1V3; UNIPARC:UPI000017B10B

Query Match 33.3%; Score 17; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;

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Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 4 DQMEH 8
Db 5 DGLKY 9

RESULT 9
A28719
thymic humoral factor gamma-2 - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: A28719
R:Burstein, Y.; Buchner, V.; Pecht, M.; Trainin, N.
Biochemistry 27, 4066-4071, 1988
A:Title: Thymic humoral factor gamma-2: purification and amino acid sequence of an immunoglobulin heavy chain diversity and
A:Reference number: A28719; MUID:88326920; PMID:3261994
A:Accession: A28719
A:Molecule type: protein
A:Residues: 1-8 <BUR>
A:Cross-references: UNIPROT:O18787; UNIPARC:UPI000002C987

Query Match 31.4%; Score 16; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 LYDGMHL 9
Db 1 LEDGPKFL 8

RESULT 10
PC4392
whey glycoprotein WGP-88 - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 10-Nov-1997 #sequence_revision 10-Nov-1997 #text_change 07-May-1999
C:Accession: PC4392
R:Hwangbo, S.; Azuma, N.; Kurisaki, J.; Kanno, C.
Biosci. Biotechnol. Biochem. 61, 1568-1574, 1997
A:Title: Purification and characterization of novel whey glycoprotein WGP-88 which binds
A:Reference number: PC4392; MUID:97480944; PMID:9339560
A:Accession: PC4392
A:Molecule type: protein
A:Residues: 1-6 <HWA>
A:Cross-references: UNIPARC:UPI000017C58E
A:Experimental source: milk
C:Comment: This protein binds to the monoclonal antibody to PAS-4 glycoprotein.

Query Match 29.4%; Score 15; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 4 DQME 7
Db 1 DGVQ 4

RESULT 11
S70334
endosperm protein, 45K - rye (fragment)
C:Species: Secale cereale (rye)
C>Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
C:Accession: S70334
R:Rocher, A.; Calero, M.; Soriano, F.; Mendez, E.
Biochim. Biophys. Acta 1295, 13-22, 1996
A:Title: Identification of major rye secalins as coeliac immunoreactive proteins.
A:Reference number: S70327; MUID:96283789; PMID:8679669
A:Accession: S70334
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <ROC>
A:Cross-references: UNIPARC:UPI000017B135
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Query Match 29.4%; Score 15; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 YDG 5
Db 7 YEG 9

RESULT 12
PT0225
Ig heavy chain CDR3 region (clone 1-103) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0225
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0225
A:Molecule type: DNA
A:Residues: 1-9 <YAM>
A:Cross-references: UNIPARC:UPI000017C1CE
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 29.4%; Score 15; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 LYDGM 6
Db 2 MFGGM 6

RESULT 13
AS6029
N-methylpurine DNA glycosylase - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C:Accession: AS6029
R:Roy, R.; Brooks, C.; Mitra, S.
Biochemistry 33, 15131-15140, 1994
A:Title: Purification and biochemical characterization of recombinant N-methylpurine-DN-
A:Reference number: AS6029; MUID:95092772; PMID:7999773
A:Accession: AS6029
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <ROY>
A:Cross-references: UNIPROT:Q7MOH1; UNIPARC:UPI000017C703

Query Match 29.4%; Score 15; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 6 MEH 8
Db 1 MDH 3

RESULT 14
PT0240
Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0240
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0240
A:Molecule type: DNA
A:Residues: 1-4 <YAM>
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A;Cross-references: UNIPARC:UPI000017C1E2
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 27.5%; Score 14; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. NO. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YDGM 6
| |
Db 1 YPGL 4

RESULT 15
JN0861
peptidyl-dipeptidase A inhibitory peptide C111 - striped bonito
C;Species: Sarda orientalis (striped bonito)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C;Accession: JN0861
R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe
A;Reference number: JN0859; MUID:94080036; PMID:7764272
A;Accession: JN0861
A;Molecule type: protein
A;Residues: 1-6 <MAT>
A;Cross-references: UNIPARC:UPI000015677C
A;Experimental source: liver
C;Comment: The carboxyl end is essential for the protein's expression of angiotensin I-c
C;Superfamily: bradykinin-potentiating peptide
C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 27.5%; Score 14; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. NO. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLY 3
| |
Db 1 GVI 3

Search completed: March 17, 2006, 22:29:25
Job time : 40 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 22:21:53 ; Search time 225 Seconds
(without alignments)
28.221 Million cell updates/sec

Title: US-09-856-812B-42
Perfect score: 51
Sequence: 1 GLYDGMHLL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 1766

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	43.1	8	Q9P285 HUMAN	Q9P285 homo sapien
2	20	39.2	9	Q9XSL0 CAPHI	Q9XSL0 capra hircu
3	19	37.3	9	Q7M2M7 BOVIN	Q7M2M7 bos taurus
4	18	35.3	8	Q5ISY8 9CALI	Q5ISY8 norovirus s
5	18	35.3	8	Q5ISY9 9CALI	Q5ISY9 norovirus s
6	18	35.3	8	Q5ISZ2 9CALI	Q5ISZ2 norovirus s
7	18	35.3	8	Q5ISZ4 9CALI	Q5ISZ4 norovirus s
8	18	35.3	8	Q5ISZ6 9CALI	Q5ISZ6 norovirus s
9	18	35.3	8	Q5IT02 9CALI	Q5IT02 norovirus s
10	18	35.3	9	FIBB PAPHA	P19343 papio hamad
11	18	35.3	9	FIBB THEGE	P19342 theropithec
12	18	35.3	9	Q7M4S2 HUMAN	Q7M4S2 homo sapien
13	17	33.3	8	DY81 LIMIN	P82079 limnodynast
14	17	33.3	8	Q7OY68 9LAMI	Q7OY68 prostanther
15	17	33.3	9	FIBB PAPAN	P19344 papio anubi
16	17	33.3	9	Q7OYA2 9LAMI	Q7OYA2 alvesia ros
17	17	33.3	9	Q7MIV3 ORYSA	Q7MIV3 oryza sativ
18	16	31.4	9	Q712A6 SINOSB	Q712A6 sinorhizobi
19	15	29.4	7	ALL7 CYDPO	P82158 cydia pomon
20	15	29.4	8	Q9TWH6 9ANNE	Q9TWH6 perinereis
21	15	29.4	8	P83158 ANASL	P83158 anabaena sp
22	15	29.4	8	Q5ISZ8 9CALI	Q5ISZ8 norovirus s
23	15	29.4	9	NSK1 SARBU	P41492 sarcophaga
24	15	29.4	9	RB842 LITRU	P82075 litorea rub
25	15	29.4	9	Q67AQ7 HUMAN	Q67AQ7 homo sapien
26	15	29.4	9	Q70SM2 HUMAN	Q70SM2 homo sapien
27	15	29.4	9	Q7M0H1 MOUSE	Q7M0H1 mus musculu
28	14	27.5	7	MNP1 LEPEDE	P42984 leptinotars
29	14	27.5	7	Q99182 9SMEG	Q99182 gnatholebia
30	14	27.5	8	GLUR HUMAN	P02729 homo sapien
31	14	27.5	8	Q80H91 9PARA	Q80H91 newcastle d

32 14 27.5 9 2 Q7S182 NEUCR Q7S182 neurospora
33 14 27.5 9 2 Q67AR4 HUMAN Q67AR4 homo sapien
34 14 27.5 9 2 Q67AR6 HUMAN Q67AR6 homo sapien
35 14 27.5 9 2 Q67AR7 HUMAN Q67AR7 homo sapien
36 14 27.5 9 2 Q67AT1 HUMAN Q67AT1 homo sapien
37 14 27.5 9 2 Q67AT2 HUMAN Q67AT2 homo sapien
38 14 27.5 9 2 Q937H9 9ENTR Q937H9 enterobact
39 14 27.5 9 2 Q937J8 9COLI Q937J8 escherichia
40 13.5 26.5 8 1 ALL5 CALVO P41841 calliphora
41 13 25.5 7 2 Q8XMS9 9ENTR Q8XMS9 enterobact
42 13 25.5 7 2 Q8K3H6 RAT Q8K3H6 rattus norv
43 13 25.5 8 1 ALL5 CYDPO Q82156 cydia pomon
44 13 25.5 8 1 FUSO FUSO P81010 fusarium so
45 13 25.5 8 2 Q7M4U4 ASPFFI Q7M4U4 aspergillus

ALIGNMENTS

RESULT 1
Q9P285 HUMAN
ID Q9P285 HUMAN PRELIMINARY; PRT; 8 AA.
AC Q9P285;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE Clotting factor VIII (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Shibata M., Shima M., Morichika S., Yoshioka A.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040872; BAA94312.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 866 MW; 1C16987AAB05BDD3 CRC64;

Query Match 43.1%; Score 22; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 DQME 7
Db 5 DQME 8

RESULT 2
Q9XSL0 CAPHI
ID Q9XSL0 CAPHI PRELIMINARY; PRT; 9 AA.
AC Q9XSL0;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Alpha 2-casein (Fragment).
GN Name=can182;
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=21313038; PubMed=11419340;
RA Ramunno L., Longobardi E., Pappalardo M., Rando A., Di Gregorio P.,
Cosenza G., Mariani P., Pastore N., Masina P.;
RT "An allele associated with a non detectable amount of a2 casein in
goat milk.";
RL Anim. Genet. 32:19-26(2001).

```
DR EMBL; AJ238475; CAB44298.1; -; Genomic DNA.
FT CHAIN <1 >9 alpha s2-Casein.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1047 MW; AAA2A5A5B051EB16 CRC64;

Query Match 39.2%; Score 20; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 MEHL 9
Db 2 MEHI 5

RESULT 3
Q7M2M7 BOVIN PRELIMINARY; PRT; 9 AA.
AC Q7M2M7
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Enamelin 1 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=90336641; PubMed=2379503;
RA Strach E., Glimcher M.J.;
RT "tooth 'enamelins' identified mainly as serum proteins. Major
RL Eur. J. Biochem. 191:47-56(1990).
DR PIR; S10784; S10784.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1036 MW; 2D867DD9C87ABB47 CRC64;

Query Match 37.3%; Score 19; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YDG 5
Db 3 YDG 5

RESULT 4
Q5ISY8_9CALI PRELIMINARY; PRT; 8 AA.
AC Q5ISY8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE RNA polymerase (Fragment).
OS Norovirus Songkhla-37/Thailand.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Norovirus.
OX NCBI_TaxID=300737;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15623956;
RA Guntapong R., Hansman G.S., Oka T., Ogawa S., Kageyama T.,
RA Pongsuwan Y., Katayama K.;
RT "Norovirus and sapovirus infections in Thailand.";
RL Jpn. J. Infect. Dis. 57:276-278(2004).
DR EMBL; AY646876; AAV69607.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 8 AA; 908 MW; 8502C87AAB1452C9 CRC64;

Query Match 35.3%; Score 18; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGME 7
Db 5 DGVE 8

RESULT 5
Q5ISY9_9CALI PRELIMINARY; PRT; 8 AA.
AC Q5ISY9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE RNA polymerase (Fragment).
OS Norovirus Songkhla-36/Thailand.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Norovirus.
OX NCBI_TaxID=300736;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15623956;
RA Guntapong R., Hansman G.S., Oka T., Ogawa S., Kageyama T.,
RA Pongsuwan Y., Katayama K.;
RT "Norovirus and sapovirus infections in Thailand.";
RL Jpn. J. Infect. Dis. 57:276-278(2004).
DR EMBL; AY646875; AAV69605.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 908 MW; 8502C87AAB1452C9 CRC64;

Query Match 35.3%; Score 18; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGME 7
Db 5 DGVE 8

RESULT 6
Q5ISZ2_9CALI PRELIMINARY; PRT; 8 AA.
AC Q5ISZ2;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE RNA polymerase (Fragment).
OS Norovirus Songkhla-34/Thailand.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Norovirus.
OX NCBI_TaxID=300735;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15623956;
RA Guntapong R., Hansman G.S., Oka T., Ogawa S., Kageyama T.,
RA Pongsuwan Y., Katayama K.;
RT "Norovirus and sapovirus infections in Thailand.";
RL Jpn. J. Infect. Dis. 57:276-278(2004).
DR EMBL; AY646874; AAV69603.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 908 MW; 8502C87AAB1452C9 CRC64;

Query Match 35.3%; Score 18; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGME 7
Db 5 DGVE 8
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RESULT 7
Q5ISZ4_9CALI
ID Q5ISZ4_9CALI PRELIMINARY; PRT; 8 AA.
AC Q5ISZ4_
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DE RNA polymerase (Fragment).
OS Norovirus Sakaao-61/Thailand.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Norovirus.
OX NCBI_TaxID=300734;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sakaao-61/Thailand;
RX PubMed=15623956;
RA Guntapong R., Hansman G.S., Oka T., Ogawa S., Kageyama T.,
RA Pongsuwan Y., Katayama K.;
RA "Norovirus and sapovirus infections in Thailand.";
RL Jpn. J. Infect. Dis. 57:276-278(2004).
DR EMBL; AV646873; AAV69600.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 8 AA; 908 MW; 8502C87AAB1452C9 CRC64;

Query Match 35.3%; Score 18; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGME 7
Db |||
5 DGVE 8

RESULT 8
Q5ISZ6_9CALI
ID Q5ISZ6_9CALI PRELIMINARY; PRT; 8 AA.
AC Q5ISZ6_
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DE RNA polymerase (Fragment).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Norovirus.
OX NCBI_TaxID=300733;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sakaao-57/Thailand;
RX PubMed=15623956;
RA Guntapong R., Hansman G.S., Oka T., Ogawa S., Kageyama T.,
RA Pongsuwan Y., Katayama K.;
RA "Norovirus and sapovirus infections in Thailand.";
RL Jpn. J. Infect. Dis. 57:276-278(2004).
DR EMBL; AV646872; AAV69599.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 8 AA; 908 MW; 8502C87AAB1452C9 CRC64;

Query Match 35.3%; Score 18; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGME 7
Db |||
5 DGVE 8

RESULT 9
Q5IT02_9CALI
ID Q5IT02_9CALI PRELIMINARY; PRT; 8 AA.
AC Q5IT02_
DT 10-MAY-2005 (TReMBLrel. 30, Created)
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DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE RNA polymerase (Fragment).
OS Norovirus Sakaao-52/Thailand.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Norovirus.
OX NCBI_TaxID=300730;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sakaao-52/Thailand;
RX PubMed=15623956;
RA Guntapong R., Hansman G.S., Oka T., Ogawa S., Kageyama T.,
RA Pongsuwan Y., Katayama K.;
RA "Norovirus and sapovirus infections in Thailand.";
RL Jpn. J. Infect. Dis. 57:276-278(2004).
DR EMBL; AY646869; AAV69593.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 8 AA; 908 MW; 8502C87AAB1452C9 CRC64;

Query Match 35.3%; Score 18; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGME 7
Db |||
5 DGVE 8

RESULT 10
FIBB_PAPHA
ID FIBB_PAPHA STANDARD; PRT; 9 AA.
AC FIBB_PAPHA
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN Name=FGB;
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecinae; Papio.
OX NCBI_TaxID=99557;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RA "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada); their amino acid sequences and evolutionary
RT rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978(1983).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: Heterohexamer; disulfide linked. Contains 2 sets of 3
CC nonidentical chains (alpha, beta and gamma). The 2 heterotrimers
CC are in head to head conformation with the N-termini in a small
CC central domain (by similarity).
CC -!- DOMAIN: A long coiled coil structure formed by 3 polypeptide
CC chains connects the central module to the C-terminal domains
CC (distal modules). The long C-terminal ends of the alpha chains
CC fold back, contributing a fourth strand to the coiled coil
CC structure.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
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DR PIR; E28854; E28854.
 DR InterPro; IPR002181; Fibrinogen C.
 DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
 KW Blood coagulation; Coiled coil; Direct protein sequencing; Plasma.
 FT PEPTIDE 1 9 Fibrinopeptide B.
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1057 MW; DDFE71E9C7287B06 CRC64;

Query Match 35.3%; Score 18; DB 1; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLYDGG 5
 ||:|
 Db 4 GLFHGG 8

RESULT 11
 FIBB_THEGE STANDARD; PRT; 9 AA.
 AC F19342;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-2005 (Rel. 46, Last annotation update)
 DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
 GN Name=FGB;
 OS Theropithecus gelada (Gelada baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecidae; Cercopithecinae; Theropithecus.
 OX NCBI_TaxID=9565;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=84161822; PubMed=6423621;
 RA Nakamura S., Takenaka O., Takahashi K.;
 RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
 RT and Theropithecus gelada): their amino acid sequences and evolutionary
 RT rates and a molecular phylogeny for the baboons.";
 RL J. Biochem. 94:1973-1978 (1983).
 CC -!- FUNCTION: Fibrinogen has a double function: Yielding monomers that
 CC polymerize into fibrin and acting as a cofactor in platelet
 CC aggregation.
 CC -!- SUBUNIT: Heterohexamer; disulfide linked. Contains 2 sets of 3
 CC nonidentical chains (alpha, beta and gamma). The 2 heterotrimers
 CC are in head to head conformation with the N-termini in a small
 CC central domain (by similarity).
 CC -!- DOMAIN: A long coiled coil structure formed by 3 polypeptide
 CC chains connects the central node to the C-terminal domains
 CC (distal nodes). The long C-terminal ends of the alpha chains
 CC fold back, contributing a fourth strand to the coiled coil
 CC structure.
 CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,
 CC and thus exposes the N-terminal polymerization sites responsible
 CC for the formation of the soft clot.
 CC -----
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 CC removed.
 CC -----
 CC PIR; F28854; F28854.
 DR InterPro; IPR002181; Fibrinogen C.
 DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
 KW Blood coagulation; Coiled coil; Direct protein sequencing; Plasma.
 FT PEPTIDE 1 9 Fibrinopeptide B.
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 977 MW; DDFE7879C7287B06 CRC64;

Query Match 35.3%; Score 18; DB 1; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLYDGG 5
 ||:|
 Db 4 GLFHGG 8

RESULT 12
 Q7M4S2 HUMAN PRELIMINARY; PRT; 9 AA.
 AC Q7M4S2;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Macrophage chemotactic factor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=89376581; PubMed=2505934;
 RA Yoshizuka N., Yoshimura M., Tsuchiya S., Okamoto K., Kobayashi Y.,
 RA Osawa T.;
 RT "Macrophage chemotactic factor (MCF) produced by a human T cell
 RT hybridoma clone.";
 RL Cell. Immunol. 123:212-225 (1989).
 DR PIR; A37027; A37027.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1048 MW; 44CEB87AB9940877 CRC64;

Query Match 35.3%; Score 18; DB 2; Length 9;
 Best Local Similarity 57.1%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLYDGG 7
 ||:|
 Db 3 GRZDGE 9

RESULT 13
 DYS1 LIMIN STANDARD; PRT; 8 AA.
 AC P82079;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Dynastin-1.
 OS Limnodynastes interioris (Giant banjo frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Limnodynastinae; Limnodynastes.
 OX NCBI_TaxID=30362;
 RN [1]
 RP PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-Tibial gland;
 RA Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structure of the dynastins from
 RT the banjo frogs Limnodynastes interioris, Limnodynastes dumerilii and
 RT Limnodynastes terraereginae.";
 RL Aust. J. Chem. 46:833-842 (1993).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin glands.
 CC -!- MASS SPECTROMETRY: MW=729; METHOD=FAB; RANGE=1-8; NOTE=Ref.1.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC Direct protein sequencing.

SEQ	SEQUENCE	8 AA; 729 MW; 7C28772865B72728 CRC64;
Query Match	33.3%; Score 17; DB 1; Length 8;	
Best Local Similarity	50.0%; Pred. No. 2.2e+06;	
Matches	3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
QY	1 GLYDGM 6	
DB	1 GLLSGL 6	
RESULT 14		
Q70Y68_9LAMI		
ID	Q70Y68_9LAMI PRELIMINARY; PRT; 8 AA.	
AC	Q70Y68;	
DT	05-JUL-2004 (TrEMBLrel. 27, Created)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	
DE	Ribosomal protein (Fragment).	
GN	Name=rp16;	
OS	Prosthanthera nivea (snowy mintbush).	
OG	Chloroplast.	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;	
OC	Lamiales; Lamiales; Lamiaceae; Prostantheroideae; Westringiaceae;	
OC	Prostanthera.	
OX	NCBI_TaxID=38863;	
RP	[1] RN	
RP	NUCLEOTIDE SEQUENCE.	
RX	PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;	
RA	Faton A., Springate D.A., Suddle S., Otieno D., Grayer R., Harley M.M.,	
RA	Willis F., Simmonds M.S.J., Powell M.P., Savolainen V.;	
RT	"Phylogeny and evolution of basilias and allies (Oclmeae, Labiatae)	
RT	based on three plastid DNA regions.";	
RL	Mol. Phylogenet. Evol. 31:277-299(2004).	
DR	EMBL; AJ505403; CAD45523.1; -; Genomic DNA.	
DR	GO; GO:0003735; F:structural constituent of ribosome; IEA.	
KW	Ribosomal protein.	
FT	NON_TER 1	
FT	NON_TER 8	
FT	NON_TER 8	
SEQ	SEQUENCE 8 AA; 838 MW; C821F2C058786415 CRC64;	
Query Match	33.3%; Score 17; DB 2; Length 8;	
Best Local Similarity	60.0%; Pred. No. 2.2e+06;	
Matches	3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
QY	5 GMEHL 9	
DB	4 GIVHL 8	
RESULT 15		
FIBB_PAPAN		
ID	FIBB_PAPAN STANDARD; PRT; 9 AA.	
AC	P19344;	
DT	01-NOV-1990 (Rel. 16, Created)	
DT	01-NOV-1990 (Rel. 16, Last sequence update)	
DT	01-FEB-2005 (Rel. 46, Last annotation update)	
DE	Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).	
GN	Name=FGB;	
OS	Papio anubis (Olive baboon).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
OC	Cercopithecoidea; Cercopithecinae; Papio.	
OX	NCBI_TaxID=9555;	
RP	[1] RN	
RP	PROTEIN SEQUENCE.	
RX	MEDLINE=84161822; PubMed=6423621;	
RA	Nakamura S., Takenaka O., Takahashi K.;	
RT	"Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,	
RT	and Theropithecus gelada): their amino acid sequences and evolutionary	
RT	rates and a molecular phylogeny for the baboons.";	
RL	J. Biochem. 94:1978-1978(1983).	

SEQ	SEQUENCE	8 AA; 729 MW; 7C28772865B72728 CRC64;
Query Match	33.3%; Score 17; DB 1; Length 8;	
Best Local Similarity	50.0%; Pred. No. 2.2e+06;	
Matches	3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
QY	1 GLYDGM 6	
DB	1 GLLSGL 6	
RESULT 14		
Q70Y68_9LAMI		
ID	Q70Y68_9LAMI PRELIMINARY; PRT; 8 AA.	
AC	Q70Y68;	
DT	05-JUL-2004 (TrEMBLrel. 27, Created)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	
DE	Ribosomal protein (Fragment).	
GN	Name=rp16;	
OS	Prosthanthera nivea (snowy mintbush).	
OG	Chloroplast.	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;	
OC	Lamiales; Lamiales; Lamiaceae; Prostantheroideae; Westringieae;	
OC	Prostanthera.	
OX	NCBI_TaxID=38863;	
RP	[1] RN	
RP	NUCLEOTIDE SEQUENCE.	
RX	PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;	
RA	Faton A., Springate D.A., Suddle S., Otieno D., Grayer R., Harley M.M.,	
RA	Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;	
RT	"Phylogeny and evolution of basilias and allies (Oclmeae, Labiatae)	
RT	based on three plastid DNA regions.";	
RL	Mol. Phylogenet. Evol. 31:277-299(2004).	
DR	EMBL; AJ505403; CAD45523.1; -; Genomic DNA.	
DR	GO; GO:0003735; F:structural constituent of ribosome; IEA.	
KW	Ribosomal protein.	
FT	NON_TER 1	
FT	NON_TER 8	
FT	NON_TER 8	
SEQ	SEQUENCE 8 AA; 838 MW; C821F2C058786415 CRC64;	
Query Match	33.3%; Score 17; DB 2; Length 8;	
Best Local Similarity	60.0%; Pred. No. 2.2e+06;	
Matches	3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
QY	5 GMEHL 9	
DB	4 GIVHL 8	
RESULT 15		
FIBB_PAPAN		
ID	FIBB_PAPAN STANDARD; PRT; 9 AA.	
AC	P19344;	
DT	01-NOV-1990 (Rel. 16, Created)	
DT	01-NOV-1990 (Rel. 16, Last sequence update)	
DT	01-FEB-2005 (Rel. 46, Last annotation update)	
DE	Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).	
GN	Name=FGB;	
OS	Papio anubis (Olive baboon).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
OC	Cercopithecoidea; Cercopithecinae; Papio.	
OX	NCBI_TaxID=9555;	
RP	[1] RN	
RP	PROTEIN SEQUENCE.	
RX	MEDLINE=84161822; PubMed=6423621;	
RA	Nakamura S., Takenaka O., Takahashi K.;	
RT	"Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,	
RT	and Theropithecus gelada): their amino acid sequences and evolutionary	
RT	rates and a molecular phylogeny for the baboons.";	
RL	J. Biochem. 94:1978-1978(1983).	

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OM protein - protein search, using sw model

Run on: March 17, 2006, 22:33:19 ; Search time 188 Seconds
(without alignments)
862.398 Million cell updates/sec

Title: US-09-856-812B-1
Perfect score: 369
Sequence: 1 MPAPKRCRMPEELQSQS.....DTTAMASASSSATGFSFSYPE 369

Scoring table: {OLIGO }
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003s.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	369	100.0	369	3	AAY71485 Human MAG
2	369	100.0	369	4	AAB80297 Human pro
3	369	100.0	369	6	ABR48215 Human bla
4	369	100.0	369	6	ABU56516 Lung can
5	362	98.1	383	8	ABO58424 Human gen
6	29	7.9	82	8	ABO59333 Human gen
7	29	7.9	151	8	ABO59726 Human gen
8	29	7.9	315	3	AAB08735 Amino aci
9	29	7.9	315	6	ABU56684 Lung can
10	29	7.9	315	6	ABU56484 Lung can
11	29	7.9	315	6	ADA83772 Human MAG
12	29	7.9	315	6	ABU04413 Human exp
13	29	7.9	315	6	ABU04425 Human exp
14	29	7.9	315	6	ABU04416 Human exp
15	29	7.9	315	6	ABU04421 Human exp
16	29	7.9	315	6	ABU04456 Human exp
17	29	7.9	315	6	ABU04454 Human exp
18	29	7.9	315	6	ABO25122 Human MAG
19	29	7.9	315	7	ADN39048 Cancer/an
20	28	7.6	28	2	AAW54400 MAGE-10 t
21	28	7.6	28	3	AAV99875 Human MAG
22	26	7.0	317	2	AAV06998 MAGE-4 pr
23	26	7.0	317	6	ABU56545 Lung can
24	26	7.0	317	6	ADA83770 Human MAG

25	26	7.0	317	8	ADO43756	Ado43756 Human MAG
26	26	7.0	317	8	ADO59164	Ado59164 Human MAG
27	17	4.6	30	5	AAU85060	Aau85060 Human MAG
28	17	4.6	105	8	ABO57647	Abos7647 Human gen
29	17	4.6	119	8	ADP80501	Adp80501 Human epi
30	17	4.6	126	2	AAW16330	Aaw16330 Human MAG
31	17	4.6	155	8	ABO59360	Abos9360 Human gen
32	17	4.6	221	4	AAE10673	Aae10673 Human mel
33	17	4.6	221	6	ABU04432	Abu04432 Human exp
34	17	4.6	282	5	AAU98924	Aau98924 Human mel
35	17	4.6	282	5	AAU98925	Aau98925 Human mel
36	17	4.6	292	4	AAW18492	Aaw18492 Peptide #
37	17	4.6	292	4	AAW30960	Aaw30960 Peptide #
38	17	4.6	292	4	ABB22826	Abb22826 Protein #
39	17	4.6	299	7	ADC35109	Adc35109 Human bre
40	17	4.6	314	2	AAW01720	Aaw01720 The MAGE-
41	17	4.6	314	3	AAW02565	Aaw02565 Human MAG
42	17	4.6	314	4	AAW02080	Aaw02080 MAGE-12 h
43	17	4.6	314	4	AAW84515	Aaw84515 MAGE3 (me
44	17	4.6	314	4	AAW99725	Aaw99725 MAGE2 (me
45	17	4.6	314	4	AAW12997	Aaw12997 Human MAG

ALIGNMENTS

RESULT 1
AAY71485
ID AAY71485 standard; protein; 369 AA.
XX AC AAY71485;
XX DT 12-OCT-2000 (first entry)
XX DE Human MAGE-A10 protein.
XX KW MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
KW immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
KW cancer; TNF; tumour necrosis factor; cytostatic.
XX OS Homo sapiens.
XX PN WO200032769-A2.
XX PD 08-JUN-2000.
XX PF 26-NOV-1999; 99WO-IB002018.
XX PR 27-NOV-1999; 98GB-00026143.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
WPI; 2000-412317/35.
XX N-PSDB; AAD01311, AAD01312, AAD01313.
XX PT Novel polypeptides expressed in tumor cells useful for treating cancers
PT have an ability to complex with a major histocompatibility complex
PT molecule and comprises a specific unbroken amino acid sequence.
XX PS Claim 1; Fig 7; 80pp; English.
XX CC The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
CC decapeptide sequences, that function as tumour rejection antigens (TRAs).
CC These peptides are capable of forming a complex with major
CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
CC Antigen), that are recognised by T-lymphocytes and elicit an immune
CC response from cytolytic T-lymphocytes (CTL). They function as an immune
CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
CC therapy and diagnosis of tumours and are effective in controlling or
CC preventing tumour growth. The present sequence is the human MAGE-A10

CC protein, comprising nonapeptides and decapeptides, that serve as tumour
CC rejection antigens (TAA). The novel TAA encoded by MAGE-A10 is
CC identified using melanoma cell line (LB1751-MEL), stimulated by
CC autologous CTL clone (447A/5) to produce TNF (tumour necrosis factor).
CC Expression of MAGE-A10 has been detected in a variety of tumours like
CC melanomas, carcinomas of the head and neck, bladder and prostate,
CC myelomas and lung cancer. The only normal tissue expressing MAGE-A10 is
CC the testis
XX
XX
SQ Sequence 369 AA;

Query Match 100.0%; Score 369; DB 3; Length 369;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAKRCRCMPEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSFPSSPSSSSSS 60
DB 1 MPRAKRCRCMPEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSFPSSPSSSSSS 60
QY 61 SSCYPLIPSTPEVSADDETPNPQSAQIACSSPSVVASLPLDQSDGSSSOKESPSTL 120
DB 61 SSCYPLIPSTPEVSADDETPNPQSAQIACSSPSVVASLPLDQSDGSSSOKESPSTL 120
QY 121 QVLPDSESLPRSEIDKVTDLVQFLLFKYQMKPEITKAEILSVIKNYEDHPFLFSEAS 180
DB 121 QVLPDSESLPRSEIDKVTDLVQFLLFKYQMKPEITKAEILSVIKNYEDHPFLFSEAS 180
QY 181 ECMLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMGLSDVQSMKPTGLILILSIIFIEGYC 240
DB 181 ECMLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMGLSDVQSMKPTGLILILSIIFIEGYC 240
QY 241 TPEEVIWEALNMWGLYDGMHEHLYGEPKLLTQDWQVQENLYEYRQVPGSDPARYEFLWGP 300
DB 241 TPEEVIWEALNMWGLYDGMHEHLYGEPKLLTQDWQVQENLYEYRQVPGSDPARYEFLWGP 300
QY 301 RAHAETKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEERAQDRIATTTDDTTAMASASSS 360
DB 301 RAHAETKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEERAQDRIATTTDDTTAMASASSS 360
QY 361 ATGSFSYPE 369
DB 361 ATGSFSYPE 369

RESULT 2
ID AAB80297
XX AAB80297 standard; protein; 369 AA.
XX
XX AAB80297;
XX
XX
XX Human prostate cancer antigen #25.
XX
XX Immunosuppressive; neutrotropic; neuroprotective; antiviral; vulnery;
XX antineoplastic; antibacterial; antifungal; antiparasitic; cardiac;
XX immune vulsant; cardiovascular disorder; neurological disease;
XX infection; cancer; cytostatic; antiarthritic; antitumouric;
XX antiasthmatic; anticonvulsant; vasotropic; vulnery; human;
XX secreted protein; prostate cancer antigen.
XX
XX Homo sapiens.
XX
XX WO200107476-A1.
XX
XX 01-FEB-2001.
XX
XX 20-JUL-2000; 2000WO-US019666.
XX
XX 21-JUL-1999; 99US-0144972P.
XX 13-AUG-1999; 99US-0148681P.
XX 17-AUG-1999; 99US-0149173P.
XX 06-OCT-1999; 99US-0158004P.

PR 05-APR-2000; 2000US-0194689P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
XX Rosen CA, Birse C;
XX PI
XX WPI; 2001-138554/14.
DR N-PSDB; AAF72765.
XX
XX New nucleic acid molecule encoding human secreted prostate cancer
PT antigens, useful for the diagnosis and treatment of disorders such as
PT cancer, leukemia and autoimmune disease.
XX
XX Claim 11; Page 399-400; 433pp; English.

XX The present invention relates to human secreted prostate cancer antigen
CC coding sequences (AAF72741-AAF72789) and proteins (AAB80273-AAB80321).
CC The coding sequences and proteins of the present invention are useful for
CC preventing, treating or ameliorating a medical condition; and for the
CC diagnosis and treatment of diseases and disorders. Diseases and disorders
CC that can be diagnosed and treated include (auto)immune diseases (e.g.
CC graft versus host disease and rheumatoid arthritis), inflammatory and
CC allergic disorders (e.g. asthma), hyperproliferative disorders (e.g.
CC cancers and leukemias), cardiovascular disorders (e.g. heart attacks and
CC arrhythmias), cerebrovascular disorders (e.g. stroke), arterial occlusive
CC disorders (e.g. arteriosclerosis), angiogenesis related disorders (e.g.
CC retinopathy and keloid scars), ocular disorders (e.g. glaucoma),
CC neurological disorders (e.g. Alzheimer's, Parkinson's disease, epilepsy
CC and Creutzfeld-Jakob disease) and infections caused by bacteria, fungi,
CC viruses or parasites. They may also be useful for wound healing,
CC epithelial cell proliferation, supporting cell culture, tissue
CC regeneration, birth control and as a food additive or preservative

SQ Sequence 369 AA;

Query Match 100.0%; Score 369; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAKRCRCMPEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSFPSSPSSSSSS 60
DB 1 MPRAKRCRCMPEDLQSQSETQGLEGAQAPLAVEEDASSSTSTSSFPSSPSSSSSS 60
QY 61 SSCYPLIPSTPEVSADDETPNPQSAQIACSSPSVVASLPLDQSDGSSSOKESPSTL 120
DB 61 SSCYPLIPSTPEVSADDETPNPQSAQIACSSPSVVASLPLDQSDGSSSOKESPSTL 120
QY 121 QVLPDSESLPRSEIDKVTDLVQFLLFKYQMKPEITKAEILSVIKNYEDHPFLFSEAS 180
DB 121 QVLPDSESLPRSEIDKVTDLVQFLLFKYQMKPEITKAEILSVIKNYEDHPFLFSEAS 180
QY 181 ECMLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMGLSDVQSMKPTGLILILSIIFIEGYC 240
DB 181 ECMLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMGLSDVQSMKPTGLILILSIIFIEGYC 240
QY 241 TPEEVIWEALNMWGLYDGMHEHLYGEPKLLTQDWQVQENLYEYRQVPGSDPARYEFLWGP 300
DB 241 TPEEVIWEALNMWGLYDGMHEHLYGEPKLLTQDWQVQENLYEYRQVPGSDPARYEFLWGP 300
QY 301 RAHAETKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEERAQDRIATTTDDTTAMASASSS 360
DB 301 RAHAETKMSLLKFLAKVNGSDPRSPFLWYEEALKDEEERAQDRIATTTDDTTAMASASSS 360
QY 361 ATGSFSYPE 369
DB 361 ATGSFSYPE 369

RESULT 3
ABR48215
ID ABR48215 standard; protein; 369 AA.
XX

AC ABR48215;
XX 12-JUN-2003 (first entry)
XX Human bladder cancer associated protein sequence SEQ ID NO:149.
DE Human; bladder cancer; cytostatic; gene therapy; vaccine.
KW Homo sapiens.
OS WO2003003906-A2.
XX 16-JAN-2003.
XX 03-JUL-2002; 2002WO-US021338.
XX 03-JUL-2001; 2001US-0302814P.
PR 03-AUG-2001; 2001US-0310099P.
PR 08-NOV-2001; 2001US-0343705P.
PR 13-NOV-2001; 2001US-0350666P.
PR 12-APR-2002; 2002US-0372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX Mack DH, Aziz N;
PI WPI; 2003-201532/19.
XX N-PSDB; ACC51029.
XX Detecting a bladder cancer-associated transcript in a cell from a
PT patient, comprises contacting a biological sample from the patient with a
PT bladder cancer-associated polynucleotide or antibody.
XX Claim 10; Page 282; 307pp; English.
XX The present invention describes a method for detecting a bladder cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with a polynucleotide
CC that selectively hybridizes to a sequence that is 80 % identical to a
CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
CC encode the human bladder cancer-associated proteins given in ABR48146 to
CC ABR48242). Bladder cancer-associated sequences from the present invention
CC have cytostatic activities, and can be used in antisense gene therapy and
CC in vaccine production. The method can be used for detecting a bladder
CC cancer-associated transcript in a cell from a patient. The method is
CC useful in diagnosing or treating bladder cancer and in screening for
CC compounds that modulate bladder cancer, such as hormones or antibodies.
CC The nucleic acid molecules from the present invention may be used in
CC various screening and diagnostic methods, and for gene therapy, vaccine
CC and/or antisense/inhibition applications
XX Sequence 369 AA;
Query Match 100.0%; Score 369; DB 6; Length 369;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAKRCMPDEELQSQSETQGLGAQAPLAVEDASSSTSTSSPPSPSSSSSS 60
DB 1 MPRAKRCMPDEELQSQSETQGLGAQAPLAVEDASSSTSTSSPPSPSSSSSS 60
QY 61 SSCYPLIPSTPEVSADDETPNPQSAQACSSPSVVASLPLDQSDGSSSQKESPS 120
DB 61 SSCYPLIPSTPEVSADDETPNPQSAQACSSPSVVASLPLDQSDGSSSQKESPS 120
QY 121 QVLPDSESLPRSEIDKVTDLVQFLLFYQKMEPTTKABILESVKNVEDHPPLFSEAS 180
DB 121 QVLPDSESLPRSEIDKVTDLVQFLLFYQKMEPTTKABILESVKNVEDHPPLFSEAS 180
QY 181 ECKMLVFGIDVKEVDPDTHGSHFVLVSLGLTYDGMISDVQSMPTKGLILILSIIFIEGVC 240
DB 181 ECKMLVFGIDVKEVDPDTHGSHFVLVSLGLTYDGMISDVQSMPTKGLILILSIIFIEGVC 240

QY 241 TPEEVIWEALNMGLYDGMHEHLIYGEPRKLLTQDWQVQENYLYRQVPGSDPARYEFLWGP 300
DB 241 TPEEVIWEALNMGLYDGMHEHLIYGEPRKLLTQDWQVQENYLYRQVPGSDPARYEFLWGP 300
QY 301 RAHAERIKWMSLLKFLAKVNGSDPRSPFLWYBEALKDEEERAQDRITATDDTTAMASASSS 360
DB 301 RAHAERIKWMSLLKFLAKVNGSDPRSPFLWYBEALKDEEERAQDRITATDDTTAMASASSS 360
QY 361 ATGSFSYPE 369
DB 361 ATGSFSYPE 369
RESULT 4
ABUS6516
ID ABUS6516 standard; protein; 369 AA.
XX
AC ABUS6516;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polypeptide #109.
XX
KW Lung cancer-associated polypeptide; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
FN WO200286443-A2.
XX
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US012476.
XX
PR 18-APR-2001; 2001US-0284770P.
PR 10-MAY-2001; 2001US-0290492P.
PR 09-NOV-2001; 2001US-0339245P.
PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334370P.
PR 12-APR-2002; 2002US-0372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
DR WPI; 2003-093161/08.
DR N-PSDB; ABX76240.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
PS Claim 27; Page 276-277; 453pp; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridizes
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful

CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
CC invention
XX
SQ Sequence 369 AA;
Query Match 100.0%; Score 369; DB 6; Length 369;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPAPKRCMPEDLQSQSETQGLEGAQAPLAVERDASSSTSTSSFFSPSSSSSS 60
DB 1 MPAPKRCMPEDLQSQSETQGLEGAQAPLAVERDASSSTSTSSFFSPSSSSSS 60
QY 61 SSCYPLIPSTPEVSADDETPNPQSAQIACSSPSVVASLPLDQSDGSSSQKEESPSTL 120
DB 61 SSCYPLIPSTPEVSADDETPNPQSAQIACSSPSVVASLPLDQSDGSSSQKEESPSTL 120
QY 121 QVLPDSESLPRSEIDKVTDLVQFLFKYQMKPEPTKAILLESVIKNYEDHPPLFSEAS 180
DB 121 QVLPDSESLPRSEIDKVTDLVQFLFKYQMKPEPTKAILLESVIKNYEDHPPLFSEAS 180
QY 181 ECMLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMLSDVQSMPTGILLILSIIFIEGYC 240
DB 181 ECMLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMLSDVQSMPTGILLILSIIFIEGYC 240
QY 241 TPEEVIWEALNMWGLYDGMHEHLIYGEPRKLLTQDWQVQENYLEYRQVPGSDPARYEFLWGP 300
DB 241 TPEEVIWEALNMWGLYDGMHEHLIYGEPRKLLTQDWQVQENYLEYRQVPGSDPARYEFLWGP 300
QY 301 RAHAERKMSLLKFLAKVNGSDPRSFPPLWYEALKDEEERAQDRIATDDTTAMASASS 360
DB 301 RAHAERKMSLLKFLAKVNGSDPRSFPPLWYEALKDEEERAQDRIATDDTTAMASASS 360
QY 361 ATGSPSYPE 369
DB 361 ATGSPSYPE 369
RESULT 5
ID ABO58424 standard; protein; 383 AA.
XX ABO58424;
AC ABO58424;
XX
DT 29-JUL-2004 (first entry)
XX Human genome derived single exon protein #4658.
XX Human; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
XX Homo sapiens.
XX OS
XX US2003194704-A1.
XX
XX 16-OCT-2003.
XX
XX 03-APR-2002; 2002US-00029386.
XX
XX 03-APR-2002; 2002US-00029386.
XX
XX (PENN/) PENN S G.
XX (RANK/) RANK D R.
XX (HANZ/) HANZEL D K.
XX
XX Penn SG, Rank DR, Hanzel DK;
XX WPI; 2004-119264/12.
XX
XX New human genome-derived single exon nucleic acid probes useful for human
XX gene expression analysis, for identifying or characterizing alternative
PT

PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX Claim 45; SEQ ID NO 32058; 80pp; English.
XX
CC The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridizes under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above, a
CC method of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subcription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe protein of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
SQ Sequence 383 AA;
Query Match 98.1%; Score 362; DB 8; Length 383;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPAPKRCMPEDLQSQSETQGLEGAQAPLAVERDASSSTSTSSFFSPSSSSSS 60
DB 22 MPAPKRCMPEDLQSQSETQGLEGAQAPLAVERDASSSTSTSSFFSPSSSSSS 81
QY 61 SSCYPLIPSTPEVSADDETPNPQSAQIACSSPSVVASLPLDQSDGSSSQKEESPSTL 120
DB 82 SSCYPLIPSTPEVSADDETPNPQSAQIACSSPSVVASLPLDQSDGSSSQKEESPSTL 141
QY 121 QVLPDSESLPRSEIDKVTDLVQFLFKYQMKPEPTKAILLESVIKNYEDHPPLFSEAS 180
DB 142 QVLPDSESLPRSEIDKVTDLVQFLFKYQMKPEPTKAILLESVIKNYEDHPPLFSEAS 201
QY 181 ECMLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMLSDVQSMPTGILLILSIIFIEGYC 240
DB 202 ECMLLVFGIDVKEVDPTGHSFVLVTSGLTYDGMLSDVQSMPTGILLILSIIFIEGYC 261
QY 241 TPEEVIWEALNMWGLYDGMHEHLIYGEPRKLLTQDWQVQENYLEYRQVPGSDPARYEFLWGP 300
DB 262 TPEEVIWEALNMWGLYDGMHEHLIYGEPRKLLTQDWQVQENYLEYRQVPGSDPARYEFLWGP 321
QY 301 RAHAERKMSLLKFLAKVNGSDPRSFPPLWYEALKDEEERAQDRIATDDTTAMASASS 360
DB 322 RAHAERKMSLLKFLAKVNGSDPRSFPPLWYEALKDEEERAQDRIATDDTTAMASASS 381
QY 361 AT 362
XX |||

Db 382 AT 383

RESULT 6

ABO59333

ID ABO59333 standard; protein; 82 AA.

AC ABO59333;

XX 29-JUL-2004 (first entry)

XX Human genome derived single exon protein #5567.

XX Human; gene expression; single exon probe; microarray;

KW alternative splicing event; genomic alteration.

XX Homo sapiens.

XX US2003194704-A1.

XX 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX (PENN/) PENN S G.

PA (RANK/) RANK D R.

PA (HANZ/) HANZEL D K.

XX Penn SG, Rank DR, Hanzel DK;

XX WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human

PT gene expression analysis, for identifying or characterizing alternative

PT splicing events, for assessing genomic alterations or as tools for

PT surveying tissues.

XX Claim 45; SEQ ID NO 32967; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene

CC expression, comprising any of the 27,400 fully defined nucleotide

CC sequences in the specification, or their complements or fragments, and

CC encoding at least 8 amino acids of any of the 688 amino acid sequences

CC fully defined in the specification. The probe is a single exon probe that

CC hybridizes under high stringency conditions to a nucleic acid molecule

CC expressed in human cells or tissues. Also included are a spatially-

CC addressable set of single exon nucleic acid probes for measuring human

CC gene expression (comprising a plurality of single exon nucleic acid

CC probes cited above, where each of the plurality of probes is separately

CC and addressably isolatable or amplifiable from the plurality), a single

CC exon microarray for measuring human gene expression, a method of

CC measuring human gene expression, a vector comprising the single exon

CC probe cited above, an ORF-encoded peptide comprising at least 8

CC contiguous amino acids of any of the above-mentioned amino acid

CC sequences (optionally with conservative amino acid substitutions), an

CC isolated antibody that binds specifically to a peptide cited above,

CC methods of selling and/or licensing single exon probes or microarrays to

CC a customer desiring to measure gene expression, a method of providing

CC human gene expression data by subscription, and a computer-readable

CC storage medium which contains a database having a plurality of records

CC (each record including data on the expression of a single exon probe

CC cited above. The probe, methods and apparatus are useful in gene

CC expression analysis. The probes may be used as tools for surveying

CC tissues to detect the presence of expressed messages that contain their

CC specific exon, or in constructing genome-derived single exon microarrays.

CC In addition, the probes are used in identifying and characterizing

CC alternative splicing events, in detecting and characterizing gross

CC alterations in the genomic locus that includes their exon, in assessing

CC smaller genomic alterations, in priming the synthesis of nucleic acids,

CC or in expressing the ORF-encoded peptide. The present sequence is a human

CC single exon probe protein of the invention. Note: The sequence data for

CC this patent did not form part of the printed specification, but was

CC obtained in electronic format directly from USPTO at

CC seqdata.uspto.gov/sequence.html?DocID=20030194704

XX Sequence 82 AA;

XX Query Match 7.9%; Score 29; DB 8; Length 82;

XX Best Local Similarity 100.0%; Pred. No. 2.2e-19;

XX Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPRKLLTQDWQENYLEYRVPGSDPA 292

DB 5 YGEPRKLLTQDWQENYLEYRVPGSDPA 33

RESULT 7

ABO59726

ID ABO59726 standard; protein; 151 AA.

XX ABO59726;

XX 29-JUL-2004 (first entry)

XX Human genome derived single exon protein #5960.

XX Human; gene expression; single exon probe; microarray;

KW alternative splicing event; genomic alteration.

XX Homo sapiens.

XX US2003194704-A1.

XX 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX (PENN/) PENN S G.

PA (RANK/) RANK D R.

PA (HANZ/) HANZEL D K.

XX Penn SG, Rank DR, Hanzel DK;

XX WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human

PT gene expression analysis, for identifying or characterizing alternative

PT splicing events, for assessing genomic alterations or as tools for

PT surveying tissues.

XX Claim 45; SEQ ID NO 33360; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene

CC expression, comprising any of the 27,400 fully defined nucleotide

CC sequences in the specification, or their complements or fragments, and

CC encoding at least 8 amino acids of any of the 688 amino acid sequences

CC fully defined in the specification. The probe is a single exon probe that

CC hybridizes under high stringency conditions to a nucleic acid molecule

CC expressed in human cells or tissues. Also included are a spatially-

CC addressable set of single exon nucleic acid probes for measuring human

CC gene expression (comprising a plurality of single exon nucleic acid

CC probes cited above, where each of the plurality of probes is separately

CC and addressably isolatable or amplifiable from the plurality), a single

CC exon microarray for measuring human gene expression, a method of

CC measuring human gene expression, a vector comprising the single exon

CC probe cited above, an ORF-encoded peptide comprising at least 8

CC contiguous amino acids of any of the above-mentioned amino acid

CC sequences (optionally with conservative amino acid substitutions), an

CC isolated antibody that binds specifically to a peptide cited above,

CC methods of selling and/or licensing single exon probes or microarrays to

CC a customer desiring to measure gene expression, a method of providing

CC human gene expression data by subscription, and a computer-readable

CC storage medium which contains a database having a plurality of records

CC (each record including data on the expression of a single exon probe

CC cited above. The probe, methods and apparatus are useful in gene

CC expression analysis. The probes may be used as tools for surveying

CC tissues to detect the presence of expressed messages that contain their

CC specific exon, or in constructing genome-derived single exon microarrays.

CC In addition, the probes are used in identifying and characterizing

CC alternative splicing events, in detecting and characterizing gross

CC alterations in the genomic locus that includes their exon, in assessing

CC smaller genomic alterations, in priming the synthesis of nucleic acids,

CC or in expressing the ORF-encoded peptide. The present sequence is a human

CC single exon probe protein of the invention. Note: The sequence data for

CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe protein of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
SQ Sequence 151 AA;

Query Match 7.9%; Score 29; DB 8; Length 151;
Best Local Similarity 100.0%; Pred. No. 4e-19; 0; Mismatches 0; Gaps 0;
Matches 29; Conservative 0;

QY 264 YGEPKLLTQDWQENYLEYRQVPGSDPA 292
|||||
DB 74 YGEPKLLTQDWQENYLEYRQVPGSDPA 102
|||||

RESULT 8
AAB08735
ID AAB08735 standard; protein; 315 AA.
XX
AC AAB08735;
XX
DT 02-JAN-2001 (first entry)
XX
DE Amino acid sequence of a human MAGE-A9 polypeptide.
XX
MAGE-A5; MAGE-A8; MAGE-A9; MAGE-A11; tumour rejection antigen;
KW human leukocyte antigen; HLA; T cell response; region q28; X chromosome;
KW cancer.
XX
OS Homo sapiens.
XX
PN WO200052163-A1.
XX
PD 08-SEP-2000.
XX
PF 01-MAR-2000; 2000WO-US005346.
XX
PR 02-MAR-1999; 99US-00260978.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
Serrano A, Lethe B, Lurquin C, De Plaen E, Rimoldi D;
PI Boon-Falleur T;
PI
XX WPI; 2000-579285/54.
DR N-PSDB; AAA64634.
XX
PT Complementary polynucleotide of MAGE family, useful in the diagnosis of
XX cancer in a patient.
XX
XX Example 4; Page 64-66; 72pp; English.

XX The present sequence represents a human MAGE-A9 polypeptide. The
XX specification also describes MAGE-A5, MAGE-A8, MAGE-A9, and MAGE-A11
XX polypeptides. The MAGE genes encode tumour rejection antigens which
XX complex to human leukocyte antigens (HLAs), and provoke response by
XX autologous, cytolytic T cells. The genes are located in region q28 of the
XX X chromosome. The MAGE polynucleotides are useful for diagnosis of cancer
XX in a patient
XX
SQ Sequence 315 AA;

Query Match 7.9%; Score 29; DB 3; Length 315;
Best Local Similarity 100.0%; Pred. No. 7.8e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 264 YGEPKLLTQDWQENYLEYRQVPGSDPA 292
|||||
DB 238 YGEPKLLTQDWQENYLEYRQVPGSDPA 266
|||||
RESULT 9
ABU56684
ID ABU56684 standard; protein; 315 AA.
XX
AC ABU56684;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polypeptide #277.
XX
KW Lung cancer-associated polypeptide; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
PN WO200286443-A2.
XX
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US012476.
XX
PR 18-APR-2001; 2001US-0284770P.
PR 10-MAY-2001; 2001US-0290492P.
PR 09-NOV-2001; 2001US-0339245P.
PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334370P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
XX WPI; 2003-093161/08.
DR N-PSDB; ABX76413.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
PS Claim 27; Page 401; 453pp; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABU56408-ABU56745 represent lung cancer-associated polypeptides of the

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CC invention
XX
SQ Sequence 315 AA;
    Query Match          7.9%; Score 29; DB 6; Length 315;
    Best Local Similarity 100.0%; Pred. No. 7.8e-19;
    Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPKLLTQDWQENYLEYRQVPGSDPA 292
    |||||
DB 238 YGEPKLLTQDWQENYLEYRQVPGSDPA 266

RESULT 10
ABU56484
ID ABU56484 standard; protein; 315 AA.
XX
AC ABU56484;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polypeptide #77.
XX
KW Lung cancer-associated polypeptide; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
PN WO200286443-A2.
XX
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US012476.
XX
PR 18-APR-2001; 2001US-0284770P.
PR 10-MAY-2001; 2001US-0290492P.
PR 09-NOV-2001; 2001US-0339245P.
PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334370P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
WPI; 2003-093161/08.
DR N-PSDB; ABX76208.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
PS Claim 27; Page 248; 453pp; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
```

```
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABU56408-ABU56745 represent lung cancer-associated polypeptides of the
CC invention
XX
SQ Sequence 315 AA;
    Query Match          7.9%; Score 29; DB 6; Length 315;
    Best Local Similarity 100.0%; Pred. No. 7.8e-19;
    Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPKLLTQDWQENYLEYRQVPGSDPA 292
    |||||
DB 238 YGEPKLLTQDWQENYLEYRQVPGSDPA 266

RESULT 11
ADA83772
ID ADA83772 standard; protein; 315 AA.
XX
AC ADA83772;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MAGEA9 protein.
XX
KW human; marker; expressed sequence tag; EST; arabidopsis; tumour;
KW stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
KW vaccine.
XX
OS Homo sapiens.
XX
PN WO2002103028-A2.
XX
PD 27-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-IB004189.
XX
PR 30-MAY-2001; 2001US-0293999P.
PR 22-OCT-2001; 2001US-0330457P.
PR 19-FEB-2002; 2002US-0357144P.
XX
PA (BIOM-) BIOMEDICAL CENT.
XX
PI Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;
XX
WPI; 2003-175241/17.
DR N-PSDB; ADA83771.
XX
PT Determining if a nucleic acid is a marker for a phenotype/cell type of
PT interest, by global comparison of expressed sequence tags known to be
PT expressed in the phenotype/cell type with all ESTs expressed in normal
PT tissue.
XX
PS Claim 29; Page 159-160; 516pp; English.
XX
CC The invention relates to a novel method for determining if a nucleic acid
CC is a marker for a predetermined phenotype/cell type of interest from a
CC biological species. The method comprises performing a global comparison
CC of a group of expressed sequence tags (ESTs) known to be expressed in the
CC phenotype/cell type of interest with all ESTs expressed in normal tissue
CC in order to identify ESTs that are preferentially expressed in the
CC phenotype/cell of interest. A method of the invention is useful for
CC determining whether a nucleic acid is a marker for a predetermined
CC phenotype or cell type of interest from a biological species, preferably
CC Arabidopsis or human. The cell type of interest is an abnormal cell such
CC as a tumour cell, and the predetermined phenotype is a stress-induced
CC phenotype such as hyperosmotic stress or high salt conditions. A method
CC of the invention is also useful for determining the progression of colon
CC cancer in a human, for detecting a tumour cell, and for regulating or
CC preventing the growth of a tumour cell. An antibody of the invention is
CC useful for detecting the absence or presence of peptides encoded by
CC tumour-associated markers. A polypeptide of the invention is useful as an
```

CC immunogen for vaccinating an animal. The present sequence represents a
CC tumour-associated antigen of the invention.

XX
SQ Sequence 315 AA;

Query Match 7.9%; Score 29; DB 6; Length 315;
Best Local Similarity 100.0%; Pred. No. 7.8e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPRKLLTQDWQENYLEYRQVPGSDPA 292
|||||
DB 238 YGEPRKLLTQDWQENYLEYRQVPGSDPA 266

RESULT 12

ABU04413
ID ABU04413 standard; protein; 315 AA.

XX
AC ABU04413;

XX
DT 29-JAN-2003 (first entry)

XX
DE Human expressed protein tag (EPT) #1079.

XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX
OS Homo sapiens.

XX
PN WO200278524-A2.

XX
PD 10-OCT-2002.

XX
PF 28-MAR-2002; 2002WO-US009671.

XX
PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX
PA (ZYCO-) ZYCOS INC.

XX
PI Chicx RM, Tomlinson AJ, Urban RG;

XX
DR WPI; 2003-040607/03.

XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.

XX
PS Example 2; SEQ ID NO 1079; 134pp; English.

XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed

CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 315 AA;

Query Match 7.9%; Score 29; DB 6; Length 315;
Best Local Similarity 100.0%; Pred. No. 7.8e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPRKLLTQDWQENYLEYRQVPGSDPA 292
|||||
DB 238 YGEPRKLLTQDWQENYLEYRQVPGSDPA 266

RESULT 13

ABU04425

ID ABU04425 standard; protein; 315 AA.

XX
AC ABU04425;

XX
DT 29-JAN-2003 (first entry)

XX
DE Human expressed protein tag (EPT) #1091.

XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX
OS Homo sapiens.

XX
PN WO200278524-A2.

XX
PD 10-OCT-2002.

XX
PF 28-MAR-2002; 2002WO-US009671.

XX
PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX
PA (ZYCO-) ZYCOS INC.

XX
PI Chicx RM, Tomlinson AJ, Urban RG;

XX
DR WPI; 2003-040607/03.

XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.

XX
PS Example 2; SEQ ID NO 1091; 134pp; English.

XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed

CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 315 AA;

Query Match 7.9%; Score 29; DB 6; Length 315;
Best Local Similarity 100.0%; Pred. No. 7.8e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPRKLLTQDWQENYLEYRQVPGSDPA 292
|||||
Db 238 YGEPRKLLTQDWQENYLEYRQVPGSDPA 266
|||||

RESULT 14
ABU04416
ID ABU04416 standard; protein; 315 AA.
XX
AC ABU04416;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1082.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.

XX Example 2; SEQ ID NO 1082; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed

CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 315 AA;

Query Match 7.9%; Score 29; DB 6; Length 315;
Best Local Similarity 100.0%; Pred. No. 7.8e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPRKLLTQDWQENYLEYRQVPGSDPA 292
|||||
Db 238 YGEPRKLLTQDWQENYLEYRQVPGSDPA 266
|||||

RESULT 15

ABU04421

ID ABU04421 standard; protein; 315 AA.

XX AC ABU04421;

XX 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1087.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.

XX Example 2; SEQ ID NO 1087; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed

CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 315 AA;

Query Match 7.9%; Score 29; DB 6; Length 315;
Best Local Similarity 100.0%; Pred. No. 7.8e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPRKLLTQDWVQENYLEYRQVPGSDPA 292
|||
Db 238 YGEPRKLLTQDWVQENYLEYRQVPGSDPA 266
|||

Search completed: March 17, 2006, 22:36:51
Job time : 196 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 22:42:34 ; Search time 23 Seconds
(without alignments)
459.211 Million cell updates/sec

Title: US-09-856-812B-1
Perfect score: 369
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 169630 seqs, 28622889 residues

Word size : 0
Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications_AA_New.*
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2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US05_NEW_PUB.pep.*
6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	17	4.6	314	6	US-10-510-101-69 Sequence 69, Appl
2	17	4.6	314	7	US-11-155-288-6 Sequence 6, Appli
3	14	3.8	309	7	US-11-155-288-5 Sequence 5, Appli
4	12	3.3	1006	7	US-11-203-251A-90 Sequence 90, Appl
5	11	3.0	1142	7	US-11-044-051-73 Sequence 73, Appl
6	10	2.7	10	7	US-11-044-051-83 Sequence 83, Appl
7	10	2.7	57	7	US-11-096-568A-3481 Sequence 3481, Ap
8	10	2.7	179	7	US-11-096-568A-19169 Sequence 19169, A
9	10	2.7	209	7	US-11-096-568A-22097 Sequence 22097, A
10	10	2.7	228	7	US-11-096-568A-7793 Sequence 7793, Ap
11	10	2.7	235	7	US-11-096-568A-22096 Sequence 22096, A
12	10	2.7	247	7	US-11-096-568A-7792 Sequence 7792, Ap
13	10	2.7	258	7	US-11-072-512-3034 Sequence 3034, Ap
14	10	2.7	259	7	US-11-096-568A-22095 Sequence 22095, A
15	10	2.7	286	6	US-10-714-887-196 Sequence 196, App
16	10	2.7	302	7	US-11-096-568A-28036 Sequence 28036, A
17	10	2.7	352	7	US-11-096-568A-28035 Sequence 28035, A
18	10	2.7	371	7	US-11-096-568A-31720 Sequence 31720, A
19	10	2.7	373	7	US-11-044-051-71 Sequence 71, Appl
20	10	2.7	373	7	US-11-044-051-105 Sequence 105, App
21	10	2.7	374	6	US-10-537-094-6 Sequence 6, Appli
22	10	2.7	374	6	US-10-537-094-8 Sequence 8, Appli
23	10	2.7	377	7	US-11-096-568A-28034 Sequence 28034, A
24	10	2.7	387	7	US-11-096-568A-6334 Sequence 6334, Ap
25	10	2.7	406	7	US-11-096-568A-1547 Sequence 1547, Ap

ALIGNMENTS

RESULT 1

US-10-510-101-69
; Sequence 69, Application US/10510101
; Publication No. US20060018915A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Ishioka, Glenn
; APPLICANT: Fikes, John
; APPLICANT: Tangri, Shabnam
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Heterocyclic Analogs and Related Methods
; FILE REFERENCE: 2060.009PC05
; CURRENT APPLICATION NUMBER: US/10/510,101
; CURRENT FILING DATE: 2004-10-05
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/413,471
; PRIOR APPLICATION NUMBER: US 10/116,118
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-510-101-69

Query Match 4.6%; Score 17; DB 6; Length 314;
Best Local Similarity 100.0%; Pred. No. 8.5e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 VQENYLEYRQVPGSDPA 292
DB 251 VQENYLEYRQVPGSDPA 267

RESULT 2

US-11-155-288-6
; Sequence 6, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MAN/K.050A
; CURRENT APPLICATION NUMBER: US/11/155,288
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969

; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-6

Query Match 4.6%; Score 17; DB 7; Length 314;
Best Local Similarity 100.0%; Pred. No. 8.5e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 VOENYLEYRQVGSDDPA 292
|||
DB 251 VOENYLEYRQVGSDDPA 267

RESULT 3
US-11-155-288-5
; Sequence 5, Application US/11155288
; Publication No. US2006008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANKK.050A
; CURRENT APPLICATION NUMBER: US/11/155,288
; PRIOR FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-5

Query Match 3.8%; Score 14; DB 7; Length 309;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 SDPARYEFLWGPPRA 302
|||
DB 257 SDPARYEFLWGPPRA 270

RESULT 4
US-11-203-251A-90
; Sequence 90, Application US/11203251A
; Publication No. US20060039904A1
; GENERAL INFORMATION:
; APPLICANT: MedImmune Inc.
; TITLE OF INVENTION: EPH RECEPTOR PC VARIANTS WITH ENHANCED ANTIBODY DEPENDENT
; TITLE OF INVENTION: CELL-MEDIATED CYTOTOXICITY ACTIVITY
; FILE REFERENCE: AE7020US
; CURRENT APPLICATION NUMBER: US/11/203,251A
; CURRENT FILING DATE: 2005-08-15
; PRIOR APPLICATION NUMBER: 60/601,634
; PRIOR FILING DATE: 2004-08-16
; PRIOR APPLICATION NUMBER: 60/608,852
; PRIOR FILING DATE: 2004-09-13
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 90
; LENGTH: 1006
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-203-251A-90

Query Match 3.3%; Score 12; DB 7; Length 1006;

Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 51 SFPSSSSSSSSSS 62
|||
DB 148 SFPSSSSSSSSSS 159

RESULT 5
US-11-044-051-73
; Sequence 73, Application US/11044051
; Publication No. US2005025553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: GODELAINE, Danisle
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459,263
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-044-051-73

Query Match 3.0%; Score 11; DB 7; Length 1142;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 RYEFLLMGPPRAH 303
|||
DB 1066 RYEFLLMGPPRAH 1076

RESULT 6
US-11-044-051-83
; Sequence 83, Application US/11044051
; Publication No. US2005025553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: GODELAINE, Danisle
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459,263
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-044-051-83

Query Match 2.7%; Score 10; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 LVFGIDVKEV 194
|||
DB 1 LVFGIDVKEV 10

RESULT 7
US-11-096-568A-3481
; Sequence 3481, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 3481
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(57)
; OTHER INFORMATION: Ceres Seq. ID no. 12609928
US-11-096-568A-3481

Query Match 2.7%; Score 10; DB 7; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.011; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 PSSSSSSSSS 62
|||||
Db 34 PSSSSSSSSS 43

RESULT 8
US-11-096-568A-19169
; Sequence 19169, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19169
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(179)
; OTHER INFORMATION: Ceres Seq. ID no. 12369262
US-11-096-568A-19169

Query Match 2.7%; Score 10; DB 7; Length 179;
Best Local Similarity 100.0%; Pred. No. 0.035; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 PSSSSSSSSS 62
|||||
Db 2 PSSSSSSSSS 11

RESULT 9
US-11-096-568A-22097
; Sequence 22097, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A

; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22097
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(209)
; OTHER INFORMATION: Ceres Seq. ID no. 12407535
US-11-096-568A-22097

Query Match 2.7%; Score 10; DB 7; Length 209;
Best Local Similarity 100.0%; Pred. No. 0.04; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 PSSSSSSSSS 62
|||||
Db 36 PSSSSSSSSS 45

RESULT 10
US-11-096-568A-7793
; Sequence 7793, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 7793
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(228)
; OTHER INFORMATION: Ceres Seq. ID no. 15175769
US-11-096-568A-7793

Query Match 2.7%; Score 10; DB 7; Length 228;
Best Local Similarity 100.0%; Pred. No. 0.044; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 PSSSSSSSSS 62
|||||
Db 27 PSSSSSSSSS 36

RESULT 11
US-11-096-568A-22096
; Sequence 22096, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22096
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(235)
; OTHER INFORMATION: Ceres Seq. ID no. 12407534
US-11-096-568A-22096

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Query Match          2.7%; Score 10; DB 7; Length 235;
Best Local Similarity 100.0%; Pred. No. 0.045; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 PSSSSSSSSSS 62
Db 62 PSSSSSSSSSS 71

RESULT 12
US-11-096-568A-7792
; Sequence 7792, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 7792
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(247)
; OTHER INFORMATION: Ceres Seq. ID no. 15175768
US-11-096-568A-7792

Query Match          2.7%; Score 10; DB 7; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.047; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 PSSSSSSSSSS 62
Db 46 PSSSSSSSSSS 55

RESULT 13
US-11-072-512-3034
; Sequence 3034, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYU
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3034
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3034

Query Match          2.7%; Score 10; DB 7; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.05; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 PSSSSSSSSSS 62
Db 92 PSSSSSSSSSS 101

RESULT 14
US-11-096-568A-22095
; Sequence 22095, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22095
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(259)
; OTHER INFORMATION: Ceres Seq. ID no. 12407533
US-11-096-568A-22095

Query Match          2.7%; Score 10; DB 7; Length 259;
Best Local Similarity 100.0%; Pred. No. 0.05; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 PSSSSSSSSSS 62
Db 86 PSSSSSSSSSS 95

RESULT 15
US-10-714-887-196
; Sequence 196, Application US/10714887
; Publication No. US20060015972A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: HEARD, Jacqueline
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: CREELMAN, Robert
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: CANALES, Roger
; APPLICANT: REPETTI, Peter
; APPLICANT: KUMIMOTO, Roderick W
; APPLICANT: GUTTERSON, Neal
; APPLICANT: REUBER, T. Lynne
; APPLICANT: PINEDA, Omaira
; APPLICANT: SHERMAN, Bradley K
; TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF DROUGHT STRESS
; FILE REFERENCE: MB10058-CIP
; CURRENT APPLICATION NUMBER: US/10/714,887
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 10/412,699
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/135,134
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; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/125,814
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 196
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: G3772 polypeptide Orthologous to G3086
US-10-714-887-196

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Query Match      2.7%; Score 10; DB 6; Length 286;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      53 PSSSSSSSSS 62
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Db       3 PSSSSSSSSS 12

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Search completed: March 17, 2006, 22:45:37
Job time : 25 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: March 17, 2006, 22:33:43 ; Search time 228 Seconds
(without alignments)
1141.842 Million cell updates/sec
Title: US-09-856-812B-1
Perfect score: 369
Sequence: 1 MPAPKRCMPEDLQSQS.....DTTANASASSATGFSFSYPE 369

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 2166443 seqs, 705528306 residues
Word size : 0
Total number of hits satisfying chosen parameters: 2166443
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 45 summaries
Database : UniProt.05.80:*
1: uniprot_prot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	369	100.0	369	1	MAGAA_HUMAN
2	29	7.9	315	1	MAGAA_HUMAN
3	29	7.9	315	2	Q725K4_HUMAN
4	26	7.0	317	1	MAGAA_HUMAN
5	26	7.0	317	2	Q14798_HUMAN
6	17	4.6	314	1	MAGAA_HUMAN
7	17	4.6	314	1	MAGAA_HUMAN
8	17	4.6	314	1	MAGAA_HUMAN
9	17	4.6	314	1	MAGAA_HUMAN
10	17	4.6	314	2	Q6FGT7_HUMAN
11	17	4.6	314	2	Q6FHI5_HUMAN
12	17	4.6	314	2	Q6FHH8_HUMAN
13	17	4.6	314	2	Q53EX0_HUMAN
14	17	4.6	314	2	Q96E03_HUMAN
15	17	4.6	314	2	Q6P448_HUMAN
16	17	4.6	314	2	Q6FHI6_HUMAN
17	17	4.6	314	2	Q6NW44_HUMAN
18	17	4.6	314	2	Q60763_MOUSE
19	16	4.3	330	2	Q8JZK8_MOUSE
20	16	4.3	330	2	Q8K315_MOUSE
21	16	4.3	330	2	Q99PF1_MOUSE
22	16	4.3	330	2	Q9D2H4_MOUSE
23	15	4.1	346	1	MAGB3_HUMAN
24	14	3.8	309	1	MAGAA_HUMAN
25	14	3.8	316	2	Q8WHH6_HUMAN
26	14	3.8	330	2	Q6XZC3_MOUSE
27	14	3.8	330	2	Q4U221_MOUSE
28	14	3.8	330	2	Q60761_MOUSE
29	13	3.5	343	2	Q96M61_HUMAN
30	13	3.5	344	2	Q4R998_MACFA
31	12	3.3	319	1	MAGAB_HUMAN

RESULT 1
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ID MAGAA_HUMAN STANDARD; PRT; 369 AA.
AC P43363;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Melanoma-associated antigen 10 (MAGE-10 antigen).
GN Name=MAGEA10; Synonyms=MAGEB10;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95012457; PubMed=7927540;
RA de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,
RA de Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C.,
RA Brasseur R., Chomez P., de Backer O., Cavenne W., Boon T.;
RT "Structure, chromosomal localization, and expression of 12 genes of
the MAGE family."
RL Immunogenetics 40:360-369(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
TX TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McWen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.J., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Not known, though may play a role in embryonal
development and tumor transformation or aspects of tumor
progression.
CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
such as melanoma, head and neck squamous cell carcinoma, lung
carcinoma and breast carcinoma, but not in normal tissues except
for testes and placenta.

ALIGNMENTS

```
CC  -1- SIMILARITY: Contains 1 MAGE domain.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
CC  EMBL; U10685; AA68869.1; -; Genomic DNA.
CC  EMBL; BC004105; AAH04105.1; -; mRNA.
CC  PIR; I38659; I38659.
CC  Ensembl; ENSG00000124260; Homo sapiens.
CC  HGNC; HGNC:6797; MAGEA10.
CC  H-InvDB; HIX0017116; -.
CC  MIM; 300343; -.
CC  InterPro; IPR002190; MAGE.
CC  PANTHER; PTHR11736; MAGE; 2.
CC  Pfam; PF01454; MAGE; 1.
CC  PROSITE; PS50838; MAGE; 1.
CC  Antigen; Multigene family; Tumor antigen.
CC  DOMAIN 134 333
CC  COMPIAS 54 62 Poly-Ser.
CC  SEQUENCE 369 AA; 40767 MW; 16FA3301CAB7116A6 CRC64;
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CC  Query Match 100.0%; Score 369; DB 1; Length 369;
CC  Best Local Similarity 100.0%; Pred. No. 0;
CC  Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MPRAPKRCMPEDLQSQSETQGLGAQAPLAVEEDASSSTSTSSFFSPSSSSSS 60
QY 61 SSCYPLIPSTPEVSADDETPNPQSAQIACSPSVVASLPLDQSDGSSQKEESPSTL 120
DB 61 SSCYPLIPSTPEVSADDETPNPQSAQIACSPSVVASLPLDQSDGSSQKEESPSTL 120
QY 121 QVLPDSESLPRSIDKVTDLQVFLFKYQMKPITKAETLESVKNYEDHPFLPSEAS 180
DB 121 QVLPDSESLPRSIDKVTDLQVFLFKYQMKPITKAETLESVKNYEDHPFLPSEAS 180
QY 181 ECLMLVFGIDVKEVDPTGHSFVLVTSIGLYDQMLSDVQSMPTKGLILILSIPIEGYC 240
DB 181 ECLMLVFGIDVKEVDPTGHSFVLVTSIGLYDQMLSDVQSMPTKGLILILSIPIEGYC 240
QY 241 TPEVITWEALNMGLVDGMEHLIYGBPRKLLTQDWQVQENLYEYRQVPGSDPARYEFLWGP 300
DB 241 TPEVITWEALNMGLVDGMEHLIYGBPRKLLTQDWQVQENLYEYRQVPGSDPARYEFLWGP 300
QY 301 RAHAETKMSLLKFLAKVNGSDPRSPLWVEEAKDDEERAQDIATDDTTTAMASASS 360
DB 301 RAHAETKMSLLKFLAKVNGSDPRSPLWVEEAKDDEERAQDIATDDTTTAMASASS 360
QY 361 ATGSFVSYPE 369
DB 361 ATGSFVSYPE 369
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RESULT 2
MAGA9 HUMAN
ID MAGA9 HUMAN STANDARD; PRT; 315 AA.
AC P43362; Q92910;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Melanoma-associated antigen 9 (MAGE-9 antigen).
GN Name=MAGEA9; Synonyms=MAGE9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
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RX MEDLINE=95012457; PubMed=7927540;
RA de Plaan E., Arden K., Traverari C., Gaforio J.J., Szikora J.-P.,
RA Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C.,
RA Brasseur R., Chomez P., de Backer O., Cavenese W., Boon T.;
RT "Structure, chromosomal localization, and expression of 12 genes of
RT the MAGE family.";
RL Immunogenetics 40:360-369(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Timms K.M., Bondeason M.L., Ansari-Lari M.A., Lagerstedt K.,
RA Nelson D.L., Petheress U., Gibbs R.A.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Lung;
RX MEDLINE=223868257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Not known, though may play a role in embryonal
CC development and tumor transformation or aspects of tumor
CC progression.
CC -1- TISSUE SPECIFICITY: Expressed in many tumors of several types,
CC such as melanoma, head and neck squamous cell carcinoma, lung
CC carcinoma and breast carcinoma, but not in normal tissues except
CC for testes and placenta.
CC -1- SIMILARITY: Contains 1 MAGE domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U10694; AA68877.1; -; Genomic DNA.
CC EMBL; U66083; AAB67888.1; -; Genomic DNA.
CC EMBL; BC002351; AAH02351.1; -; mRNA.
CC PIR; I38668; I38668.
CC HGNC; HGNC:6807; MAGEA9.
CC H-InvDB; HIX0017105; -.
CC MIM; 300342; -.
CC InterPro; IPR002190; MAGE.
CC PANTHER; PTHR11736; MAGE; 1.
CC Pfam; PF01454; MAGE; 1.
CC PROSITE; PS50838; MAGE; 1.
CC Antigen; Multigene family; Tumor antigen.
CC DOMAIN 108 307
CC COMPIAS 34 37 Poly-Glu.
CC FT COMPBIAS 87 90 Poly-Glu.
CC SEQUENCE 315 AA; 35088 MW; 7FD2ED10D680D928 CRC64;
CC
CC 7.9%; Score 29; DB 1; Length 315;
CC Query Match 100.0%; Pred. No. 1.6e-18;
CC Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
CC Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
QY 264 YGEPRKLLTQDWVQENLYEYRQVPGSDPA 292
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Db 238 YGEPKLLTQDWQVQENYLEYRQVPGSDPA 266
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RESULT 3
Q725K4 HUMAN
ID Q725K4_HUMAN PRELIMINARY; PRT; 315 AA.
AC Q725K4;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Melanoma antigen family A 9 (Fragment).
GN Name=MAGEA9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Zhu J., Feng Z., Guan X.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AV310325; AAP82171.1; -; mRNA.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
FT NON TER 315
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Query Match 7.9%; Score 29; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.6e-18;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPKLLTQDWQVQENYLEYRQVPGSDPA 292
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Db 238 YGEPKLLTQDWQVQENYLEYRQVPGSDPA 266

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ID MAGA4_HUMAN STANDARD; PRT; 317 AA.
AC P43358;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Melanoma-associated antigen 4 (MAGE-4 antigen) (MAGE-X2) (MAGE-41).
GN Name=MAGEA4; Synonyms=MAGE4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=95012457; PubMed=7927540;
RA de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,
RA de Smet C., Brasseur P., van der Bruggen P., Lethe B., Lurquin C.,
RA Brasseur R., Chomez P., de Backer O., Cavenee W., Boon T.;
RT "Structure, chromosomal localization, and expression of 12 genes of
RT the MAGE family.";
RT Immunogenetics 40:360-369(1994).
RN [2]_
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=94311935; PubMed=8037761;
RA Ding M., Beck R.J., Keller C.J., Fenton R.G.;
RT "Cloning and analysis of MAGE-1-related genes.";
RL Biochem. Biophys. Res. Commun. 202:549-555(1994).
RN [3]_
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95369706; PubMed=7642112; DOI=10.1016/0378-1119(94)00680-Q;
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RA Imai Y., Shichijo S., Yamada A., Katayama T., Yano H., Itoh K.;
RT "Sequence analysis of the MAGE gene family encoding human tumor-
RL rejection antigens.";
RL Gene 160:287-290(1995).
RN [4]_
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Ductenun;
RX MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ushin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquell N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Not known, though may play a role in embryonal
CC development and tumor transformation or aspects of tumor
CC progression.
CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
CC such as melanoma, head and neck squamous cell carcinoma, lung
CC carcinoma and breast carcinoma, but not in normal tissues except
CC for testes and placenta.
CC -!- SIMILARITY: Contains 1 MAGE domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U10687; AAA68871.1; -; Genomic DNA.
CC EMBL; U10688; AAA68872.1; -; Genomic DNA.
CC EMBL; U10340; AAA19007.1; -; mRNA.
CC EMBL; D32077; BAA06843.1; -; mRNA.
CC EMBL; BC017723; AAH17723.1; -; mRNA.
CC F1R; I38661; I38661.
CC PDB; 1I4F; X-ray; C=230-239.
CC Ensembl; ENSG00000198681; Homo sapiens.
CC HGNC; HGNC:6802; MAGEA4.
CC H-InvDB; HIX0017115; -.
CC MIM; 300175; -.
CC InterPro; IPR002190; MAGE.
CC PANTHER; PTHR11736; MAGE; 1.
CC Pfam; PF01454; MAGE; 1.
CC PROSITE; PS50838; MAGE; 1.
KW 3D-structure; Antigen; Multigene family; Polymorphism; Tumor antigen.
FT DOMAIN 110 309
FT COMBIAS 41 44 Poly-Ser.
FT VARIANT 173 173 T -> A.
FT CONFLICT 307 307 /FTID=VAR 004284.
FT SEQUENCE 317 AA; 34929 MW; 3CFAC0E2B696257C CRC64;
SQ
Query Match 7.0%; Score 26; DB 1; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.1e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPKLLTQDWQVQENYLEYRQVPGS 289
|||||
Db 240 YGEPKLLTQDWQVQENYLEYRQVPGS 265
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```

Genome Res. 10:758-775 (2000).
[3]
RN  MUTAGENESIS.
RP  TISSUE=Blood;
RC  MEDLINE=94157413; PubMed=8113684; DOI=10.1084/jem.179.3.921;
RX  Gaugler B., van den Eynde B., van der Bruggen P., Romero P.,
RA  Gaforio J.J., de Plaen E., Lethe B., Brasseur F., Boon T.;
RT  "Human gene MAGE-3 codes for an antigen recognized on a melanoma by
RT  autologous cytolytic T lymphocytes.";
RL  J. Exp. Med. 179:921-930 (1994).
CC  -!- FUNCTION: Not known, though may play a role in embryonal
CC  development and tumor transformation or aspects of tumor
CC  progression. Antigen recognized on a melanoma by autologous
CC  cytolytic T lymphocytes.
CC  -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
CC  such as melanoma, head and neck squamous cell carcinoma, lung
CC  carcinoma and breast carcinoma, but not in normal tissues except
CC  for testes.
CC  -!- SIMILARITY: Contains 1 MAGE domain.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
DR  EMBL; L18920; AAA17729.1; -; Unassigned_DNA.
DR  EMBL; U82671; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR  PIR; I68889; I68889.
DR  HGNC; HGNC:6800; MAGEA2.
DR  HGNC; HGNC:19340; MAGEA2B.
DR  H-InvDB; HIX0017118; -.
DR  MIM; 300173; -.
DR  InterPro; IPR002190; MAGE.
DR  PANTHER; PTHR11736; MAGE; 1.
DR  Pfam; PF01454; MAGE; 1.
DR  PROSITE; PS50838; MAGE; 1.
KW  Antigen; Multigene family; Tumor antigen.
FT  DOMAIN 109..308
FT  COMPBIAS 40..43 Poly-Ser.
FT  MUTAGEN 170..170 V->D: Improves ability to bind to HLA-A1.
SQ  SEQUENCE 314 AA; 35055 MW; 844F16335A2BCE7 CRC64;

Query Match 4.6%; Score 17; DB 1; Length 314;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 VQENYLEYRQVFGSDPA 292
Db 251 VQENYLEYRQVFGSDPA 267

RESULT 7
MAGA3 HUMAN
ID MAGA3 HUMAN STANDARD; PRT; 314 AA.
AC P43357;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Melanoma-associated antigen 3 (MAGE-3 antigen) (Antigen M22-D).
DE Name=MAGEA3; Synonyms=MAGE3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND MUTAGENESIS.
RC TISSUE=Blood;
RX MEDLINE=94157413; PubMed=8113684; DOI=10.1084/jem.179.3.921;
RA Gaugler B., van den Eynde B., van der Bruggen P., Romero P.,
RA Gaforio J.J., de Plaen E., Lethe B., Brasseur F., Boon T.;
RT "Human gene MAGE-3 codes for an antigen recognized on a melanoma by
RT autologous cytolytic T lymphocytes.";
RL J. Exp. Med. 179:921-930 (1994).
CC  -!- FUNCTION: Not known, though may play a role in embryonal
CC  development and tumor transformation or aspects of tumor
CC  progression. Antigen recognized on a melanoma by autologous
CC  cytolytic T lymphocytes.
CC  -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
CC  such as melanoma, head and neck squamous cell carcinoma, lung
CC  carcinoma and breast carcinoma, but not in normal tissues except
CC  for testes.
CC  -!- SIMILARITY: Contains 1 MAGE domain.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
DR  EMBL; L18920; AAA17729.1; -; Unassigned_DNA.
DR  EMBL; U82671; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR  PIR; I68889; I68889.
DR  HGNC; HGNC:6800; MAGEA2.
DR  HGNC; HGNC:19340; MAGEA2B.
DR  H-InvDB; HIX0017118; -.
DR  MIM; 300173; -.
DR  InterPro; IPR002190; MAGE.
DR  PANTHER; PTHR11736; MAGE; 1.
DR  Pfam; PF01454; MAGE; 1.
DR  PROSITE; PS50838; MAGE; 1.
KW  Antigen; Multigene family; Tumor antigen.
FT  DOMAIN 109..308
FT  COMPBIAS 40..43 Poly-Ser.
FT  MUTAGEN 170..170 V->D: Improves ability to bind to HLA-A1.
SQ  SEQUENCE 314 AA; 35055 MW; 844F16335A2BCE7 CRC64;

Query Match 7.0%; Score 26; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.1e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPRKLLTQDWQENYLEYRQVFGS 289
Db 240 YGEPRKLLTQDWQENYLEYRQVFGS 265

RESULT 6
MAGA2 HUMAN
ID MAGA2 HUMAN STANDARD; PRT; 314 AA.
AC P43356;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Melanoma-associated antigen 2 (MAGE-2 antigen).
DE Name=MAGEA2A; Synonyms=MAGE2, MAGEA2;
GN and
GN Name=MAGEA2B; Synonyms=MAGE2, MAGEA2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=94102805; PubMed=8276455;
RA de Smet C., Lurquin C., van der Bruggen P., de Plaen E., Brasseur F.,
RA Boon T.;
RT "Sequence and expression pattern of the human MAGE2 gene.";
RL Immunogenetics 39:121-129 (1994).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=20314869; PubMed=10854409; DOI=10.1101/gr.10.6.758;
RA Mallon A.-M., Platzer M., Bate R., Gloeckner G., Botcherby M.R.M.,
RA Nordieck G., Strivens M.A., Kioschis P., Dangel A., Cunningham D.,
RA Straw R.N.A., Weston P., Gilbert M., Fernando S., Goodall K.,
RA Hunter G., Greystrong J.S., Clarke D., Kimberley C., Goordes M.,
RA Blechschmidt K., Rump A., Hinzmann B., Mundy C.R., Miller W.,
RA Poustka A., Herman G.E., Rhodes M., Denny P., Rosenthal A.,
RA Brown S.D.M.;
RT "Comparative genome sequence analysis of the Bpa/Str region in mouse
RT and man.";

```

RT autologous cytolytic T lymphocytes.";
RL J. Exp. Med. 179:921-930(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=94311935; PubMed=8037761;
RA Ding M., Beck R.J., Keller C.J., Fenton R.G.;
RT "Cloning and analysis of MAGE-1-related genes.";
RL Biochem. Biophys. Res. Commun. 202:549-555(1994).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=20314869; PubMed=10854409; DOI=10.1101/gr.10.6.758;
RA Mallon A.-M., Platzer M., Bate R., Gloeckner G., Botcherby M.R.M.,
RN Nordiek G., Strivens M.A., Kioschis P., Dangel A., Cunningham D.,
RA Straw R.N.A., Weston P., Gilbert M., Fernando S., Goodall K.,
RA Hunter G., Greystrom J.S., Clarke D., Kimberley C., Goerdes M.,
RA Blechschmidt K., Rump A., Hinzmann B., Mundy C.R., Miller W.,
RA Poustka A., Herman G.E., Rhodes M., Denny P., Rosenthal A.,
RA Brown S.D.M.;
RT "Comparative genome sequence analysis of the Bpa/Str region in mouse
and man.";
RL Genome Res. 10:758-775(2000).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Bone marrow, Lung, Prostate, and Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RN Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RN Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RN Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano R.A., Peters G.J., Abramson R.D., Mullany S.J.,
RN Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RN Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RN Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Trichmond J.W., Green E.D., Dickson M.C.,
RN Rodriguez A.W., Goughman J.J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RN Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [1]
RP FUNCTION: Not known, though may play a role in embryonal
development and tumor transformation or aspects of tumor
progression. Antigen recognized on a melanoma by autologous
cytolytic T lymphocytes.
CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
such as melanoma, head and neck squamous cell carcinoma, lung
carcinoma and breast carcinoma, but not in normal tissues except
for testes and placenta. Never expressed in kidney tumors,
leukemias and lymphomas.
CC -!- SIMILARITY: Contains 1 MAGE domain.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

CC EMBL; U03735; AAA17446.1; -; Unassigned DNA.
CC EMBL; U82671; -; NOT ANNOTATED CDS; Genomic_DNA.
CC EMBL; BC003340; AA00340.1; -; mRNA.
CC EMBL; BC005963; AA05963.1; -; mRNA.
CC EMBL; BC011744; AA011744.1; -; mRNA.
CC EMBL; BC016803; AA016803.1; -; mRNA.
CC EMBL; BC017389; AA017389.1; -; mRNA.
CC PIR; JC2361; JC2361.
CC EnsEmbl; ENSG00000191712; Homo sapiens.
CC HGNC; HGNC:6801; MAGEA3.

DR H-InvDB; HIX0017120; -;
DR MIM; 300174; -;
DR InterPro; IPR002190; MAGE.
DR PANTHER; PTHR11736; MAGE; 1.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS08038; MAGE; 1.
KW Antigen; Multigene family; Tumor antigen.
FT DOMAIN 109 308
FT COMPIAS 40 43
FT MUTAGEN 170 170 D->A: Abolishes HLA-A1 binding.
FT MUTAGEN 176 176 Y->A: Abolishes HLA-A1 binding.
SQ SEQUENCE 314 AA; 34747 MW; 3F5EB13D1C9946A1 CRC64;
Query Match 4.6%; Score 17; DB 1; Length 314;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 276 VOENYLEYRQVPGSDPA 292
DB 251 VOENYLEYRQVPGSDPA 267
|||||
RESULT 8
MAGE6_HUMAN STANDARD; PRT; 314 AA.
ID MAGE6_HUMAN
AC P43360;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Melanoma-associated antigen 6 (MAGE-6 antigen) (MAGE3B).
GN Names=MAGE6; Synonyms=MAGE5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95012457; PubMed=7927540;
RA de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,
RN de Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C.,
RA Brasseur R., Chomez P., de Backer O., Cavenne W., Boon T.;
RT "Structure, chromosomal localization, and expression of 12 genes of
the MAGE family.";
RL Immunogenetics 40:360-369(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=94311935; PubMed=8037761;
RA Ding M., Beck R.J., Keller C.J., Fenton R.G.;
RT "Cloning and analysis of MAGE-1-related genes.";
RL Biochem. Biophys. Res. Commun. 202:549-555(1994).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95369706; PubMed=7642112; DOI=10.1016/0378-1119(94)00680-Q;
RA Imai Y., Shichiyo S., Yamada A., Katayama T., Yano H., Itoh K.;
RT "Sequence analysis of the MAGE gene family encoding human tumor-
rejection antigens.";
RL Gene 160:287-290(1995).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Oesophageal carcinoma;
RG The German CDNA consortium;
RN Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RN Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RN Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Not known, though may play a role in tumor or aspects of
CC tumor progression.
CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
CC such as melanoma, head and neck squamous cell carcinoma, lung
CC carcinoma and breast carcinoma, but not in normal tissues except
CC for testes.
CC -!- SIMILARITY: Contains 1 MAGE domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U10691; AAAG8875.1; -; Genomic_DNA.
DR EMBL; U10339; AAA19006.1; -; mRNA.
DR EMBL; D32076; BAA06842.1; -; mRNA.
DR EMBL; BX60600; CAE45706.1; -; mRNA.
DR EMBL; BC041599; AAH41599.1; -; mRNA.
DR PIR; JC2360; JC2360.
DR ENSEMBL; ENSG00000183305; Homo sapiens.
DR HGNC; HGNC:6804; MAGEA6.
DR MIM; 300176; -.
DR InterPro; IPR002190; MAGE.
DR PANTHER; PTHR11736; MAGE; 1.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
KW Antigen; Multigene family; Tumor antigen.
FT DOMAIN 109 308 MAGE.
FT COMPBIAS 40 43 Poly-Ser.
SQ SEQUENCE 314 AA; 34891 MW; 29B83C7FA6850263 CRC64;

Query Match 4.6%; Score 17; DB 1; Length 314;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 VQENYLEYRQVPGSDPA 292
|||||
Db 251 VQENYLEYRQVPGSDPA 267

RESULT 9
ID MAGAC HUMAN STANDARD; PRT; 314 AA.
AC P43365; Q9NSD3;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Melanoma-associated antigen 12 (MAGE-12 antigen) (MAGE12F).
GN Name=MAGEA12; Synonyms=MAGE12;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
OX [1]
RP NUCLEOTIDE SEQUENCE.
RP MEDLINE=94102805; PubMed=8276455;

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RA de Smet C., Lurquin C., van der Bruggen P., de Plaen E., Brasseur F.,
RA Boon T.;
RT "Sequence and expression pattern of the human MAGE2 gene.";
RL Immunogenetics 39:121-129(1994).
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=94311935; PubMed=8037761;
RA Ding M., Beck R.J., Keller C.J., Fenton R.G.;
RT "Cloning and analysis of MAGE-1-related genes.";
RL Biochem. Biophys. Res. Commun. 202:549-555(1994).
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=20314869; PubMed=10854409; DOI=10.1101/gr.10.6.758;
RA Mallon A.-M., Platzers M., Bete R., Gloeckner G., Botcherby M.R.M.,
RA Nordstiek G., Strivens M.A., Kioschis P., Dangel A., Cunningham D.,
RA Straw R.N.A., Weston P., Gilbert M., Fernando S., Goodall K.,
RA Hunter G., Greystrom J.S., Clarke D., Kimberley C., Goerdes M.,
RA Blechschmidt K., Rump A., Hinzmann B., Mundy C.R., Miller W.,
RA Poustka A., Herman G.E., Rhodes M., Denny P., Rosenthal A.,
RA Brown S.D.M.;
RT "Comparative genome sequence analysis of the Bpa/Str region in mouse
RT and man.";
RL Genome Res. 10:758-775(2000).
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSS in BD Creator(TM) system donor
RT vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Not known, though may play a role in tumor
CC transformation or aspects of tumor progression.
CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
CC such as melanoma, head and neck squamous cell carcinoma, lung
CC carcinoma and breast carcinoma, but not in normal tissues except
CC for testes.
CC -!- SIMILARITY: Contains 1 MAGE domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; LI8877; AAA19023.1; -; Unassigned DNA.
DR EMBL; U82671; -; NOT ANNOTATED_CDS; Genomic_DNA.
DR EMBL; BT007108; AAP35772.1; -; mRNA.

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DR EMBL; BC003408; AAH03408.1; -; mRNA.
DR FIR; I54519; I54519.
DR Ensembl; ENSG00000147381; Homo sapiens.
DR HGNC; HGNC:6799; MAGEA12.
DR H-InvDB; HIX0020426; -.
DR MIM; 300177; -.
DR InterPro; IPR002190; MAGE.
DR PANTHER; PTHR11736; MAGE; 1.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS08338; MAGE; 1.
KW Antigen; Multigene family; Tumor antigen.
FT DOMAIN 109 308 MAGE.
FT COMPIAS 40 43 Poly-Ser.
FT CONFLICT 10 10 C -> S (in Ref. 2).
FT CONFLICT 187 187 D -> A (in Ref. 1).
FT CONFLICT 300 300 S -> P (in Ref. 1).
SQ SEQUENCE 314 AA; 34836 MW; 7E00F7CECD8F6568 CRC64;

Query Match 4.6%; Score 17; DB 1; Length 314;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 VOENYLEYRQVPGSDPA 292
Db 251 VOENYLEYRQVPGSDPA 267

RESULT 10
Q6FGT7 HUMAN
ID Q6FGT7_HUMAN PRELIMINARY; PRT; 314 AA.
AC Q6FGT7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MAGEA6 protein (Fragment).
GN Name=MAGEA6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
RA Neubert P., Ketrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR542020; CAG46817.1; -; mRNA.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS08338; MAGE; 1.
FT NON_TER 314 314
SQ SEQUENCE 314 AA; 34842 MW; 69562C7FA6E50275 CRC64;

Query Match 4.6%; Score 17; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 VOENYLEYRQVPGSDPA 292
Db 251 VOENYLEYRQVPGSDPA 267

RESULT 11
Q6FH15 HUMAN
ID Q6FH15_HUMAN PRELIMINARY; PRT; 314 AA.
AC Q6FH15;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MAGEA6 protein.
GN Name=MAGEA6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
RA Neubert P., Ketrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR541775; CAG46574.1; -; mRNA.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS08338; MAGE; 1.
FT NON_TER 314 314
SQ SEQUENCE 314 AA; 34836 MW; 7E00F7CECD8F6568 CRC64;

Query Match 4.6%; Score 17; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 VOENYLEYRQVPGSDPA 292
Db 251 VOENYLEYRQVPGSDPA 267

RESULT 12
Q6FHH8 HUMAN
ID Q6FHH8_HUMAN PRELIMINARY; PRT; 314 AA.
AC Q6FHH8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE MAGEA12 protein (Fragment).
GN Name=MAGEA12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
RA Neubert P., Ketrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR541775; CAG46574.1; -; mRNA.
FT NON_TER 314 314
SQ SEQUENCE 314 AA; 34836 MW; 7E00F7CECD8F6568 CRC64;

Query Match 4.6%; Score 17; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 VOENYLEYRQVPGSDPA 292
Db 251 VOENYLEYRQVPGSDPA 267

RESULT 13
Q53EXO HUMAN
ID Q53EXO_HUMAN PRELIMINARY; PRT; 314 AA.
AC Q53EXO;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Melanoma antigen, family A, 3 variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
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RA Maruyama K., Sugano S.;
RT "Oligo-capping : a simple method to replace the cap structure of
RT eucaryotic mRNAs with oligoribonucleotides.";
RL Gene 138:171-174 (1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
RT "Construction and characterization of a full length-enriched and a 5'-
RT end-enriched cDNA library.";
RL Gene 200:149-156 (1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK223519; BAD97239.1; -; mRNA.
FT NON TER 1
SQ SEQUENCE 314 AA; 34807 MW; F89866B6C84F073 CRC64;

Query Match 4.6%; Score 17; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 VOENYLEYRQVPGSDPA 292
Db |||||
251 VOENYLEYRQVPGSDPA 267

RESULT 14
Q96E03 HUMAN
ID Q96E03 HUMAN PRELIMINARY; PRT; 314 AA.
AC Q96E03;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Melanoma antigen family A, 2B.
GN Name=MAGEA2B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Adrenal cortex;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalón D.K., Muzny D.M., Young A.C., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madsen A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalón D.K., Muzny D.M., Young A.C., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Breast;
RX Director MGC Project;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063681; AAH63681.1; -; mRNA.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
SQ SEQUENCE 314 AA; 35026 MW; 28810BE358FA3FE6 CRC64;

Query Match 4.6%; Score 17; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 VOENYLEYRQVPGSDPA 292
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Job time : 235 secs

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DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
SQ SEQUENCE 314 AA; 35024 MW; A94F16247D1BFBC0 CRC64;

Query Match 4.6%; Score 17; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 VOENYLEYRQVPGSDPA 292
Db |||||
251 VOENYLEYRQVPGSDPA 267

RESULT 15
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ID Q96F48 HUMAN PRELIMINARY; PRT; 314 AA.
AC Q96F48;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Melanoma antigen family A, 2.
GN Name=MAGEA2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Breast;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Gibbs R.A.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madsen A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madsen A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Gibbs R.A.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madsen A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Breast;
RX Director MGC Project;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063681; AAH63681.1; -; mRNA.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
SQ SEQUENCE 314 AA; 35026 MW; 28810BE358FA3FE6 CRC64;

Query Match 4.6%; Score 17; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 VOENYLEYRQVPGSDPA 292
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251 VOENYLEYRQVPGSDPA 267

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Job time : 235 secs

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6/12/19

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Copyright (c) 1993 - 2006 Bioceleration Ltd.
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Searched: 1867569 seqs, 417829326 residues

Word size : 0

Total number of hits satisfying chosen parameters: 180914

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Listing first 45 summaries

Database : Published Applications AA_Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	9	2.4	9	3	US-09-933-708-3
2	9	2.4	9	3	US-09-865-548A-39
3	9	2.4	9	4	US-10-117-937-119
4	9	2.4	9	4	US-10-117-937-265
5	9	2.4	9	4	US-10-164-121A-13
6	9	2.4	9	4	US-10-164-078A-12
7	9	2.4	9	4	US-10-447-161-14
8	9	2.4	9	4	US-10-447-161-29
9	9	2.4	9	4	US-10-149-135-238
10	9	2.4	9	4	US-10-149-135-429
11	9	2.4	9	4	US-10-149-135-2050
12	9	2.4	9	4	US-10-149-135-2080
13	9	2.4	9	4	US-10-149-135-2106
14	9	2.4	9	4	US-10-149-135-2135
15	9	2.4	9	4	US-10-156-527-21
16	9	2.4	9	4	US-10-753-158-42
17	9	2.4	9	4	US-10-670-472A-6
18	9	2.4	9	5	US-10-651-616-24
19	9	2.4	9	5	US-10-362-715-8
20	9	2.4	9	5	US-10-705-459-39
21	9	2.4	9	5	US-10-776-521B-392
22	9	2.4	9	5	US-10-941-150A-13
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28 8 2.2 8 4 US-10-218-095-58 Sequence 58, Appl
29 8 2.2 8 4 US-10-149-135-233 Sequence 233, App
30 8 2.2 8 4 US-10-149-135-424 Sequence 424, App
31 8 2.2 8 4 US-10-149-135-1177 Sequence 1177, Ap
32 8 2.2 8 4 US-10-149-135-1274 Sequence 1274, Ap
33 8 2.2 8 4 US-10-149-135-1297 Sequence 1297, Ap
34 8 2.2 8 4 US-10-149-135-1315 Sequence 1315, Ap
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36 8 2.2 8 4 US-10-149-135-1453 Sequence 1453, Ap
37 8 2.2 8 4 US-10-149-135-1512 Sequence 1512, Ap
38 8 2.2 8 4 US-10-149-135-1626 Sequence 1626, Ap
39 8 2.2 8 4 US-10-156-527-20 Sequence 20, Appl
40 8 2.2 8 4 US-10-444-683-25 Sequence 25, Appl
41 8 2.2 9 4 US-10-117-937-100 Sequence 100, App
42 8 2.2 9 4 US-10-117-937-163 Sequence 163, App
43 8 2.2 9 4 US-10-117-937-259 Sequence 259, App
44 8 2.2 9 4 US-10-149-135-21 Sequence 21, Appl
45 8 2.2 9 4 US-10-149-135-46 Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-09-933-708-3
; Sequence 3, Application US/09933708
; Publication No. US20020099013A1
; GENERAL INFORMATION:
; APPLICANT: PICCARIELLO, THOMAS
; APPLICANT: OLON, LAWRENCE P.
; APPLICANT: KIRK, RANDAL J.
; TITLE OF INVENTION: ACTIVE AGENT DELIVERY SYSTEMS AND METHODS FOR
; TITLE OF INVENTION: PROTECTING AND ADMINISTERING ACTIVE AGENTS
; FILE REFERENCE: 54719.000028
; CURRENT APPLICATION NUMBER: US/09/933,708
; CURRENT FILING DATE: 2003-04-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(9)
; OTHER INFORMATION: This peptide may encompass 4-9 residues
US-09-933-708-3

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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 SSSSSSSSSS 62
Db 1 SSSSSSSSSS 9

RESULT 2
US-09-865-548A-39
; Sequence 39, Application US/09865548A
; Publication No. US20030096298A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULES
; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A

; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-39

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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 GLYDGMHLL 262
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DB 1 GLYDGMHLL 9

RESULT 3
US-10-117-937-119
; Sequence 119, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLLMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-119

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DB 1 YGEPRKLLT 9

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; Sequence 265, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLLMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
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; ORGANISM: Homo sapiens
US-10-117-937-265

Query Match 2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 LVFGIDVKE 193
|||||
DB 1 LVFGIDVKE 9

RESULT 5
US-10-164-121A-13
; Sequence 13, Application US/10164121A
; Publication No. US20030228308A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Boon, Thierry
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Traversari, Catra
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-Cw6 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5771
; CURRENT APPLICATION NUMBER: US/10/164,121A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-121A-13

Query Match 2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 GLYDGMHLL 262
|||||
DB 1 GLYDGMHLL 9

RESULT 6
US-10-164-078A-12
; Sequence 12, Application US/10164078A
; Publication No. US20030228325A1
; GENERAL INFORMATION:
; APPLICANT: Bilsborough, Janine
; APPLICANT: Schultz, Erwin
; APPLICANT: Panichelli, Christophe
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Boon, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B*18 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5756
; CURRENT APPLICATION NUMBER: US/10/164,078A
; CURRENT FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:

US-10-164-078A-12

Query Match 2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 GLYDGMHL 262
|||||
DB 1 GLYDGMHL 9

RESULT 7

US-10-447-161-14
; Sequence 14, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; PRIOR FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2003-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-14

Query Match 2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 DPARYEFLW 298
|||||
DB 1 DPARYEFLW 9

RESULT 8

US-10-447-161-29
; Sequence 29, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2003-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-29

Query Match 2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 GLYDGMHL 262
|||||
DB 1 GLYDGMHL 9

RESULT 9

US-10-149-135-238
; Sequence 238, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: WAGE2/3 Using Peptide and Nucleic Acid Compositions
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 238
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-238

Query Match 2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 284 RQVPGSDPA 292
|||||
DB 1 RQVPGSDPA 9

RESULT 10

US-10-149-135-429
; Sequence 429, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: WAGE2/3 Using Peptide and Nucleic Acid Compositions
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10

;; PRIOR APPLICATION NUMBER: US 08/205,713
;; PRIOR FILING DATE: 1994-03-04
;; PRIOR APPLICATION NUMBER: US 08/159,184
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/073,205
;; PRIOR FILING DATE: 1993-06-04
;; PRIOR APPLICATION NUMBER: US 08/027,146
;; PRIOR FILING DATE: 1993-03-05
;; NUMBER OF SEQ ID NOS: 2479
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 429
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Artificial Peptide
US-10-149-135-429

Query Match 2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 284 RQVPGSDPA 292
|||||
Db 1 RQVPGSDPA 9

RESULT 11
US-10-149-135-2050
;; Sequence 2050, Application US/10149135
;; Publication No. US20040053822A1
;; GENERAL INFORMATION:
;; APPLICANT: Fikes, John
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; APPLICANT: Southwood, Scott
;; APPLICANT: Chesnut, Robert
;; APPLICANT: Celis, Esteban
;; APPLICANT: Keogh, Elissa
;; TITLE OF INVENTION: Inducing Cellular Immune Responses to
;; FILE REFERENCE: MAGE2/3 Using Peptide and Nucleic Acid Compositions
;; CURRENT APPLICATION NUMBER: US/10/149,135
;; PRIOR FILING DATE: 2000-12-11
;; PRIOR APPLICATION NUMBER: PCT/US00/33545
;; PRIOR FILING DATE: 2000-12-11
;; PRIOR APPLICATION NUMBER: US 09/458,298
;; PRIOR FILING DATE: 1999-12-10
;; PRIOR APPLICATION NUMBER: US 09/189,702
;; PRIOR FILING DATE: 1998-11-10
;; PRIOR APPLICATION NUMBER: US 08/205,713
;; PRIOR FILING DATE: 1994-03-04
;; PRIOR APPLICATION NUMBER: US 08/159,184
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/073,205
;; PRIOR FILING DATE: 1993-06-04
;; PRIOR APPLICATION NUMBER: US 08/027,146
;; PRIOR FILING DATE: 1993-03-05
;; NUMBER OF SEQ ID NOS: 2479
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 2050
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2050

Query Match 2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 281 LEYRQVPGS 289

Db |||||
1 LEYRQVPGS 9

RESULT 12
US-10-149-135-2080
;; Sequence 2080, Application US/10149135
;; Publication No. US20040053822A1
;; GENERAL INFORMATION:
;; APPLICANT: Fikes, John
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; APPLICANT: Southwood, Scott
;; APPLICANT: Chesnut, Robert
;; APPLICANT: Celis, Esteban
;; APPLICANT: Keogh, Elissa
;; TITLE OF INVENTION: Inducing Cellular Immune Responses to
;; FILE REFERENCE: MAGE2/3 Using Peptide and Nucleic Acid Compositions
;; CURRENT APPLICATION NUMBER: US/10/149,135
;; PRIOR FILING DATE: 2000-12-11
;; PRIOR APPLICATION NUMBER: PCT/US00/33545
;; PRIOR FILING DATE: 2000-12-11
;; PRIOR APPLICATION NUMBER: US 09/458,298
;; PRIOR FILING DATE: 1999-12-10
;; PRIOR APPLICATION NUMBER: US 09/189,702
;; PRIOR FILING DATE: 1998-11-10
;; PRIOR APPLICATION NUMBER: US 08/205,713
;; PRIOR FILING DATE: 1994-03-04
;; PRIOR APPLICATION NUMBER: US 08/159,184
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/073,205
;; PRIOR FILING DATE: 1993-06-04
;; PRIOR APPLICATION NUMBER: US 08/027,146
;; PRIOR FILING DATE: 1993-03-05
;; NUMBER OF SEQ ID NOS: 2479
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 2080
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2080

Query Match 2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 276 VOENYLEYR 284
|||||
Db 1 VOENYLEYR 9

RESULT 13
US-10-149-135-2106
;; Sequence 2106, Application US/10149135
;; Publication No. US20040053822A1
;; GENERAL INFORMATION:
;; APPLICANT: Fikes, John
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; APPLICANT: Southwood, Scott
;; APPLICANT: Chesnut, Robert
;; APPLICANT: Celis, Esteban
;; APPLICANT: Keogh, Elissa
;; TITLE OF INVENTION: Inducing Cellular Immune Responses to
;; FILE REFERENCE: MAGE2/3 Using Peptide and Nucleic Acid Compositions
;; CURRENT APPLICATION NUMBER: US/10/149,135
;; PRIOR FILING DATE: 2000-12-11
;; PRIOR APPLICATION NUMBER: PCT/US00/33545
;; PRIOR FILING DATE: 2000-12-11

; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2106
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2106

Query Match 2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 281 LEYRQVPGS 289
Db 1 LEYRQVPGS 9

RESULT 14
US-10-149-135-2135
; Sequence 2135, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elisa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2135
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2135

Query Match 2.4%; Score 9; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;
QY 276 VOENYLEYR 284
Db 1 VOENYLEYR 9

RESULT 15
US-10-156-527-21
; Sequence 21, Application US/10156527
; Publication No. US20040063628A1
; GENERAL INFORMATION:
; APPLICANT: PICCARELLO, THOMAS
; APPLICANT: KIRK, RANDAL
; APPLICANT: OLON, LAWRENCE
; TITLE OF INVENTION: ACTIVE AGENT DELIVERY SYSTEMS AND METHODS FOR PROTECTING AND
; FILE OF INVENTION: ADMINISTERING ACTIVE AGENTS
; FILE REFERENCE: 54719.000063
; CURRENT APPLICATION NUMBER: US/10/156,527
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 09/986,426
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: 09/411,238
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 09/265,415
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 09/642,820
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/987,458
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/988,071
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 09/988,034
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 09/933,708
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/43089
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: PCT/US01/43117
; PRIOR FILING DATE: 2001-11-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: this peptide may encompass 4-9 residues according to the
; OTHER INFORMATION: specification as filed
US-10-156-527-21

Query Match 2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 54 SSSSSSSSS 62
Db 1 SSSSSSSSS 9

Search completed: March 17, 2006, 22:57:03
Job time : 162 secs

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OM protein - protein search, using sw model

Run on: March 17, 2006, 22:54:31 ; Search time 23 Seconds
(without alignments)
459.211 Million cell updates/sec

Title: US-09-856-812B-1
Perfect score: 369
Sequence: 1 MPRAPKRCMPEDLQSQS.....DTTAMASASSATGFSFSYPE 369

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 169630 seqs, 28622889 residues

Word size : 0
Total number of hits satisfying chosen parameters: 37190

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Listing first 45 summaries

- Database : Published Applications_AA_New.*
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 - 2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 4: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 5: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	2.4	9	6	US-10-994-204-11 Sequence 11, Appl
2	9	2.4	9	7	US-11-032-498-14 Sequence 14, Appl
3	9	2.4	9	7	US-11-044-051-6 Sequence 6, Appl
4	8	2.2	9	7	US-11-044-051-48 Sequence 48, Appl
5	7	1.9	9	6	US-10-517-784-33 Sequence 33, Appl
6	7	1.9	9	6	US-10-962-951-12 Sequence 12, Appl
7	7	1.9	9	6	US-10-602-663-31 Sequence 31, Appl
8	7	1.9	9	7	US-11-032-498-8 Sequence 8, Appl
9	7	1.9	9	7	US-11-032-498-11 Sequence 11, Appl
10	7	1.9	9	7	US-11-044-051-49 Sequence 49, Appl
11	7	1.9	9	7	US-11-044-051-50 Sequence 50, Appl
12	7	1.9	9	7	US-11-240-341-5 Sequence 5, Appl
13	7	1.9	9	7	US-11-240-341-7 Sequence 7, Appl
14	6	1.6	8	6	US-10-510-101-114 Sequence 114, App
15	6	1.6	8	6	US-10-517-784-30 Sequence 30, Appl
16	6	1.6	9	6	US-10-510-101-23 Sequence 23, Appl
17	6	1.6	9	7	US-11-032-498-20 Sequence 20, Appl
18	6	1.6	9	7	US-11-044-051-8 Sequence 8, Appl
19	6	1.6	9	7	US-11-044-051-10 Sequence 10, Appl
20	6	1.6	9	7	US-11-240-341-4 Sequence 4, Appl
21	6	1.6	9	7	US-11-188-849-1 Sequence 1, Appl
22	5	1.4	9	6	US-10-491-096-100 Sequence 100, App
23	5	1.4	9	6	US-10-491-096-165 Sequence 165, App
24	5	1.4	9	6	US-10-510-101-20 Sequence 20, Appl
25	5	1.4	9	6	US-10-510-101-21 Sequence 21, Appl

ALIGNMENTS

RESULT 1

US-10-994-204-11
; Sequence 11, Application US/10994204
; Publication No. US20050271679A1
; GENERAL INFORMATION:
; APPLICANT: DADAGLIO, GILLES
; APPLICANT: LECLERC, CLAUDE
; APPLICANT: LADANT, DANIEL
; APPLICANT: VAN DEN ENDE, BENOIT
; APPLICANT: MOREL, SANDRA
; APPLICANT: BAUCHE, CECILE
; TITLE OF INVENTION: RECOMBINANT ADENYLATE CYCLASE TOXIN OF BORDETTELLA
; TITLE OF INVENTION: INDUCES T CELL RESPONSES AGAINST TUMORAL ANTIGENS
; FILE REFERENCE: 03495.0327
; CURRENT APPLICATION NUMBER: US/10/994,204
; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: 60/523,632
; PRIOR FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-994-204-11

Query Match 2.4%; Score 9; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 GLYDGMHEHL 262

Db 1 GLYDGMHEHL 9

RESULT 2

US-11-032-498-14
; Sequence 14, Application US/11032498
; Publication No. US20050249743A1
; GENERAL INFORMATION:
; APPLICANT: Boon-Faller, Thierry
; APPLICANT: Van der Bruggen, Pierre
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-A24 Molecule and Uses Thereof
; FILE REFERENCE: LUD 5861
; CURRENT APPLICATION NUMBER: US/11/032,498

; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: US 60/535,751
; PRIOR FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MAGE-A10 peptide
US-11-032-498-14

Query Match 2.4%; Score 9; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 254 GLYDGMHL 262
Db 1 GLYDGMHL 9

RESULT 3

US-11-044-051-6
; Sequence 6, Application US/11044051
; Publication No. US2005025553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: CODELAINE, Danisle
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459,263
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-044-051-6

Query Match 2.4%; Score 9; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 333 ALKDEERA 341
Db 1 ALKDEERA 9

RESULT 4

US-11-044-051-48
; Sequence 48, Application US/11044051
; Publication No. US2005025553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: CODELAINE, Danisle
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459,263
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 48
; LENGTH: 9
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Antigenic peptide
US-11-044-051-48

Query Match 2.2%; Score 8; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 333 ALKDEER 340
Db 1 ALKDEER 8

RESULT 5

US-10-517-784-33
; Sequence 33, Application US/10517784
; Publication No. US20060003315A1
; GENERAL INFORMATION:
; APPLICANT: GROSS, Gideon
; APPLICANT: MARGALIT, Alon
; TITLE OF INVENTION: MEMBRANE-ANCHORED BETA-2 MICROGLOBULIN COVALENTLY LINKED TO MHC
; TITLE OF INVENTION: PEPTIDE EPITOPES
; FILE REFERENCE: GAVISH-004 US
; CURRENT APPLICATION NUMBER: US/10/517,784
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US 60/389,273
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/IL03/00501
; PRIOR FILING DATE: 2003-06-12
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-517-784-33

Query Match 1.9%; Score 7; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 296 FLWGPRA 302
Db 1 FLWGPRA 7

RESULT 6

US-10-962-951-12
; Sequence 12, Application US/10962951
; Publication No. US20060029610A1
; GENERAL INFORMATION:
; APPLICANT: Argon, Yair
; APPLICANT: Gidalevitz, Tali
; APPLICANT: Biswas, Chhanda
; APPLICANT: Simen, Birgitte B.
; APPLICANT: Wanderling, Sherry
; APPLICANT: Ostrovsky, Olga
; TITLE OF INVENTION: GRP94-BASED COMPOSITIONS AND METHODS OF
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: 3460-CHOP.C-2060US
; CURRENT APPLICATION NUMBER: US/10/962,951
; CURRENT FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US/10/844,711
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/469,723
; PRIOR FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/477,990

; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: 60/478,149
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: 60/556,362
; PRIOR FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: 60/566,363
; PRIOR FILING DATE: 2004-04-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MAGE 3
US-10-962-951-12

Query Match 1.9%; Score 7; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 FLWGPRA 302
Db 1 FLWGPRA 7

RESULT 7
US-10-602-663-31
; Sequence 31, Application US/10602663
; Publication No. US20060040347A1
; GENERAL INFORMATION:
; APPLICANT: CHARNEAU, PIERRE
; APPLICANT: ZENNOU, VERONIQUE
; APPLICANT: FIRAT, HUSYIN
; TITLE OF INVENTION: USE OF TRIPLEX STRUCTURE DNA SEQUENCES FOR TRANSFERRING
; FILE OF INVENTION: NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 03495.0199
; CURRENT APPLICATION NUMBER: US/10/602,663
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US/09/688,990
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: PCT/FR99/00974
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Melanoma
; OTHER INFORMATION: peptide
US-10-602-663-31

Query Match 1.9%; Score 7; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 FLWGPRA 302
Db 1 FLWGPRA 7

RESULT 8
US-11-032-498-8
; Sequence 8, Application US/11032498
; Publication No. US20050249743A1
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Van der Bruggen, Pierre
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-A24 Molecule and Uses Thereof
; FILE REFERENCE: LUD 5881
; CURRENT APPLICATION NUMBER: US/11/032,498

; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: US 60/535,751
; PRIOR FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: MAGE-A3 peptide
US-11-032-498-8

Query Match 1.9%; Score 7; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 FLWGPRA 302
Db 1 FLWGPRA 7

RESULT 9
US-11-032-498-11
; Sequence 11, Application US/11032498
; Publication No. US20050249743A1
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Van der Bruggen, Pierre
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-A24 Molecule and Uses Thereof
; FILE REFERENCE: LUD 5881
; CURRENT APPLICATION NUMBER: US/11/032,498
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: US 60/535,751
; PRIOR FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MAGE-A12 peptide
US-11-032-498-11

Query Match 1.9%; Score 7; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 FLWGPRA 302
Db 1 FLWGPRA 7

RESULT 10
US-11-044-051-49
; Sequence 49, Application US/11044051
; Publication No. US2005025553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: GODELAINE, DaniSle
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459,263
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49

; LENGTH: 9
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Antigenic peptide
US-11-044-051-49

Query Match 1.9%; Score 7; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

QY 333 ALKDEEE 339
Db 1 ALKDEEE 7

RESULT 11
US-11-044-051-50
; Sequence 50, Application US/11044051
; Publication No. US2005025553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: GODELAINE, Danisle
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459,263
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 9
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Antigenic peptide
US-11-044-051-50

Query Match 1.9%; Score 7; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

QY 333 ALKDEEE 339
Db 1 ALKDEEE 7

RESULT 12
US-11-240-341-5
; Sequence 5, Application US/11240341
; Publication No. US20060024742A1
; GENERAL INFORMATION:
; APPLICANT: Martelange, Valerie
; APPLICANT: De Smet, Charles
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: L0461.70047US01
; CURRENT APPLICATION NUMBER: US/11/240,341
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US 09/183,789
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: US 09/060,706
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-240-341-5

Query Match 1.9%; Score 7; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

QY 264 YGEPRKL 270
Db 3 YGEPRKL 9

RESULT 13
US-11-240-341-7
; Sequence 7, Application US/11240341
; Publication No. US20060024742A1
; GENERAL INFORMATION:
; APPLICANT: Martelange, Valerie
; APPLICANT: De Smet, Charles
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: L0461.70047US01
; CURRENT APPLICATION NUMBER: US/11/240,341
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US 09/183,789
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: US 09/060,706
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-240-341-7

Query Match 1.9%; Score 7; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

QY 296 FLWGPRA 302
Db 1 FLWGPRA 7

RESULT 14
US-10-510-101-114
; Sequence 114, Application US/10510101
; Publication No. US20060018915A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Ishioke, Glenn
; APPLICANT: Fikes, John
; APPLICANT: Tangri, Shabnam
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
; FILE REFERENCE: 2060.009PC05
; CURRENT APPLICATION NUMBER: US/10/510,101
; CURRENT FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: US 60/413,471
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 10/116,118
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide derived from Homo sapiens melanoma antigens
US-10-510-101-114

Query Match 1.6%; Score 6; DB 6; Length 8;

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Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 297 LMGPR 302
Db 1 LMGPR 6

RESULT 15
US-10-517-784-30
; Sequence 30, Application US/10517784
; Publication No. US20060003315A1
; GENERAL INFORMATION:
; APPLICANT: GROSS, Gideon
; TITLE OF INVENTION: MEMBRANE-ANCHORED BETA-2 MICROGLOBULIN COVALENTLY LINKED TO MHC
; FILE REFERENCE: GAVISH-004 US
; CURRENT APPLICATION NUMBER: US/10/517,784
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US 60/388,273
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/IL03/00501
; PRIOR FILING DATE: 2003-06-12
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-517-784-30

Query Match 1.6%; Score 6; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 195 DPTGHS 200
Db 3 DPTGHS 8
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Job time : 24 secs

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OM protein - protein search, using sw model

Run on: March 17, 2006, 22:49:05 ; Search time 39 Seconds
(without alignments)
910.359 Million cell updates/sec

Title: US-09-856-812B-1
Perfect score: 369
Sequence: 1 MPRAPKRCMPEDLQSQS.....DTTAMASASSSGTSFSYPE 369

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 791

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	1.1	4	2 I40697	biotin A - Citropa
2	4	1.1	5	2 PT0651	T-cell receptor be
3	4	1.1	6	2 PT0593	T-cell receptor be
4	4	1.1	6	4 A35039	hypothetical colla
5	4	1.1	7	2 A11483	aspartate transami
6	4	1.1	7	2 B39040	calsequestrin, fas
7	4	1.1	8	2 PT0691	T-cell receptor be
8	4	1.1	8	2 S29272	tocopherol-binding
9	4	1.1	8	2 S65647	2-hydroxyglutaryl-
10	4	1.1	8	2 I57018	gene cfr protein
11	4	1.1	9	2 B45796	dihydrolipoamide S
12	4	1.1	9	2 PT0670	T-cell receptor be
13	4	1.1	9	2 PH0902	T-cell receptor be
14	4	1.1	9	2 B41983	orf downstream to b
15	3	0.8	3	3 PT0636	T-cell receptor be
16	3	0.8	3	3 PT0622	T-cell receptor be
17	3	0.8	3	3 B23751	spinal cord peptid
18	3	0.8	4	2 B43848	cell surface adhes
19	3	0.8	4	2 I40505	hypothetical prote
20	3	0.8	4	2 I61883	protamine P1 - ora
21	3	0.8	4	2 I37013	protamine P1 - Car
22	3	0.8	4	2 I84439	protamine P1 - sav
23	3	0.8	4	2 PT0696	T-cell receptor be
24	3	0.8	4	2 PT0645	T-cell receptor be
25	3	0.8	4	2 PT0712	T-cell receptor be
26	3	0.8	4	2 PT0698	T-cell receptor be
27	3	0.8	4	2 PT0551	tyrosine-melanocyt
28	3	0.8	4	2 A32039	URF2 protein - Xan
29	3	0.8	5	2 S70154	

30	3	0.8	5	2 A44955	alkanal monooxygen
31	3	0.8	5	2 I39964	ribosomal protein
32	3	0.8	5	2 I39966	ribosomal protein
33	3	0.8	5	2 I39965	ribosomal protein
34	3	0.8	5	2 B60274	major protein anti
35	3	0.8	5	2 D60274	major protein anti
36	3	0.8	5	2 E60274	major protein anti
37	3	0.8	5	2 P80324	ribulose-bisphosph
38	3	0.8	5	2 I50385	myosin light chain
39	3	0.8	5	2 PT0596	T-cell receptor be
40	3	0.8	5	2 PT0610	T-cell receptor be
41	3	0.8	5	2 PT0597	T-cell receptor be
42	3	0.8	5	2 PT0729	T-cell receptor be
43	3	0.8	5	2 PT0624	T-cell receptor be
44	3	0.8	5	2 PT0625	T-cell receptor be
45	3	0.8	5	2 PT0672	T-cell receptor be

ALIGNMENTS

RESULT 1

I40697
biotin A - Citrobacter freundii (fragment)
C:Species: Citrobacter freundii
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40697
R:Shiuan, D.; Campbell, A.
Gene 67, 203-211, 1988
A>Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter
A:Reference number: I40697; MUID:89006280; PMID:2971595
A:Accession: I40697
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: UNIPROT:P13071; UNIPARC:UPI000017AA21; GB:M21922; NID:g144434

Query Match 1.1%; Score 4; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 347 TTDD 350
DB 1 TTDD 4

RESULT 2

PT0651
T-cell receptor beta chain V-D-J region (121-1C) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0651
R:Peeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A>Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0651
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FEE>
A:Cross-references: UNIPARC:UPI000017C7EE
A:Experimental source: day 4 postnatal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 1.1%; Score 4; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 ASAS 358
DB 1 ASAS 4

```
RESULT 3
PT0593
T-cell receptor beta chain V-D-J region (159-1P) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0593
R:Peeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0593
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <PEE>
A:Cross-references: UNIPARC:UPI000017C83P
A:Experimental source: day 19 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      1.1%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      38 ASSS 41
      |||||
Db       1 ASSS 4

RESULT 4
A35039
hypothetical collagen alpha 2(I) intron 2 protein 1 - chicken
C:Species: Gallus gallus (chicken)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: A35039
R:Bennett, V.D.; Adams, S.L.
J. Biol. Chem. 265, 2223-2230, 1990
A:Title: Identification of a cartilage-specific promoter within intron 2 of the chick alpha 2(I) collagen gene.
A:Reference number: A35039; MUID:90130479; PMID:1688851
A:Accession: A35039
A:Molecule type: mRNA
A:Residues: 1-6 <BEN>
A:Cross-references: UNIPARC:UPI000017CEB1; GB:M33382; NID:g211043
A:Note: This ORF is not translated in GenBank entry CHKA21CG
C:Comment: This sequence is the translation of a cartilage specific alternative transcript
C:Keywords: alternative splicing; cartilage

Query Match      1.1%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      98 ASLP 101
      |||||
Db       2 ASLP 5

RESULT 5
A11483
aspartate transaminase (EC 2.6.1.1), mitochondrial - sheep (fragment)
N:Alternate names: aspartate aminotransferase, mitochondrial
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 20-Aug-1999
C:Accession: A11483
R:Campos-Cavieiro, M.; Milestein, C.P.
Biochem. J. 147, 275-281, 1975
A:Title: The sequences of the coenzyme-binding peptide in the cytoplasmic and the mitochondrial aspartate aminotransferase from sheep.
A:Reference number: A11483; MUID:76039441; PMID:11180894
A:Accession: A11483
A:Molecule type: protein
A:Residues: 1-7 <CAM>
A:Cross-references: UNIPARC:UPI000017C59C
A:Experimental source: liver
C:Keywords: aminotransferase; mitochondrion; phosphoprotein; pyridoxal phosphate
F:2/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental
```

```
Query Match      1.1%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      253 MGLY 256
      |||||
Db       4 MGLY 7

RESULT 6
B39040
calsequestrin, fast skeletal muscle - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997
C:Accession: B39040
R:Calais, S.E.; Jones, L.R.
J. Biol. Chem. 266, 391-398, 1991
A:Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein kinase II.
A:Reference number: A39040; MUID:91093153; PMID:1985907
A:Accession: B39040
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <CAL>
A:Cross-references: UNIPARC:UPI000017C58C
C:Keywords: phosphoprotein; skeletal muscle

Query Match      1.1%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 EEDL 16
      |||||
Db       3 EEDL 6

RESULT 7
PT0691
T-cell receptor beta chain V-D-J region (154-2K) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0691
R:Peeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0691
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-8 <PEE>
A:Cross-references: UNIPARC:UPI000017C83D
A:Experimental source: day 18 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      1.1%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      265 GEPR 268
      |||||
Db       3 GEPR 6

RESULT 8
S29272
tocopherol-binding protein, s1k - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 12-Apr-1996
C:Accession: S29272
R:Nalecz, K.A.; Nalecz, M.J.; Azzi, A.
Eur. J. Biochem. 209, 37-42, 1992
A:Title: Isolation of tocopherol-binding proteins from the cytosol of smooth muscle A7r: cells.
A:Reference number: S29272; MUID:93011150; PMID:1396710
A:Accession: S29272
```

A:Molecule type: protein
A:Residues: 1-8 <NAL>
A:Cross-references: UNIPARC:UPI000017CA08
A:Experimental source: smooth muscle A7r5 cells

Query Match 1.1%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PEED 15
DB 1 PEED 4

RESULT 9
S65647
2-hydroxyglutaryl-CoA dehydratase - Acidaminococcus fermentans (fragment)
C:Species: Acidaminococcus fermentans
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S65647
R:Mueller, U.; Buckel, W.
Eur. J. Biochem. 230, 698-704, 1995
A:Title: Activation of (R)-2-hydroxyglutaryl-CoA dehydratase from Acidaminococcus fermentans
A:Reference number: S65647; MUID:95331308; PMID:7607244
A:Accession: S65647
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <MUE>
A:Cross-references: UNIPROT:Q7M1C5; UNIPARC:UPI000017AB76

Query Match 1.1%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 GIDV 191
DB 4 GIDV 7

RESULT 10
IS7018
gene Cfr protein - mouse (fragment)
C:Species: Mus sp. (mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: IS7018
R:Dorin, J.R.; Stevenson, B.J.; Fleming, S.; Alton, E.W.; Dickinson, P.; Porteous, D.J.
Mamm. Genome 5, 465-472, 1994
A:Title: Long-term survival of the exon 10 insertional cystic fibrosis mutant mouse is a result of a mutation in the Cfr gene
A:Reference number: IS7018; MUID:95037043; PMID:7949729
A:Accession: IS7018
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-8 <RES>
A:Cross-references: UNIPROT:Q7M056; UNIPARC:UPI000017C895; GB:S74246; NID:g710482
A:Genetics: Cfr

Query Match 1.1%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 LPDS 126
DB 1 LPDS 4

RESULT 11
B45796
dihydrolipoamide S-succinyltransferase (EC 2.3.1.61) - Pseudomonas fluorescens (fragment)
C:Species: Pseudomonas fluorescens
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
A:Accession: B45796
R:Benen, J.A.E.; Van Berkel, W.J.H.; Van Dongen, W.M.A.M.; Mueller, F.; De Kok, A.

A:Molecule type: protein
A:Residues: 1-8 <NAL>
A:Cross-references: UNIPARC:UPI000017CA08
A:Experimental source: smooth muscle A7r5 cells

Query Match 1.1%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PEED 15
DB 1 PEED 4

RESULT 9
S65647
2-hydroxyglutaryl-CoA dehydratase - Acidaminococcus fermentans (fragment)
C:Species: Acidaminococcus fermentans
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S65647
R:Mueller, U.; Buckel, W.
Eur. J. Biochem. 230, 698-704, 1995
A:Title: Activation of (R)-2-hydroxyglutaryl-CoA dehydratase from Acidaminococcus fermentans
A:Reference number: S65647; MUID:95331308; PMID:7607244
A:Accession: S65647
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <MUE>
A:Cross-references: UNIPROT:Q7M1C5; UNIPARC:UPI000017AB76

Query Match 1.1%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 GIDV 191
DB 4 GIDV 7

RESULT 10
IS7018
gene Cfr protein - mouse (fragment)
C:Species: Mus sp. (mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: IS7018
R:Dorin, J.R.; Stevenson, B.J.; Fleming, S.; Alton, E.W.; Dickinson, P.; Porteous, D.J.
Mamm. Genome 5, 465-472, 1994
A:Title: Long-term survival of the exon 10 insertional cystic fibrosis mutant mouse is a result of a mutation in the Cfr gene
A:Reference number: IS7018; MUID:95037043; PMID:7949729
A:Accession: IS7018
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-8 <RES>
A:Cross-references: UNIPROT:Q7M056; UNIPARC:UPI000017C895; GB:S74246; NID:g710482
A:Genetics: Cfr

Query Match 1.1%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 LPDS 126
DB 1 LPDS 4

RESULT 11
B45796
dihydrolipoamide S-succinyltransferase (EC 2.3.1.61) - Pseudomonas fluorescens (fragment)
C:Species: Pseudomonas fluorescens
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
A:Accession: B45796
R:Benen, J.A.E.; Van Berkel, W.J.H.; Van Dongen, W.M.A.M.; Mueller, F.; De Kok, A.

J. Gen. Microbiol. 135, 1787-1797, 1989
A:Title: Molecular cloning and sequence determination of the lpd gene encoding liposamidase
A:Reference number: A45796; MUID:90132584; PMID:2515251
A:Accession: B45796
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-9 <BEN>
A:Cross-references: UNIPROT:Q51765; UNIPARC:UPI000008D216; GB:M28356; NID:g151343; PIDN:1836012
C:Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology
C:Keywords: acyltransferase; coenzyme A; liposamide; tricarboxylic acid cycle

Query Match 1.1%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 DPAR 293
DB 1 DPAR 4

RESULT 12
PT0670
T-cell receptor beta chain V-D-J region (121-1BN) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0670
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0670
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-9 <FEE>
A:Cross-references: UNIPARC:UPI000017C7EC
A:Experimental source: day 4 postnatal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 1.1%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ASSS 41
DB 1 ASSS 4

RESULT 13
PH0902
T-cell receptor beta chain V-D-J region (hybridoma S23F4F4) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0902
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0902
A:Molecule type: mRNA
A:Residues: 1-9 <GOL>
A:Cross-references: UNIPARC:UPI000017C9F1
A:Experimental source: myelin basic protein-immunized T-cell
C:Keywords: T-cell receptor

Query Match 1.1%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 SSTS 43
DB 3 SSTS 6

RESULT 14

B41983
 orf downstream to bacterioferritin - Azotobacter vinelandii (fragment)
 C:Species: Azotobacter vinelandii
 C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: B41983
 R:Grossman, M.J.; Hinton, S.M.; Minak-Bernero, V.; Slaughtter, C.; Stiefel, E.I.
 Proc. Natl. Acad. Sci. U.S.A. 89, 2419-2423, 1992
 A:Title: Unification of the ferritin family of proteins.
 A:Reference number: A41983; MUID:92196129; PMID:1549605
 A:Accession: B41983
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid; protein
 A:Residues: 1-9 <GRO>
 A:Cross-references: UNIPROT:P25825; UNIPARC:UPI000013A327; GB:M83692; NID:g142297; PIDN:
 A:Note: sequence extracted from NCBI backbone (NCBIP:88442)

Query Match 1.1%; Score 4; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 TSTS 45
 ||||
 Db 6 TSTS 9

RESULT 15

PT0636
 T-cell receptor beta chain V-D-J region (100-2AT) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C:Accession: PT0636
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0636
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-3 <FEE>
 A:Cross-references: UNIPARC:UPI000017CE9E
 A:Experimental source: newborn thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 0.8%; Score 3; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 361 ATG 363
 ||||
 Db 1 ATG 3

Search completed: March 17, 2006, 22:53:25
 Job time : 40 secs

GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM protein - protein search, using sw model
 Run on: March 17, 2006, 22:45:50 ; Search time 228 Seconds
 (without alignments)
 1141.842 Million cell updates/sec
 Title: US-09-856-812B-1
 Perfect score: 369
 Sequence: 1 MPRAKRCRCPEEDLQSQS.....DTTAMASASSATGFSFSYPE 369

Scoring table: OLI³⁰ Gapop 60.0 , Gapext 60.0
 Searched: 2166443 seqs, 705528306 residues
 Word size : 0
 Total number of hits satisfying chosen parameters: 1766
 Minimum DB seq length: 0
 Maximum DB seq length: 9
 Post-processing: Listing first 45 summaries
 Database : UniProt 05.80.*
 1: uniprot_sprot.*
 2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	5	1.4	Q70Y81_9LAMI	Q70Y81 plectranth
2	5	1.4	Q9FXL0_LILLO	Q9FXL0 lilium long
3	4	1.1	P13071_CITR	P13071 citrobacter
4	4	1.1	P70804_AZOVI	P70804 azotobacter
5	4	1.1	Q9P285_HUMAN	Q9P285 homo sapien
6	4	1.1	Q53TMC_HUMAN	Q53TMC homo sapien
7	4	1.1	P82324_PEA	P82324 pisum sativ
8	4	1.1	O87471_HABIN	O87471 haemophilus
9	4	1.1	Q7M1C5_ACIFE	Q7M1C5 acidaminoco
10	4	1.1	Q78DX6_RAT	Q78DX6 rattus norv
11	4	1.1	Q7M056_9MURI	Q7M056 mus sp. gen
12	4	1.1	Q35835_9MURI	Q35835 rattus sp.
13	4	1.1	R133_BOVIN	P82926 bos taurus
14	4	1.1	YBFR_AZOVI	P25825 azotobacter
15	4	1.1	Q51LX3_MAGGR	Q51LX3 magnaporthe
16	4	1.1	Q15891_HUMAN	Q15891 homo sapien
17	4	1.1	Q6QF45_HUMAN	Q6QF45 homo sapien
18	4	1.1	Q9UCS8_HUMAN	Q9UCS8 homo sapien
19	4	1.1	Q28112_BOVIN	Q28112 bos taurus
20	4	1.1	Q5ZES4_BOVIN	Q5ZES4 bos taurus
21	4	1.1	Q42452_WHEAT	Q42452 triticum ae
22	4	1.1	P83529_LACSN	P83529 lactobacill
23	4	1.1	Q5U4H1_XANMA	Q5U4H1 xanthomonas
24	4	1.1	Q51765_PSEFL	Q51765 pseudomonas
25	4	1.1	Q81182_MOUSE	Q81182 mus musculu
26	4	1.1	Q72P19_9HIV1	Q72P19 human immun
27	3	0.8	AP21_EISFO	P84182 eisenia foe
28	3	0.8	FARP_CHICK	P83308 gallus gall
29	3	0.8	TRAM3_ECOLI	P13973 escherichia
30	3	0.8	ACPH_RABIT	P25154 oryctolagus
31	3	0.8	UN06_CLOPA	P81351 clostridium

32	3	0.8	7	1	CCF1_ENTFA	P20104 enterococcu
33	3	0.8	7	1	CIA_ENTFA	P11932 enterococcu
34	3	0.8	7	1	LANC_CARUI	P36960 carnobacter
35	3	0.8	7	1	MNP1_LEPDE	P42984 leptinotars
36	3	0.8	7	1	UF03_MOUSE	P38641 mus musculu
37	3	0.8	7	1	UH11_RAT	P56576 rattus norv
38	3	0.8	7	1	Q15897_HUMAN	Q15897 homo sapien
39	3	0.8	7	2	Q9BRY4_HUMAN	Q9BRY4 homo sapien
40	3	0.8	7	2	Q28742_RABIT	Q28742 oryctolagus
41	3	0.8	7	2	P84495_CUCMA	P84495 cucurbita m
42	3	0.8	7	2	Q8MPY6_9ASTR	Q8MPY6 taraxacum (
43	3	0.8	7	2	Q47029_ENTCL	Q47029 enterobacte
44	3	0.8	7	2	Q8GL04_BORBU	Q8GL04 borrelia bu
45	3	0.8	7	2	Q8GL12_BORBU	Q8GL12 borrelia bu

ALIGNMENTS

RESULT 1
 Q70Y81_9LAMI PRELIMINARY; PRT; 9 AA.
 AC Q70Y81.
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DE Ribosomal protein (Fragment).
 GN Name=rp16;
 OS Plectranthus gillettii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Plectranthus.
 OX NCBI_TaxID=204186;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;
 RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
 RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
 RT "Phylogeny and evolution of basilis and allies (Ocimeae, Labiatae)
 based on three plastid DNA regions.";
 RL Mol. Phylogenet. Evol. 31:277-299(2004).
 DR EMBL; AJ505385; CAD45506.1; -; Genomic DNA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 KW Ribosomal protein.
 FT NON_TER 1
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1016 MW; 66D6205861A3333B CRC64;
 Query Match 1.4%; Score 5; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 223 KTGIL 227
 DB 4 KTGIL 8
 RESULT 2
 Q9FXL0_LILLO PRELIMINARY; PRT; 9 AA.
 ID Q9FXL0.
 AC Q9FXL0.
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DE LIM8 protein (Fragment).
 GN Name=LIM8;
 OS Lilium longiflorum (Trumpet lily).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.
 OX NCBI_TaxID=4650;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

```

RA Uefuji H., Minami M., Takase H., Hiratsuka K.;
RT "Isolation of a Promoter that Directs Microsporogenesis-Associated
RT Gene Expression in Lillium longiflorum.";
RL Plant Biotechnol. 18:151-156(2001).
DR EMBL; AB050987; BAB17856.1; -; Genomic_DNA.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1021 MW; 6F8BD76685A6C2CB CRC64;

Query Match 1.4%; Score 5; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 VQSMP 222
DB 3 VQSMP 7

RESULT 3
BIOA_CITFR STANDARD; PRT; 5 AA.
AC P13071;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
DE (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
DE aminotransferase) (Fragment).
DE Name=bioA;
GN Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=89006280; PubMed=2971595; DOI=10.1016/0378-1119(88)90397-6;
RA Shivan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
CC oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
CC diaminononanoate.
CC -!- COFACTOR: Pyridoxal phosphate.
CC -!- PATHWAY: Cofactor biosynthesis; biotin biosynthesis; biotin from
CC 6-carboxyhexanoyl-CoA: step 2.
CC -!- SUBUNIT: Homodimer.
CC -!- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent
CC aminotransferase family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; M21922; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR PIR; I40697; I40697.
DR InterPro; IPR005814; Aminotrans_3.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
KW Aminotransferase; Biotin biosynthesis; Pyridoxal phosphate;
KW Transferase.
FT NON_TER 5
SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 1.1%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 347 TTDD 350
DB 2 TTDD 5

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RESULT 4
P70804 AZOVI PRELIMINARY; PRT; 7 AA.
AC P70804;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Algt protein (Fragment).
DE Name=algt;
GN Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E; 96427318; PubMed=8830682;
RX MEDLINE=96427318; PubMed=8830682;
RA Rehm B.H.A., Ertesvaag H., Valla S.;
RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algC) is
RT part of an alg gene cluster physically organized in a manner similar
RT to that in Pseudomonas aeruginosa.";
RL J. Bacteriol. 178:5884-5889(1996).
DR EMBL; X87973; CAA61230.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 7 AA; 684 MW; 71B5A5A5A2D1AED0 CRC64;

Query Match 1.1%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 SSST 42
DB 4 SSST 7

RESULT 5
Q9P285 HUMAN PRELIMINARY; PRT; 8 AA.
AC Q9P285;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Clotting factor VIII (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Shibata M., Shima M., Morichika S., Yoshiola A.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040872; BAA94312.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 866 MW; 1C16987AAB05BDD3 CRC64;

Query Match 1.1%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 DGWE 260
DB 5 DGWE 8

RESULT 6
Q53TM6 HUMAN PRELIMINARY; PRT; 8 AA.
AC Q53TM6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

```

Best Local Similarity 100.0%; Pred. No. 2.2e+06;			
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	95 SVVA 98		
DB	1 SVVA 4		
RESULT 8			
O87471_HABIN			
ID	O87471_HABIN PRELIMINARY;	PRT;	8 AA.
AC	O87471;		
DT	01-NOV-1998 (TrEMBLrel. 08, Created)		
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)		
DT	01-NOV-1998 (TrEMBLrel. 08, Last annotation update)		
DE	Hifa (Fragment).		
GN	Name-hifa;		
OS	Haemophilus influenzae.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;		
OC	Pasteurellaceae; Haemophilus.		
NCBI_TaxID=727;			
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=Eagan;		
RX	MEDLINE=98389689; PubMed=9721313;		
RA	Mhlanga-Mutangadura T., Morlin G., Smith A.L., Eisenstark A.,		
RA	Golomb M.;		
RT	"Evolution of the major pilus gene cluster of Haemophilus		
RT	influenzae.";		
RL	J. Bacteriol. 180:4693-4703 (1998).		
DR	EMBL; AF071762; AAC35830.1; -; Genomic_DNA.		
FT	NON_TER 1		
SEQ	SEQUENCE 8 AA; 876 MW; DAB44451A7272325 CRC64;		
Query Match 1.1%; Score 4; DB 2; Length 8;			
Best Local Similarity 100.0%; Pred. No. 2.2e+06;			
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	269 KLIT 272		
DB	2 KLIT 5		
RESULT 9			
Q7M1C5_ACIFE			
ID	Q7M1C5_ACIFE PRELIMINARY;	PRT;	8 AA.
AC	Q7M1C5;		
DT	01-MAR-2004 (TrEMBLrel. 26, Created)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	2-hydroxyglutaryl-CoA dehydratase (Fragment).		
OS	Acidaminococcus fermentans		
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Acidaminococcaceae;		
OC	Acidaminococcus.		
NCBI_TaxID=905;			
RN	[1]		
RP	PROTEIN SEQUENCE.		
RX	MEDLINE=95331308; PubMed=7607244;		
RA	Mueller U., Buckel W.;		
RT	"Activation of (R)-2-hydroxyglutaryl-CoA dehydratase from		
RT	Acidaminococcus fermentans.";		
RL	Eur. J. Biochem. 230:698-704 (1995).		
DR	PIR; S65647; S65647.		
FT	NON_TER 1		
FT	NON_TER 8		
SEQ	SEQUENCE 8 AA; 761 MW; C762CAA0587731B5 CRC64;		
Query Match 1.1%; Score 4; DB 2; Length 8;			
Best Local Similarity 100.0%; Pred. No. 2.2e+06;			
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	188 GIDV 191		

```
Db          4 CIDV 7

RESULT 10
Q78DX6_RAT PRELIMINARY; PRT; 8 AA.
AC Q78DX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Vasopressin V2 receptor (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX MEDLINE=95396550; PubMed=7667072;
RA Mandon B., Bellanger A.C., Elalouf J.M.;
RT "Inverse-PCR-mediated cloning of the promoter for the rat vasopressin
RL V2 receptor gene.";
RL Pfluegers Arch. 430:12-18(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RA Elalouf J.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; X83264; CAA58238.1; -; Genomic DNA.
DR GO; GO:0004872; Fireceptor activity; IEA.
KW Receptor.
FT NON TER
SQ SEQUENCE 8 AA; 849 MW; ECA2D1B5A2C72726 CRC64;

Query Match 1.1%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 MLIV 186
DB 1 MLIV 4

RESULT 11
Q7M056_9MURI PRELIMINARY; PRT; 8 AA.
AC Q7M056;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Gene Cfr protein (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95037043; PubMed=7949729;
RA Dorin J.R., Stevenson B.J., Fleming S., Alton E.W., Dickinson P.,
RA Porteous D.J.;
RT "Long-term survival of the exon 10 insertion cystic fibrosis mutant
RT mouse is a consequence of low level residual wild-type Cfr gene
RT expression.";
RL Mamm. Genome 5:465-472(1994).
DR FIR; I57018; I57018.
FT NON TER
SQ SEQUENCE 8 AA; 874 MW; 180EA5A775BAB767 CRC64;

Query Match 1.1%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db          4 CIDV 7

RESULT 12
Q35835_9MURI PRELIMINARY; PRT; 8 AA.
AC Q35835;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF1 protein.
GN Name=ORF1;
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=98008057; PubMed=9581555;
RA Hospital V., Prat A., Joulie C., Cherif D., Day R., Cohen P.;
RT "Human and rat testis express two mRNA species encoding variants of
RT NR1 convertase, a metalloendopeptidase of the insulinase family.";
RL Biochem. J. 327:773-779(1997).
DR EMBL; X93208; CAA63695.1; -; mRNA.
SQ SEQUENCE 8 AA; 886 MW; EA7EA1B1ADC5A5B6 CRC64;

Query Match 1.1%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 SSAT 362
DB 2 SSAT 5

RESULT 13
RT33_BOVIN STANDARD; PRT; 9 AA.
AC R82326;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).
GN Name=MRPS33;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP PROTEIN SEQUENCE.
RX TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123; DOI=10.1074/jbc.M100727200;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
```

KW Direct protein sequencing; Mitochondrion; Ribonucleoprotein;
 KW Ribosomal protein.
 FT NON TER 1
 FT NON TER 9
 SQ SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;

Query Match 1.1%; Score 4; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 LPSE 178
 |||||

Db 1 LPSE 4

RESULT 14

YBPR_AZ0VI
 ID YBPR_AZ0VI STANDARD; PRT; 9 AA.
 AC P25825;
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Hypothetical protein in bfr 3'region (Fragment).
 OS Azotobacter vinelandii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Azotobacter.
 OX NCBI_TaxID=354;
 RN [1]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX MEDLINE=92196129; PubMed=1549605;
 RA Grossman M.J.; Hinton S.N.; Minak-Bernero V.; Slaughter C.,
 RA Stiefel E.I.;
 RT "Unification of the ferritin family of proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----

DR EMBL; M83692; AAA22122.1; -; Genomic_DNA.

DR FIR; B41983; B41983.

KW Hypothetical protein.

FT NON TER 9

SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B41776D CRC64;

Query Match 1.1%; Score 4; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 TSTS 45
 |||||

Db 6 TSTS 9

RESULT 15

Q51LX3_MAGGR
 ID Q51LX3_MAGGR PRELIMINARY; PRT; 9 AA.
 AC Q51LX3;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=MG02768.4;
 OS Magnaporthe grisea 70-15.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.
 OX NCBI_TaxID=242507;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Birren B.; Nusbaum C.; Abebe A.; Abouelleil A.; Adekoya E.,

RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
 RA Arachchi H., Ambruster J., Bachantsang P., Baldwin J., Barry A.,
 RA Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavskiy L.,
 RA Borowsky M., Boukgalter B., Brunache A., Butler J., Calixte N.,
 RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
 RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
 RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
 RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
 RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
 RA Gnitke A., Goyette A., Graham J., Grandbois E., Gyalteen K., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
 RA Honan T., Horn A., Houde N., Hughes L., Huime W., Husby E., Iliev I.,
 RA Jaffe D., Jones C., Kamal M., Kamat A., Kamvysellis M., Karlsson E.,
 RA Kellis C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
 RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
 RA Lindblad-toh K., Liu X., Lokvitsang T., Lokvitsang Y., Lucien O.,
 RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
 RA Manning J., Marabella R., Maru K., Matthews C., Maucell E.,
 RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
 RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mienga V., Moru K.,
 RA Mozes J., Multain L., Munson G., Naylor J., News C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
 RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
 RA O'Neill K., Oman S., Parker S., Ferrin D., Phunkhang P., Pignani B.,
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
 RA Rettig R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
 RA Rutman M., Schubach R., Seaman C., Settipalli S., Sharpe T.,
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
 RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
 RA Stenson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
 RA Tensing P., Tesfaye S., Theodore J., Thoulteang Y., Topham K.,
 RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zenbeck L.,
 RA Zimmer A., Zody M., Lander E.;
 RA "The genome sequence of Magnaporthe grisea.";
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Zhu H., Blackmon B.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; ACU01001555; EAA47525.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 9 AA; 1003 MW; DF9FCSA6D1F5BDC6 CRC64;

Query Match 1.1%; Score 4; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 QSQS 20
 |||||

Db 6 QSQS 9

Search completed: March 17, 2006, 22:52:45
 Job time : 235 secs

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	29	7.9	82	8	AB059333	Human gen
2	28	7.6	28	2	AAW54400	MAGE-10 t
3	28	7.6	28	3	AAI99875	Human MAG
4	17	4.6	30	5	AAU85060	Human MAG
5	16	4.3	16	3	AAU802636	MAGE-A3 H
6	16	4.3	16	8	ADL17869	Tumour as
7	16	4.3	16	8	ADO23376	Human MAG
8	15	4.1	15	4	AA884542	MAGE2 DR
9	15	4.1	15	4	AA884598	MAGE3 DR
10	14	3.8	16	3	AAI92308	MAGE-A1 a
11	14	3.8	30	5	AAU85041	Human MAG
12	14	3.8	30	5	AAU85061	Human MAG
13	12	3.3	15	4	AA884627	MAGE3 DR
14	12	3.3	15	4	AA884572	MAGE2 DR
15	12	3.3	16	3	AAI92309	MAGE-A4 a
16	12	3.3	16	3	AAI92307	MAGE-A1 a
17	12	3.3	16	3	AAU802635	MAGE-A3 H
18	12	3.3	16	8	ADL17868	Tumour as
19	12	3.3	16	8	ADO23374	Human MAG
20	12	3.3	30	5	AAU85040	Human MAG
21	11	3.0	15	3	AAI99900	HLA class
22	11	3.0	15	4	AA884892	MAGE2 DR3
23	11	3.0	15	4	AA884648	MAGE2 DR
24	11	3.0	15	4	AA884658	MAGE3 DR

CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subcription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe protein of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
XX
SQ Sequence 82 AA;

Query Match 7.9%; Score 29; DB 8; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 264 YGEPRKLTQDWQENLYEYRQVPGSDPA 292
DB 5 YGEPRKLTQDWQENLYEYRQVPGSDPA 33
RESULT 2
AAW54400
ID AAW54400 standard; peptide; 28 AA.
AC AAW54400;
DT 14-SEP-1998 (first entry)
XX
DE MAGE-10 tumour rejection antigen precursor-derived peptide.
KW MAGE-10; tumour rejection antigen precursor; TRAP; human; cancer;
KW melanoma; diagnosis.
XX
OS Homo sapiens.
XX
FN WO9814463-A1.
XX
PD 09-APR-1998.
XX
PF 10-SEP-1997; 97WO-US015981.
XX
PR 03-OCT-1996; 96US-00724774.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Rimoldi D, Jongeneel V, Coullie P, Cerrottini J, Carrel S, Reed D;
XX
DR WPI; 1998-240013/21.
XX
PT New cDNA encoding MAGE-10 tumour rejection antigen precursor - useful in
PT immunogenic compositions for, e.g. diagnosis and monitoring of cancer.
XX
PS Claim 9; Page 14; 28pp; English.
XX
CC This peptide is an antigenic portion of the deduced amino acid sequence

CC of the human MAGE-10 tumour rejection antigen precursor. Polyclonal
CC antisera raised against this peptide, or against hybrids of the peptide
CC with helper peptide P-30 (see AAW54401), were tested for reactivity with
CC MAGE-10 in various assays. The antiserum recognised a 72 kDa band from
CC melanoma lysates that was identified as MAGE-10. MAGE-10 and its
CC antigenic peptide are used in claimed immunogenic compositions.
CC Polyclonal antiserum obtained by immunising a non-human animal with the
CC claimed peptide is also claimed and can be used to determine the presence
CC of MAGE-10 tumour rejection antigen precursor in a sample e.g. for
CC diagnosing and monitoring of cancer
XX
SQ Sequence 28 AA;

Query Match 7.6%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 7.5e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 342 QDIRATDDTTAMASASSSATGFSYPE 369
DB 1 QDIRATDDTTAMASASSSATGFSYPE 28
RESULT 3
AAAY99875
ID AAAY99875 standard; protein; 28 AA.
XX
AC AAAY99875;
XX
DT 03-OCT-2000 (first entry)
XX
DE Human MAGE-10 derived immunogenic peptide.
XX
KW Human; MAGE-10; tumour rejection antigen precursor; bladder cancer;
KW prostate cancer; lung cancer; cancer detection; oesophageal cancer;
XX head and neck cancer; melanoma; myeloma; sarcoma; immunogen.
XX
OS Homo sapiens.
XX
FN WO200026407-A1.
XX
PD 11-MAY-2000.
XX
PF 15-OCT-1999; 99WO-US024258.
XX
PR 30-OCT-1998; 98US-00183714.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Boon-Falleur T, Brasseur F, Rimoldi D, Deplaen E;
XX
DR WPI; 2000-451624/39.
XX
PT Determining presence of cancer in samples, especially useful for
PT detecting bladder, prostate and lung cancer comprises assaying sample for
PT expression of tumor rejection antigen precursor MAGE-10.
XX
PS Example 12; Page 14; 26pp; English.
XX
CC The present sequence is an immunogenic peptide derived from tumour
CC rejection antigen precursor MAGE-10. It was used to generate polyclonal
CC antiserum against MAGE-10. MAGE-10 binding monoclonal antibodies can be
CC used to detect MAGE-10 expression. A correlation between MAGE-10
CC expression and cancer has been discovered and thus by determining the
CC presence of MAGE-10, the presence of cancer can be determined. MAGE-10
CC expression can be detected using an immunoassay, an oligonucleotide
CC hybridisation assay or via other standard techniques. This method is
CC especially useful for determining the presence of bladder, oesophageal,
CC head and neck, prostate or lung cancer, or melanoma, myeloma or sarcoma
XX
SQ Sequence 28 AA;

Query Match 7.6%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 7.5e-19;


```

RESULT 6
ADL17869
ID ADL17869 standard; peptide; 16 AA.
XX
AC ADL17869;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human MAGE HLA class II-binding peptide #24.
XX
KW MAGE; human leukocyte antigen; HLA class II; T lymphocyte;
KW CD4+ T lymphocyte; cancer; tumour; human.
XX
OS Homo sapiens.
XX
PN US2004077045-A1.
XX
PD 22-APR-2004.
XX
PF 23-MAY-2003; 2003US-00444683.
XX
PR 18-MAY-2001; 2001US-00860840.
XX
PA (ZHAN/) ZHANG Y.
PA (CHAU/) CHAU P.
PA (BOON/) BOON-FALLEUR T.
PA (VBRU/) VAN DER BRUGGEN P.
XX
PI Zhang Y, Chau P, Boon-Falleur T, Van Der Bruggen P;
XX
DR WPI; 2004-340002/31.
XX
PT New isolated MAGE human leukocyte antigens (HLA) class II-binding
PT peptides and encoding genes, useful for diagnosing or treating diseases
PT associated with aberrant expression or activity of the MAGE genes, such
PT as tumors and cancers.
XX
PS Claim 2; SEQ ID NO 31; 59pp; English.
XX
CC The invention relates to an isolated MAGE human leukocyte antigen (HLA)
CC class II-binding peptide, where the MAGE HLA class II-binding peptide
CC does not include a full length MAGE protein. Also described are the
CC following: (i) a composition comprising an isolated HLA class I-binding
CC peptide and an isolated MAGE HLA class II-binding peptide cited above;
CC (ii) a composition comprising one or more of the isolated MAGE HLA class
CC II-binding peptides cited above complexed with one or more isolated HLA
CC class II molecules; (iii) an isolated nucleic acid molecule encoding the
CC MAGE HLA class II-binding peptide cited above; (iv) an expression vector
CC comprising the isolated nucleic acid molecule of (iii) operably linked to
CC a promoter; (v) a method for enriching selectively a population of T
CC lymphocytes with CD4+ T lymphocytes specific for a MAGE HLA class II-
CC binding peptide, comprising contacting a population of T lymphocytes with
CC an agent presenting a complex of the MAGE HLA class II-binding peptide
CC and an HLA class II molecule to selectively enrich the isolated
CC population of T lymphocytes with the CD4+ T lymphocytes; (vi) a method
CC for diagnosing a cancer characterised by expression of a MAGE protein.
CC The methods and compositions of the present invention are useful for the
CC diagnosis and/or treatment of diseases or conditions associated with
CC aberrant expression or activity of MAGE genes, such as tumours and
CC cancers. The present sequence represents a human MAGE class II-binding
CC peptide.
XX
SQ Sequence 16 AA;
Query Match 4.3%; Score 16; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 VOENYLEYRQVPGSDP 291
Db 1 VOENYLEYRQVPGSDP 16
|||||
|||||

RESULT 7
AD023376
ID AD023376 standard; peptide; 16 AA.

```

XX AAG84542;
AC
XX 10-SEP-2001 (first entry)
XX
XX MAGE2 DR supermotif binding peptide #7.
DE
XX Human; human leukocyte antigen; HLA epitope; cytotoxic T lymphocyte; CTL;
KW MAGE2; MAGE3; melanoma antigen gene; immune response; vaccine; cancer;
KW cytostatic; immunostimulant.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200142267-A1.
PN
XX 14-JUN-2001.
PD
XX 11-DEC-2000; 2000WO-US033545.
PF
XX 10-DEC-1999; 99US-00458298.
PR
XX (EPIM-) EPIMMUNE INC.
PA
XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cellis E;
PI Keogh E;
PI
XX WPI; 2001-375002/39.
DR
XX An isolated prepared MAGE2/3 epitope (I) for use in pharmaceuticals for
PT the treatment and prevention of cancer.
PT
XX Disclosure; Page 134; 171pp; English.
XX
XX The present invention describes MAGE2/3 epitopes (I). Also described are:
CC (1) a clonal cytotoxic T lymphocyte (CTL) that is cultured in vivo and
CC binds to a complex of (I); (2) a peptide (II) comprising (I) and a second
CC epitope and has less than 50 contiguous amino acids; (3) a vaccine
CC composition comprising (II), a unit dose of a peptide with at least 50
CC contiguous amino acids with 100% identity to the native peptide sequence
CC of MAGE2/3, and a pharmaceutical excipient; (4) an isolated nucleic acid
CC encoding (I); and (5) an isolated nucleic acid encoding (II). (I) has
CC cytostatic activity, and can be used in vaccines and as an
CC immunostimulant. A vaccine of (3) is useful for the treatment and
CC immune response by incubating a T-lymphocyte sample from a patient with
CC (I) that binds to an human leukocyte antigen (HLA) allele present in the
CC patient and detecting the presence of the T-lymphocyte that binds to the
CC peptide. The vaccine allows the opportunity to combine epitopes derived
CC from multiple tumour-associated molecules reducing the likelihood of
CC tumour escape due to antigen loss. AAG84515 to AAG84909 and AAB99725
CC represent amino acid sequences used in the exemplification of the present
XX invention
XX
SQ Sequence 15 AA;
Query Match 4.1%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 278 ENLEYRQVPGSDPA 292
Db 1 ENLEYRQVPGSDPA 15
RESULT 9
AAG84598
ID AAG84598 standard; peptide; 15 AA.
XX
AC AAG84598;
XX
XX 10-SEP-2001 (first entry)
DT
XX

DE MAGE3 DR supermotif binding peptide #9.
XX
XX Human; human leukocyte antigen; HLA epitope; cytotoxic T lymphocyte; CTL;
KW MAGE2; MAGE3; melanoma antigen gene; immune response; vaccine; cancer;
KW cytostatic; immunostimulant.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200142267-A1.
PN
XX 14-JUN-2001.
PD
XX 11-DEC-2000; 2000WO-US033545.
PF
XX 10-DEC-1999; 99US-00458298.
PR
XX (EPIM-) EPIMMUNE INC.
PA
XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cellis E;
PI Keogh E;
PI
XX WPI; 2001-375002/39.
DR
XX An isolated prepared MAGE2/3 epitope (I) for use in pharmaceuticals for
PT the treatment and prevention of cancer.
PT
XX Disclosure; Page 138; 171pp; English.
XX
XX The present invention describes MAGE2/3 epitopes (I). Also described are:
CC (1) a clonal cytotoxic T lymphocyte (CTL) that is cultured in vivo and
CC binds to a complex of (I); (2) a peptide (II) comprising (I) and a second
CC epitope and has less than 50 contiguous amino acids; (3) a vaccine
CC composition comprising (II), a unit dose of a peptide with at least 50
CC contiguous amino acids with 100% identity to the native peptide sequence
CC of MAGE2/3, and a pharmaceutical excipient; (4) an isolated nucleic acid
CC encoding (I); and (5) an isolated nucleic acid encoding (II). (I) has
CC cytostatic activity, and can be used in vaccines and as an
CC immunostimulant. A vaccine of (3) is useful for the treatment and
CC immune response by incubating a T-lymphocyte sample from a patient with
CC (I) that binds to an human leukocyte antigen (HLA) allele present in the
CC patient and detecting the presence of the T-lymphocyte that binds to the
CC peptide. The vaccine allows the opportunity to combine epitopes derived
CC from multiple tumour-associated molecules reducing the likelihood of
CC tumour escape due to antigen loss. AAG84515 to AAG84909 and AAB99725
CC represent amino acid sequences used in the exemplification of the present
XX invention
XX
SQ Sequence 15 AA;
Query Match 4.1%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 278 ENLEYRQVPGSDPA 292
Db 1 ENLEYRQVPGSDPA 15
RESULT 10
AAY92308
ID AAY92308 standard; peptide; 16 AA.
XX
AC AAY92308;
XX
XX 10-AUG-2000 (first entry)
DT
XX MAGE-A1 antigenic peptide epitope (residues 257-272).
DE
XX MAGE-A1; antigen; epitope; cytotoxic T lymphocyte; CTL; complex;
KW human leukocyte antigen; HLA.
XX

```

OS Homo sapiens.
XX WO200020445-A2.
XX PD 13-APR-2000.
XX PF 15-SEP-1999; 99WO-IB001664.
XX PR 02-OCT-1998; 98US-00165863.
XX PR 09-APR-1999; 99US-00289350.
XX (CHAU/) CHAUX P.
XX PA (LUIT/) LUITEN R.
XX PA (DEMO/) DEMOTTE N.
XX PA (DUFF/) DUFFOUR M.
XX PA (LURQ/) LURQUIN C.
XX PA (STRO/) TRAVERSARI C.
XX PA (STRO/) STROOBANT V.
XX PA (CORN/) CORNELIS G R.
XX PA (BOON/) BOON-FALLEUR T.
XX PA (VBRU/) VAN DER BRUGGEN P.
XX PA (SCHU/) SCHULTZ E.
XX PA (WARN/) WARNIER G.
XX Chaux P, Luiten R, Demotte N, Duffour M, Lurquin C, Traversari C;
XX Stroobant V, Cornelis GR, Boon-Falleur T, Van Der Bruggen P;
XX Schultz E, Warnier G;
XX WPI; 2000-303739/26.
XX Isolation of cytotoxic T-lymphocytes clones by successive steps of
XX stimulation and testing of lymphocytes with antigen presenting cells
XX PT which present antigens derived from different expression systems.
XX PS Example 8; Page 56; 99pp; English.
XX A novel method of isolation of cytotoxic T-lymphocytes (CTL) clones
XX CC comprises successive steps of stimulation and testing of lymphocytes with
XX CC antigen presenting cells (APCs) which present antigens derived from
XX CC different expression systems. The CTL clones isolated recognize specific
XX CC antigenic peptides of proteins, preferably of the MAGE family. The APC is
XX CC autologous and each expression systems is different from at least one of
XX CC the other expression systems, therefore isolating a cytotoxic T cell
XX CC clone specific for the protein. The method can also be used to identify
XX CC an antigenic peptide epitope. Isolated CTL clones specific for a
XX CC peptide/human leukocyte antigen (HLA) complex are claimed. The CTL cells
XX CC specific for the complexes, peptides or cells which present the complexes
XX CC on the cell surface are useful for treating pathological conditions
XX CC characterized by abnormal expression of the complexes
XX SQ Sequence 16 AA;
Query Match 3.8%; Score 14; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 289 SDPARYEFLWGPPRA 302
DB 1 SDPARYEFLWGPPRA 14
RESULT 11
AAU85041
ID AAU85041 standard; peptide; 30 AA.
XX AC AAU85041;
XX DT 08-MAY-2002 (first entry)
XX DE Human MAGE-1 segment 18.
XX KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
XX viral infection; human immunodeficiency virus; melanoma;
KW bacterial infection; Salmonella; Legionella; parasitic infection;
KW Trypanosoma; Toxoplasma; Giardia.
XX Homo sapiens.
XX WO200190197-A1.
XX PD 29-NOV-2001.
XX PF 25-MAY-2001; 2001WO-AU000622.
XX PR 26-MAY-2000; 2000AU-00007761.
XX PA (AUSU ) UNIV AUSTRALIAN NAT.
XX Thomson SA, Ramshaw IA;
XX WPI; 2002-147575/19.
XX N-PSDB; ABK36861.
XX New synthetic polypeptides having several different segments of at least
XX one parent polypeptide linked together differently compared to the
XX linkage in the parent polypeptide, for inducing immune response against a
XX pathogen or cancer.
XX Example 3; Fig 27; 364pp; English.
XX The invention relates to a new synthetic polypeptide (I) comprising
XX several different segments of at least one parent polypeptide linked
XX together in a different relationship relative to their linkage in the
XX parent polypeptide to impede, abrogate or otherwise alter at least one
XX function associated with the parent polypeptide and for inducing an
XX immune response against a pathogen or cancer. Also included are a
XX synthetic polynucleotide encoding and a computer system for designing the
XX synthetic polypeptides. The synthetic polypeptides and polynucleotides
XX are referred to as a Savine. The synthetic polypeptide is useful for
XX modulating immune responses preferably directed against a pathogen or a
XX cancer. (e.g., cancers of the lung, breast, ovary, cervix, colon, head
XX and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
XX oesophagus, brain, testicle, uterus), as potentiating agents.
XX Compositions comprising the polypeptide may be used in the treatment or
XX prophylaxis against viral (such as infections caused by HIV (human
XX immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
XX virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
XX (e.g., infections caused by Neisseria, Meningococcus, Haemophilus,
XX Salmonella, Streptococcus, Legionella and Mycobacterium or parasitic
XX (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
XX Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
XX a peptide derived from a parent protein used to construct a Savine of the
XX invention
XX SQ Sequence 30 AA;
Query Match 3.8%; Score 14; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 289 SDPARYEFLWGPPRA 302
DB 4 SDPARYEFLWGPPRA 17
RESULT 12
AAU85061
ID AAU85061 standard; peptide; 30 AA.
XX AC AAU85061;
XX DT 08-MAY-2002 (first entry)
XX DE Human MAGE-3 segment 18.
XX KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;

```


OS Synthetic.
 XX WO200142267-A1.
 XX PD 14-JUN-2001.
 XX PF 11-DEC-2000; 2000WO-US033545.
 XX PR 10-DEC-1999; 99US-00458298.
 XX PA (EPIM-) EPIMUNE INC.
 XX PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cellis E;
 PI Keogh E;
 XX WPI; 2001-375002/39.
 XX PT An isolated prepared MAGE2/3 epitope (I) for use in pharmaceuticals for
 PT the treatment and prevention of cancer.
 XX PS Disclosure; Page 134; 171pp; English.
 XX CC The present invention describes MAGE2/3 epitopes (I). Also described are:
 CC (1) a clonal cytotoxic T lymphocyte (CTL) that is cultured in vivo and
 CC binds to a complex of (I); (2) a peptide (II) comprising (I) and a second
 CC epitope and has less than 50 contiguous amino acids; (3) a vaccine
 CC composition comprising (III), a unit dose of a peptide with at least 50
 CC contiguous amino acids with 100% identity to the native peptide sequence
 CC of MAGE2/3, and a pharmaceutical excipient; (4) an isolated nucleic acid
 CC encoding (I); and (5) an isolated nucleic acid encoding (II). (I) has
 CC cytostatic activity, and can be used in vaccines and as an
 CC immunostimulant. A vaccine of (3) is useful for the treatment and
 CC prevention of cancer. (I) is useful for monitoring or evaluating an
 CC immune response by incubating a T-lymphocyte sample from a patient with
 CC (I) that binds to an human leukocyte antigen (HLA) allele present in the
 CC patient and detecting the presence of the T-lymphocyte that binds to the
 CC peptide. The vaccine allows the opportunity to combine epitopes derived
 CC from multiple tumour-associated molecules reducing the likelihood of
 CC tumour escape due to antigen loss. AAG84515 to AAG84909 and AAB99725
 CC represent amino acid sequences used in the exemplification of the present
 CC invention
 XX CC
 SQ Sequence 15 AA;
 Query Match 3.3%; Score 12; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.00098;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 276 VOENYLEYRQVP 287
 DB 4 VOENYLEYRQVP 15
 RESULT 15
 AAY92309
 ID AAY92309 standard; peptide; 16 AA.
 XX AC AAY92309;
 XX AC AAY92309;
 DT 10-AUG-2000 (first entry)
 XX DE MAGE-A4 antigenic peptide epitope (residues 264-279).
 XX KW MAGE-A4; antigen; epitope; cytotoxic T lymphocyte; CTL; complex;
 KW human leukocyte antigen; HLA.
 XX OS Homo sapiens.
 XX PN WO200020445-A2.
 XX PD 13-APR-2000.
 XX PF 15-SEP-1999; 99WO-IB001664.

XX 02-OCT-1998; 98US-00165863.
 PR 09-APR-1999; 99US-00289350.
 XX (CHAU/) CHAUX P.
 PA (LUIT/) LUITEN R.
 PA (DEMO/) DEMOTTE N.
 PA (DUFF/) DUFFOUR M.
 PA (LURQ/) LURQUIN C.
 PA (TRAV/) TRAVERSARI C.
 PA (STRO/) STROOBANT V.
 PA (BOON/) BOON-FALLEUR T.
 PA (VBRU/) VAN DER BRUGEN P.
 PA (SCHU/) SCHULTZ E.
 PA (WARN/) WARNIER E.
 XX Chaux P, Luiten R, Demotte N, Duffour M, Lurquin C, Traversari C;
 PI Stroobant V, Cornelis GR, Boon-Falleur T, Van Der Bruggen P;
 PI Schultz E, Warnier G;
 XX WPI; 2000-303739/26.
 XX Isolation of cytotoxic T-lymphocytes clones by successive steps of
 PT stimulation and testing of lymphocytes with antigen presenting cells
 PT which present antigens derived from different expression systems.
 XX Example 8; Page 58; 99pp; English.
 XX A novel method of isolation of cytotoxic T-lymphocytes (CTL) clones
 CC comprises successive steps of stimulation and testing of lymphocytes with
 CC antigen presenting cells (APCs) which present antigens derived from
 CC different expression systems. The CTL clones isolated recognize specific
 CC antigenic peptides of proteins, preferably of the MAGE family. The APC is
 CC autologous and each expression systems is different from at least one of
 CC the other expression systems, therefore isolating a cytotoxic T cell
 CC clone specific for the protein. The method can also be used to identify
 CC an antigenic peptide epitope. Isolated CTL clones specific for a
 CC peptide/human leukocyte antigen (HLA) complex are claimed. The CTL cells
 CC specific for the complexes, peptides or cells which present the complexes
 CC on the cell surface are useful for treating pathological conditions
 CC characterized by abnormal expression of the complexes
 XX CC
 SQ Sequence 16 AA;
 Query Match 3.3%; Score 12; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 291 PARYEFLMGPPRA 302
 DB 4 PARYEFLMGPPRA 15

Search completed: March 17, 2006, 23:12:43
 Job time : 190 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:16:57 ; Search time 47 Seconds
(without alignments)
649.092 Million cell updates/sec

Title: US-09-856-812B-1
Perfect score: 369
Sequence: 1 MPRAKRCRQMPEDLQSQS.....DTTAWASASSATGFSFSYPE 369

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 357358

Minimum DB seq length: 0
Maximum DB seq length: 93

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	7.6	28	1 US-08-724-774B-4	Sequence 4, Appli
2	28	7.6	28	2 US-09-089-593-4	Sequence 4, Appli
3	28	7.6	28	2 US-09-382-855-4	Sequence 4, Appli
4	28	7.6	28	2 US-09-183-714B-4	Sequence 4, Appli
5	28	7.6	28	2 US-09-642-281-4	Sequence 4, Appli
6	28	7.6	28	2 US-09-589-717-4	Sequence 4, Appli
7	16	4.3	16	2 US-09-396-315-85	Sequence 85, Appl
8	14	3.8	16	2 US-09-165-863-39	Sequence 39, Appl
9	14	3.8	16	2 US-09-289-350-39	Sequence 39, Appl
10	14	3.8	16	2 US-09-806-769-39	Sequence 39, Appl
11	14	3.8	58	1 US-08-465-167A-1	Sequence 1, Appli
12	14	3.8	58	2 US-08-627-820-1	Sequence 1, Appli
13	12	3.3	16	2 US-09-165-863-38	Sequence 38, Appl
14	12	3.3	16	2 US-09-165-863-40	Sequence 40, Appl
15	12	3.3	16	2 US-09-289-350-38	Sequence 38, Appl
16	12	3.3	16	2 US-09-289-350-40	Sequence 40, Appl
17	12	3.3	16	2 US-09-806-769-38	Sequence 38, Appl
18	12	3.3	16	2 US-09-806-769-40	Sequence 40, Appl
19	12	3.3	16	2 US-09-396-315-84	Sequence 84, Appl
20	11	3.0	16	1 US-08-195-186A-2	Sequence 2, Appli
21	11	3.0	16	2 US-08-292-492D-2	Sequence 2, Appli
22	11	3.0	16	2 US-09-633-994-2	Sequence 2, Appli
23	10	2.7	10	2 US-09-165-863-41	Sequence 41, Appl
24	10	2.7	10	2 US-09-289-350-41	Sequence 41, Appl
25	10	2.7	10	2 US-09-806-769-41	Sequence 41, Appl
26	9	2.4	9	2 US-09-165-863-42	Sequence 42, Appl
27	9	2.4	9	2 US-09-289-350-42	Sequence 42, Appl

28	9	2.4	9	2	US-09-533-499B-18	Sequence 18, Appl
29	9	2.4	9	2	US-09-533-499B-19	Sequence 19, Appl
30	9	2.4	9	2	US-09-533-499B-20	Sequence 20, Appl
31	9	2.4	9	2	US-09-806-769-42	Sequence 42, Appl
32	9	2.4	9	2	US-09-865-548A-39	Sequence 39, Appl
33	9	2.4	11	1	US-08-040-548-43	Sequence 43, Appl
34	9	2.4	11	1	US-08-466-344-43	Sequence 43, Appl
35	9	2.4	11	6	5206152-12	Patent No. 5206152
36	9	2.4	16	2	US-09-165-863-37	Sequence 37, Appl
37	9	2.4	16	2	US-09-289-350-37	Sequence 37, Appl
38	9	2.4	16	2	US-09-806-769-37	Sequence 37, Appl
39	9	2.4	18	2	US-08-248-058-1	Sequence 1, Appli
40	9	2.4	25	2	US-09-270-767-61229	Sequence 61229, A
41	9	2.4	43	2	US-07-757-022B-12	Sequence 12, Appl
42	9	2.4	64	2	US-09-248-796A-24834	Sequence 24834, A
43	9	2.4	69	2	US-09-248-796A-22303	Sequence 22303, A
44	9	2.4	73	2	US-09-328-352-4184	Sequence 4184, Ap
45	9	2.4	82	2	US-09-621-976-5944	Sequence 5944, Ap

ALIGNMENTS

RESULT 1
US-08-724-774B-4
; Sequence 4, Application US/08724774B
; Patent No. 5908778
; GENERAL INFORMATION:
; APPLICANT: Rimoldi, Donata; Jongeneel, Victor; Coulie,
; APPLICANT: Pierre; Cerrottini, Jean-Charles; Carrel,
; APPLICANT: Stefan; Reed, Daryl
; TITLE OF INVENTION: MAGE-10 ENCODING cDNA, The Tumor
; TITLE OF INVENTION: Rejection Antigen Precursors Mage-10,
; TITLE OF INVENTION: Antibodies Specific To The Molecule, and
; TITLE OF INVENTION: Uses thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,774B
; FILING DATE: 03-October-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5908778man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5457
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28
; TYPE: amino acid
; TOPOLOGY: linear
US-08-724-774B-4

Query Match 7.6%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.1e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 342 QDRIATDDTTAWASASSATGFSFSYPE 369

DB 1 QDRIATDDTTAWASASSATGFSFSYPE 28

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;
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/382,855
; FILING DATE: 25-August-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/089,595
; FILING DATE: 02-June-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,774
; FILING DATE: 03-October-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schofield, Mary Anne
; REGISTRATION NUMBER: 36,669
; REFERENCE/DOCKET NUMBER: LUD 5457.2 DIV - JEL/MAS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 28
; TOPOLOGY: linear
; US-09-382-855-4

Query Match 7.6%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.1e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 342 QDRIATDDTTAMASASSATGFSFSYPE 369
Db 1 QDRIATDDTTAMASASSATGFSFSYPE 28

RESULT 4
US-09-183-714B-4
; Sequence 4, Application US/09183714B
; Patent No. 6221593
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Brasseur, Francis
; APPLICANT: Rimoldi, Donata
; APPLICANT: De Plaen, Etienne
; TITLE OF INVENTION: Method for Determining Cancer by Determining Expression
; TITLE OF INVENTION: of MAGE-10
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/183,714B
; CURRENT FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: US 08/724,774
; PRIOR FILING DATE: 1996-10-03
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 4
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; US-09-183-714B-4

Query Match 7.6%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.1e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 342 QDRIATDDTTAMASASSATGFSFSYPE 369
Db 1 QDRIATDDTTAMASASSATGFSFSYPE 28

RESULT 5

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US-09-642-281-4
; Sequence 4, Application US/09642281
; Patent No. 6387698
; GENERAL INFORMATION:
; APPLICANT: Rimoldi, Donata; Jongeneel, Victor; Coulie, Pierre;
; Cerrotini, Jean-Charles; Carrel, Stefan; Reed, Daryl
; TITLE OF INVENTION: MAGE-10 ENCODING cDNA, The Tumor Rejection
; Antigen Precursors MAGE-10, Antibodies Specific To The Molecu
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/642,281
; FILING DATE: 18-Aug-2000
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/089,595
; FILING DATE: 02-June-1998
; APPLICATION NUMBER: US 08/724,774
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Schofield, Mary Anne
; REGISTRATION NUMBER: 36,669
; REFERENCE/DOCKET NUMBER: LUD 5457.2 DIV - JEL/MAS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-642-281-4
Query Match 7.6%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.1e-19; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 342 QDRIATDDTTAMASASSSATSQSFYSPE 369
Db 1 QDRIATDDTTAMASASSSATSQSFYSPE 28
RESULT 6
US-09-589-717-4
; Sequence 4, Application US/09589717
; Patent No. 6497879
; GENERAL INFORMATION:
; APPLICANT: Rimoldi, Donata; Jongeneel, Victor; Coulie,
; Pierre; Cerrotini, Jean-Charles; Carrel,
; Stefan; Reed, Daryl
; TITLE OF INVENTION: MAGE-10 ENCODING cDNA, The Tumor
; Rejection Antigen Precursors MAGE-10,
; Antibodies Specific To The Molecule, and
; Uses Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
```

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ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/589,717
; FILING DATE: 08-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/089,595
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6497879man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5457
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-589-717-4
Query Match 7.6%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.1e-19; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 342 QDRIATDDTTAMASASSSATSQSFYSPE 369
Db 1 QDRIATDDTTAMASASSSATSQSFYSPE 28
RESULT 7
US-09-396-315-85
; Sequence 85, Application US/09396315
; Patent No. 6716809
; GENERAL INFORMATION:
; APPLICANT: Schultz, Erwin S.
; APPLICANT: Van Snick, Jacques
; APPLICANT: Leth, Bernard
; APPLICANT: Chau, Pascal
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Kurthals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7067
; CURRENT APPLICATION NUMBER: US/09/396,315
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-396-315-85
Query Match 4.3%; Score 16; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 276 VQENYLEYRQVPGSDP 291
Db 1 VQENYLEYRQVPGSDP 16
RESULT 8
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US-09-165-863-39
; Sequence 39, Application US/09165863
; Patent No. 6407063
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Duffour, Marie-Therese
; APPLICANT: Demotte, Nathalie
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Cornelis, Guy
; APPLICANT: Stroobant, Vincent
; APPLICANT: Lurquin, Christophe
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Chauv, Pascal
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; FILE REFERENCE: 117272
; CURRENT APPLICATION NUMBER: US/09/165,863
; CURRENT FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human MAGE-A1 peptide
US-09-165-863-39

Query Match          3.8%; Score 14; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      289 SDPARYEFLLWGPR 302
DB      1 SDPARYEFLLWGPR 14
|||||

US-09-289-350-39
; Sequence 39, Application US/09289350
; Patent No. 6531451
; GENERAL INFORMATION:
; APPLICANT: Chauv, Pascal
; APPLICANT: Luiten, Rosalie
; APPLICANT: Demotte, Nathalie
; APPLICANT: Duffour, Marie-Therese
; APPLICANT: Lurquin, Christophe
; APPLICANT: Stroobant, Vincent
; APPLICANT: Cornelis, Guy R.
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Van Der Bruggen, Pierre
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; FILE REFERENCE: 117272
; CURRENT APPLICATION NUMBER: US/09/289,350
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/165,863
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human MAGE-A1 peptide
US-09-289-350-39

Query Match          3.8%; Score 14; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      289 SDPARYEFLLWGPR 302
DB      1 SDPARYEFLLWGPR 14
|||||

US-09-806-769-39
; Sequence 39, Application US/09806769
; Patent No. 6710172
; GENERAL INFORMATION:
; APPLICANT: Chauv, Pascal
; APPLICANT: Luiten, Rosalie
; APPLICANT: Demotte, Nathalie
; APPLICANT: Duffour, Marie-Therese
; APPLICANT: Lurquin, Christophe
; APPLICANT: Traversari, Catia
; APPLICANT: Stroobant, Vincent
; APPLICANT: Cornelis, Guy R.
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Van Der Bruggen, Pierre
; APPLICANT: Schultz, Erwin
; APPLICANT: Warnier, Guy
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; FILE REFERENCE: 117272
; CURRENT APPLICATION NUMBER: US/09/806,769
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 09/165,863
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 09/289,350
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/806,769
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human MAGE-A1 peptide
US-09-806-769-39

Query Match          3.8%; Score 14; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      289 SDPARYEFLLWGPR 302
DB      1 SDPARYEFLLWGPR 14
|||||

US-08-465-167A-1
; Sequence 1, Application US/08465167A
; Patent No. 5750395
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Sette, Alessandro D.
; APPLICANT: Sidney, John C.
; TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 98111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,167A
; FILING DATE: 05-JUN-1995
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/103,623
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; TELEPHONE/DOCKET NUMBER: 14137-60-1
; TELEPHONE: 206-467-9600
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-465-167A-1

Query Match      3.8%; Score 14; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      289 SDPARYEFLWGPR 302
DB      6 SDPARYEFLWGPR 19
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RESULT 12
US-08-621-820-1
; Sequence 1, Application US/08627820
; Patent No. 6464980
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
;               Livingston, Brian D.
;               Sette, Alessandro D.
;               Sidney, John C.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF THE
;               COMPLETE MAGE 1 GENE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/627,820
; FILING DATE: 02-Apr-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/103,623
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; TELEPHONE/DOCKET NUMBER: 14137-60
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-627-820-1

Query Match      3.8%; Score 14; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      289 SDPARYEFLWGPR 302
DB      6 SDPARYEFLWGPR 19
      |||||
RESULT 13
US-09-165-863-38
; Sequence 38, Application US/09165863
; Patent No. 6407063
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Duffour, Marie-Therese
; APPLICANT: Demotte, Nathalie
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Cornelis, Guy
; APPLICANT: Stroobant, Vincent
; APPLICANT: Lurquin, Christophe
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Chau, Pascal
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; FILE REFERENCE: 11727
; CURRENT APPLICATION NUMBER: US/09/165,863
; CURRENT FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human MAGE-A1 peptide
US-09-165-863-38

Query Match      3.3%; Score 12; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      289 SDPARYEFLWGPR 300
DB      5 SDPARYEFLWGPR 16
      |||||
RESULT 14
US-09-165-863-40
; Sequence 40, Application US/09165863
; Patent No. 6407063
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Duffour, Marie-Therese
; APPLICANT: Demotte, Nathalie
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Cornelis, Guy
; APPLICANT: Stroobant, Vincent
; APPLICANT: Lurquin, Christophe
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Chau, Pascal
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; FILE REFERENCE: 11727
; CURRENT APPLICATION NUMBER: US/09/165,863
; CURRENT FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 16
; TYPE: PRT
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; ORGANISM: Human MAGE-A4 peptide
US-09-165-863-40

Query Match      3.3%; Score 12; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      291 PARYEFLWGPR 302
Db      4 PARYEFLWGPR 15

RESULT 15
US-09-289-350-38
; Sequence 38, Application US/09289350
; Patent No. 6531451
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Luiten, Rosalie
; APPLICANT: Demotte, Nathalie
; APPLICANT: Deffour, Marie-Therese
; APPLICANT: Lurquin, Christophe
; APPLICANT: Traversari, Catia
; APPLICANT: Stroobant, Vincent
; APPLICANT: Cornelis, Guy R.
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Van Der Bruggen, Pierre
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; FILE REFERENCE: 117272
; CURRENT APPLICATION NUMBER: US/09/289,350
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/165,863
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human MAGE-A1 peptide
US-09-289-350-38

Query Match      3.3%; Score 12; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      289 SDPARYEFLWGP 300
Db      5 SDPARYEFLWGP 16

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Search completed: March 17, 2006, 23:18:10
Job time : 48 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	29	7.9	82	4	US-10-029-386-32967	Sequence 32967, A
2	28	7.6	28	4	US-10-261-208-4	Sequence 4, Appli
3	17	4.6	30	4	US-10-296-734-1314	Sequence 1314, Ap
4	16	4.3	16	4	US-10-444-683-31	Sequence 31, Appl
5	15	4.1	15	4	US-10-149-135-1919	Sequence 1919, Ap
6	15	4.1	15	4	US-10-149-135-1975	Sequence 1975, Ap
7	14	3.8	16	4	US-10-753-158-39	Sequence 39, Appl
8	14	3.8	30	4	US-10-296-734-1276	Sequence 1276, Ap
9	14	3.8	30	4	US-10-296-734-1316	Sequence 1316, Ap
10	12	3.3	15	4	US-10-149-135-1949	Sequence 1949, Ap
11	12	3.3	15	4	US-10-149-135-2004	Sequence 2004, Ap
12	12	3.3	16	4	US-10-444-683-29	Sequence 29, Appl
13	12	3.3	16	4	US-10-753-158-38	Sequence 38, Appl
14	12	3.3	16	4	US-10-753-158-40	Sequence 40, Appl
15	12	3.3	30	4	US-10-296-734-1274	Sequence 1274, Ap
16	11	3.0	11	4	US-10-149-135-259	Sequence 259, App
17	11	3.0	11	4	US-10-149-135-448	Sequence 448, App
18	11	3.0	11	4	US-10-149-135-1178	Sequence 1178, Ap
19	11	3.0	11	4	US-10-149-135-1275	Sequence 1275, Ap
20	11	3.0	15	4	US-10-149-135-2025	Sequence 2025, Ap
21	11	3.0	15	4	US-10-149-135-2035	Sequence 2035, Ap
22	11	3.0	15	4	US-10-149-135-2419	Sequence 2419, Ap
23	11	3.0	15	4	US-10-149-135-2431	Sequence 2431, Ap
24	11	3.0	16	4	US-10-164-121A-2	Sequence 2, Appli
25	11	3.0	16	4	US-10-444-683-30	Sequence 30, Appl
26	11	3.0	16	4	US-10-777-053-623	Sequence 623, App
27	11	3.0	16	4	US-10-777-053-824	Sequence 824, App

;;
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Felfe & Lynch
;; STREET: 805 Third Avenue
;; CITY: New York City
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10022
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;; COMPUTER: IBM
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: Wordperfect
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/261,208
;; FILING DATE: 30-Sep-2002
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/589,717
;; FILING DATE: 08-Jun-2000
;; APPLICATION NUMBER: 09/089,595
;; FILING DATE: <Unknown>
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hanson, NO. US20030158388Alman D.
;; REGISTRATION NUMBER: 30,946
;; REFERENCE/DOCKET NUMBER: LUD 5457
;;
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 688-3200
;; TELEFAX: (212) 838-3884
;;
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 28
;; TYPE: amino acid
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-261-208-4

Query Match 7.6%; Score 28; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e-17; Indels 0;
Matches 28; Conservative 0; Mismatches 0; Gaps 0;

QY 342 QDRIATDDTTAMASASSATGSGFSYPE 369

DB 1 QDRIATDDTTAMASASSATGSGFSYPE 28

RESULT 3
US-10-296-734-1314
; Sequence 1314, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1314
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MAGB-3 segment 17
US-10-296-734-1314

Query Match 4.6%; Score 17; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 276 VQENYLEYRQVPGSDPA 292

DB 13 VQENYLEYRQVPGSDPA 29
RESULT 4
US-10-444-683-31
; Sequence 31, Application US/10444683
; Publication No. US20040077045A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Chau, Pascal
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: MAGB PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L00461.70146.US
; CURRENT APPLICATION NUMBER: US/10/444,683
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 09/860,840
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-444-683-31

Query Match 4.3%; Score 16; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.2e-07; Indels 0;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 292 ARYEFLWGPRAHAEIR 307

DB 1 ARYEFLWGPRAHAEIR 16

RESULT 5
US-10-149-135-1919
; Sequence 1919, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1919
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence

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;
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1919

Query Match          4.1%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 ENYLEYRQVPGSDPA 292
DB 1 ENYLEYRQVPGSDPA 15

RESULT 6
US-10-149-135-1975
; Sequence 1975, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; CURRENT APPLICATION NUMBER: US/10/149,135
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR FILING DATE: 2000-12-11
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1975
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1975

Query Match          4.1%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 ENYLEYRQVPGSDPA 292
DB 1 ENYLEYRQVPGSDPA 15

RESULT 7
US-10-753-158-39
; Sequence 39, Application US/10753158
; Publication No. US20040185033A1
; GENERAL INFORMATION:
; APPLICANT: Chauv, Pascal
; APPLICANT: Luiten, Rosalie
; APPLICANT: Demotte, Nathalie
; APPLICANT: Deffour, Marie-Therese
; APPLICANT: Lurquin, Christophe
```

```
; APPLICANT: Traversari, Catia
; APPLICANT: Stroobant, Vincent
; APPLICANT: Cornellis, Guy R.
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Van Der Bruggen, Pierre
; APPLICANT: Schultz, Erwin
; APPLICANT: Warnier, Guy
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; FILE REFERENCE: 117272v
; CURRENT APPLICATION NUMBER: US/10/753,158
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US/09/806,769
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/165,863
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 09/289,350
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/806,769
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human MAGE-A1 peptide
US-10-753-158-39

Query Match          3.8%; Score 14; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 SDPARYEFELWGPR 302
DB 1 SDPARYEFELWGPR 14

RESULT 8
US-10-296-734-1276
; Sequence 1276, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1276
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MAGE-1 segment 18
US-10-296-734-1276

Query Match          3.8%; Score 14; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 SDPARYEFELWGPR 302
DB 4 SDPARYEFELWGPR 17

RESULT 9
US-10-296-734-1316
; Sequence 1316, Application US/10296734
; Publication No. US20040054137A1
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; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1316
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MAGE-3 segment 18
US-10-296-734-1316

Query Match          3.3%; Score 14; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      279 NYLEYRQVPGSDPA 292
Db      1 NYLEYRQVPGSDPA 14

RESULT 10
US-10-149-135-1949
; Sequence 1949, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1949
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1949

Query Match          3.3%; Score 12; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      276 VOENYLEYRQVP 287
Db      4 VOENYLEYRQVP 15

RESULT 12
US-10-444-683-29
; Sequence 29, Application US/10444683
; Publication No. US20040077045A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Chauk, Pascal
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: MAGE PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L00461.70146.US
; CURRENT APPLICATION NUMBER: US/10/444,683
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 09/860,840
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29

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QY      276 VOENYLEYRQVP 287
Db      4 VOENYLEYRQVP 15

RESULT 11
US-10-149-135-2004
; Sequence 2004, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2004
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2004

Query Match          3.3%; Score 12; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      276 VOENYLEYRQVP 287
Db      4 VOENYLEYRQVP 15

RESULT 12
US-10-444-683-29
; Sequence 29, Application US/10444683
; Publication No. US20040077045A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Chauk, Pascal
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: MAGE PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L00461.70146.US
; CURRENT APPLICATION NUMBER: US/10/444,683
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 09/860,840
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29

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;
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-444-683-29

Query Match 3.3%; Score 12; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 YEFWMGPRAAH 305
Db 3 YEFWMGPRAAH 14
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RESULT 13

US-10-753-158-38
; Sequence 38, Application US/10753158
; Publication No. US2004018503A1
; GENERAL INFORMATION:

; APPLICANT: Chauv, Pascal
; APPLICANT: Luiten, Rosalie
; APPLICANT: Demotte, Nathalie
; APPLICANT: Deffour, Marie-Therese
; APPLICANT: Lurquin, Christophe
; APPLICANT: Traversari, Catia
; APPLICANT: Stroobant, Vincent
; APPLICANT: Cornelis, Guy R.
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Van Der Bruggen, Pierre
; APPLICANT: Schultz, Erwin
; APPLICANT: Warnier, Guy

; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL

; FILE REFERENCE: 11727z
; CURRENT APPLICATION NUMBER: US/10/753,158
; PRIOR FILING DATE: 2004-01-07

; PRIOR APPLICATION NUMBER: US/09/806,769
; PRIOR FILING DATE: 2001-07-30
; PRIOR FILING DATE: 1998-10-02
; PRIOR FILING DATE: 1998-04-09
; PRIOR FILING DATE: 1998-04-09
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38

; LENGTH: 16
; TYPE: PRT

; ORGANISM: Human MAGE-A1 peptide
US-10-753-158-38

Query Match 3.3%; Score 12; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 SDPARYEFLWGP 300
Db 5 SDPARYEFLWGP 16
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RESULT 14

US-10-753-158-40
; Sequence 40, Application US/10753158
; Publication No. US2004018503A1
; GENERAL INFORMATION:

; APPLICANT: Chauv, Pascal
; APPLICANT: Luiten, Rosalie
; APPLICANT: Demotte, Nathalie
; APPLICANT: Deffour, Marie-Therese
; APPLICANT: Lurquin, Christophe
; APPLICANT: Traversari, Catia
; APPLICANT: Stroobant, Vincent

; APPLICANT: Cornelis, Guy R.
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Van Der Bruggen, Pierre
; APPLICANT: Schultz, Erwin
; APPLICANT: Warnier, Guy
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; FILE REFERENCE: 11727z
; CURRENT APPLICATION NUMBER: US/10/753,158
; CURRENT FILING DATE: 2004-01-07

; PRIOR APPLICATION NUMBER: US/09/806,769
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/165,863
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 09/289,350
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/806,769
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40

; LENGTH: 16
; TYPE: PRT

; ORGANISM: Human MAGE-A4 peptide
US-10-753-158-40

Query Match 3.3%; Score 12; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 291 PARYEFLWGPRA 302
Db 4 PARYEFLWGPRA 15
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RESULT 15

US-10-296-734-1274

; Sequence 1274, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:

; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1274

; LENGTH: 30
; TYPE: PRT

; ORGANISM: Artificial
; FEATURE:

; OTHER INFORMATION: MAGE-1 segment 17
US-10-296-734-1274

Query Match 3.3%; Score 12; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 SDPARYEFLWGP 300
Db 19 SDPARYEFLWGP 30
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Job time : 165 secs

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OM protein - protein search, using sw model

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Title: US-09-856-812B-1
Perfect score: 369
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Searched: 169630 seqs, 2862289 residues

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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
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8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	2.7	10	7 US-11-044-051-83	Sequence 83, Appl
2	10	2.7	57	7 US-11-096-568A-3481	Sequence 3481, Ap
3	9	2.4	9	6 US-10-994-204-11	Sequence 11, Appl
4	9	2.4	9	7 US-11-032-498-14	Sequence 14, Appl
5	9	2.4	9	7 US-11-044-051-6	Sequence 6, Appli
6	9	2.4	20	6 US-10-506-223-29	Sequence 29, Appl
7	9	2.4	21	6 US-10-506-223-30	Sequence 30, Appl
8	9	2.4	22	6 US-10-506-223-31	Sequence 31, Appl
9	9	2.4	23	6 US-10-506-223-32	Sequence 32, Appl
10	9	2.4	24	6 US-10-506-223-33	Sequence 33, Appl
11	9	2.4	25	6 US-10-506-223-34	Sequence 34, Appl
12	9	2.4	26	6 US-10-506-223-35	Sequence 35, Appl
13	9	2.4	27	6 US-10-506-223-36	Sequence 36, Appl
14	9	2.4	37	7 US-11-004-399-3261	Sequence 3261, Ap
15	9	2.4	43	7 US-11-169-232-12	Sequence 12, Appl
16	8	2.2	9	7 US-11-044-051-48	Sequence 48, Appl
17	8	2.2	10	7 US-11-044-051-86	Sequence 86, Appl
18	8	2.2	12	7 US-11-032-498-29	Sequence 29, Appl
19	8	2.2	19	6 US-10-506-223-28	Sequence 28, Appl
20	8	2.2	55	7 US-11-166-412-109	Sequence 109, App
21	8	2.2	55	7 US-11-166-412-124	Sequence 124, App
22	8	2.2	55	7 US-11-166-412-139	Sequence 139, App
23	7	1.9	9	6 US-10-517-784-33	Sequence 33, Appl
24	7	1.9	9	6 US-10-962-951-12	Sequence 12, Appl
25	7	1.9	9	6 US-10-602-663-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1

US-11-044-051-83
; Sequence 83, Application US/11044051
; Publication No. US2005025553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: GODELAINE, Danisla
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459,263
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 83
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-044-051-83

Query Match 2.7%; Score 10; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 LVFGIDVKEV 194
DB 1 LVFGIDVKEV 10
|||||||

RESULT 2

US-11-096-568A-3481
; Sequence 3481, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: thereby
; FILE REFERENCE: 2750-1592FUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 3481
; LENGTH: 57
; TYPE: PRT


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; OTHER INFORMATION: Xaa at position 11 is Nle
US-10-506-223-29
Query Match      2.4%; Score 9; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSSSS 62
DB 2 SSSSSSSSS 10

RESULT 7
US-10-506-223-30
; Sequence 30, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; PRIOR FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 12
; OTHER INFORMATION: Xaa at position 12 is Nle
US-10-506-223-30
Query Match      2.4%; Score 9; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSSSS 62
DB 2 SSSSSSSSS 10

RESULT 8
US-10-506-223-31
; Sequence 31, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; PRIOR FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 13
; OTHER INFORMATION: Xaa at position 13 is Nle
US-10-506-223-31
Query Match      2.4%; Score 9; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSSSS 62
DB 2 SSSSSSSSS 10

RESULT 9
US-10-506-223-32
; Sequence 32, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; PRIOR FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 14
; OTHER INFORMATION: Xaa at position 14 is Nle
US-10-506-223-32
Query Match      2.4%; Score 9; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSSSS 62
DB 2 SSSSSSSSS 10

RESULT 10
US-10-506-223-33
; Sequence 33, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; PRIOR FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 15
; OTHER INFORMATION: Xaa at position 15 is Nle
US-10-506-223-33
Query Match      2.4%; Score 9; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSSSS 62
DB 2 SSSSSSSSS 10
```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 15
; OTHER INFORMATION: Xaa at position 15 is Nle
US-10-506-223-33

Query Match 2.4%; Score 9; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.047; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSSSS 62
| | | | | | | | | |
DB 2 SSSSSSSSS 10

RESULT 11
US-10-506-223-34
; Sequence 34, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 16
; OTHER INFORMATION: Xaa at position 16 is Nle
US-10-506-223-34

Query Match 2.4%; Score 9; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.049; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSSSS 62
| | | | | | | | | |
DB 2 SSSSSSSSS 10

RESULT 12
US-10-506-223-35
; Sequence 35, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31

; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 17
; OTHER INFORMATION: Xaa at position 17 is Nle
US-10-506-223-35

Query Match 2.4%; Score 9; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.051; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSSSS 62
| | | | | | | | | |
DB 2 SSSSSSSSS 10

RESULT 13
US-10-506-223-36
; Sequence 36, Application US/10506223
; Publication No. US20060009622A1
; GENERAL INFORMATION:
; APPLICANT: Fuselier, Joseph A.
; APPLICANT: Coy, David H.
; TITLE OF INVENTION: Conjugates of Therapeutic or Cytotoxic
; FILE OF INVENTION: Agents and Biologically Active Peptides
; FILE REFERENCE: 07005/007002
; CURRENT APPLICATION NUMBER: US/10/506,223
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/03/06657
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,831
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: VARIANT
; LOCATION: 18
; OTHER INFORMATION: Xaa at position 18 is Nle
US-10-506-223-36

Query Match 2.4%; Score 9; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.053; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSSSS 62
| | | | | | | | | |
DB 2 SSSSSSSSS 10

RESULT 14
US-11-004-399-3261
; Sequence 3261, Application US/11004399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye

APPLICANT: Ramalingam, Sathiskumar
APPLICANT: Poon, Leo Lit Man
APPLICANT: Peiris, Joseph Sriyal Malik
TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
TITLE OF INVENTION: Sequences and Methods of Use Thereof For Immunization Against SA
FILE REFERENCE: 2587/73166/RDK
CURRENT APPLICATION NUMBER: US/11/004,399
CURRENT FILING DATE: 2004-12-03
PRIOR APPLICATION NUMBER: US 60/527,637
PRIOR FILING DATE: 2003-12-03
NUMBER OF SEQ ID NOS: 4043
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3261
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pCV2
US-11-004-399-3261

Query Match 2.4%; Score 9; DB 7; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.072; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSSSS 62
Db 28 SSSSSSSSS 36

RESULT 15
US-11-169-232-12
Sequence 12, Application US/11169232
Publication No. US20060025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/11/169,232
APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-11-169-232-12

Query Match 2.4%; Score 9; DB 7; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.083; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSSSS 62
Db 10 SSSSSSSSS 18

Search completed: March 17, 2006, 23:21:27
Job time : 23 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:13:01 ; Search time 39 Seconds
(without alignments)
910.359 Million cell updates/sec

Title: US-09-856-812B-1
Perfect score: 369
Sequence: 1 MPAPKRCRCMPEDLQSQS.....DTTAVASASSATGSFSFSYPE 369

Scoring table: OLIGO 3.3
Gap 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0
Total number of hits satisfying chosen parameters: 33266

Minimum DB seq length: 0
Maximum DB seq length: 93
Post-processing: Listing first 45 summaries
Database : PIR 80:*
1: pirl:*
2: pirl:*
3: pirl:*
4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	2.2	54	2 T10786	conserved hypothet
2	8	2.2	62	2 H72168	A43R protein - var
3	7	1.9	15	2 A38304	heterogeneous ribo
4	7	1.9	46	2 B23184	vitellogenin - duc
5	7	1.9	65	2 S12405	7K protein - carna
6	7	1.9	70	2 T02541	hypothetical prote
7	7	1.9	75	2 PC2221	ADP-ribosylated pr
8	7	1.9	76	2 S37191	hypothetical prote
9	7	1.9	77	2 T41800	AckNPV orf55 - Bom
10	7	1.9	80	2 T27603	hypothetical prote
11	7	1.9	85	2 A86282	protein F10B6.20 [
12	6	1.6	25	2 I60083	glycophorin A - hu
13	6	1.6	34	2 S68084	probable RNA-bind
14	6	1.6	39	2 C90523	hypothetical prote
15	6	1.6	40	2 A29184	vitellogenin - tur
16	6	1.6	40	2 E72429	hypothetical prote
17	6	1.6	49	2 B56448	cofilin-like prote
18	6	1.6	49	2 B97874	degenerate transpo
19	6	1.6	54	2 T06514	hypothetical prote
20	6	1.6	52	2 C35523	hypothetical prote
21	6	1.6	58	2 I52571	glycophorin Mi1 -
22	6	1.6	60	2 H63394	hypothetical prote
23	6	1.6	62	4 T09191	hypothetical prote
24	6	1.6	65	2 B68446	hypothetical prote
25	6	1.6	67	2 H98064	hypothetical prote
26	6	1.6	67	2 F89778	hypothetical prote
27	6	1.6	68	2 H72284	hypothetical prote
28	6	1.6	69	2 H38856	B1/R protein - vari
29	6	1.6	69	2 A72174	D6R protein - vari

30	6	1.6	70	2 C97412	hypothetical prote
31	6	1.6	71	4 A42590	glycophorin B/glyc
32	6	1.6	76	2 I52570	glycophorin - huma
33	6	1.6	76	2 S63584	reverse transcript
34	6	1.6	77	2 S76483	hypothetical prote
35	6	1.6	77	2 G82169	phage shock protei
36	6	1.6	78	1 A34931	glycophorin E prec
37	6	1.6	78	2 C53216	prostaglandin E2 r
38	6	1.6	78	2 T21426	hypothetical prote
39	6	1.6	79	2 T44223	hypothetical prote
40	6	1.6	79	2 D87577	hypothetical prote
41	6	1.6	80	2 G96841	hypothetical prote
42	6	1.6	80	2 A84528	hypothetical prote
43	6	1.6	83	2 I48357	p12 GAG gene like
44	6	1.6	83	2 H90170	hypothetical prote
45	6	1.6	84	2 S78732	protein YMR122w-a

ALIGNMENTS

RESULT 1

T10786
conserved hypothetical protein - clove pink
C:Species: Dianthus caryophyllus (clove pink)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10786
R:Kim, Y.J.; Lee, M.M.; Chang, K.S.; Lee, S.H.; Park, K.Y.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z17144
A:Accession: T10786
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-54 <KIM>
A:Cross-references: UNIPROT:O24519; UNIPARC:UPI00000A17AD; EMBL:U94786; NID:g2406584; P
A:Experimental source: strain White s1m
C:Genetics:
A:Introns: 48/3
A>Note: gcsdcg

Query Match 2.2%; Score 8; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 SSSSSSSS 61
|||||||
Db 10 SSSSSSSS 17

RESULT 2

H72168
A43R protein - variola minor virus (strain Garcia-1966)
C:Species: variola minor virus
C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004
C:Accession: H72168
R:Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.P.; Lopa
submitted to GenBank, March 1998
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor.
A:Reference number: A72150
A:Accession: H72168
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <SHC>
A:Cross-references: UNIPROT:O89183; UNIPARC:UPI0000061D60; GB:Y16780; NID:g5830555; PIDP
A:Experimental source: strain Garcia-1966
C:Genetics:
A:Gene: A43R

Query Match 2.2%; Score 8; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 SSSSTSTSS 46

```

Db          49 SSSTSTSS 56
|||||
Query Match      1.9%; Score 7; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
A38304
heterogeneous ribonuclear particle protein A1 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 31-Oct-1997
C:Accession: A38304
R:Kumar, A.; Casas-Finet, J.R.; Luneau, C.J.; Karpel, R.L.; Merrill, B.M.; Williams, K.R.
J. Biol. Chem. 265, 17094-17100, 1990
A:Title: Mammalian heterogeneous nuclear ribonucleoprotein A1. Nucleic acid binding prop
A:Reference number: A38304; MUID:91009136; PMID:2145269
A:Accession: A38304
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <UM>
A:Cross-references: UNIPARC:UPI0000177219
C:Superfamily: helix-destabilizing protein; ribonucleoprotein repeat homology

Query Match      1.9%; Score 7; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          354 MASASSS 360
|||||
Db          1 MASASSS 7

RESULT 4
B29184
vitellogenin - duck (fragment)
N:Contains: phosvitin
C:Species: Anas platyrhynchos (domestic duck)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 09-Jul-2004
C:Accession: B29184
R:Clark, R.C.
Int. J. Biochem. 17, 983-988, 1985
A:Title: The primary structure of avian phosvitins. Contributions through the Edman degr
A:Reference number: A91754; MUID:86056531; PMID:4065410
A:Accession: B29184
A:Molecule type: protein
A:Residues: 1-46 <CLA>
A:Cross-references: UNIPROT:P56530; UNIPARC:UPI000013886D
C:Superfamily: vitellogenin
C:Keywords: phosphoprotein
F:13,14,15,16,17,19,20,23,24,25,26,27,28,29,31,32/Binding site: phosphate (Ser) (covalen

Query Match      1.9%; Score 7; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          54 SSSSSSSS 60
|||||
Db          23 SSSSSSSS 29

RESULT 5
S12405
7K protein - carnation latent virus
C:Species: carnation latent virus, CLV
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S12405
R:Poster, G.D.; Meehan, B.M.; Mills, P.R.
Plant Mol. Biol. 15, 937-939, 1990
A:Title: Nucleotide sequence of the 7K gene of carnation latent virus.
A:Reference number: S12405; MUID:91355918; PMID:2103483
A:Accession: S12405
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-65 <FOS>
A:Cross-references: UNIPROT:P28898; UNIPARC:UPI0000137F4E; GB:X55331; NID:g296788; PIDN:

```

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Query Match      1.9%; Score 7; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          57 SSSSSSSS 63
|||||
Db          25 SSSSSSSS 31

RESULT 6
T02541
hypothetical protein At2g37750 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein F13M22.25
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C:Accession: T02541; F84796
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, June 1998
A:Description: Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence.
A:Reference number: Z14677
A:Accession: T02541
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-70 <ROU>
A:Cross-references: UNIPROT:O80943; UNIPARC:UPI000017AF6A; EMBL:AC004684; NID:g3236234;
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, L.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: F84796
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-70 <STO>
A:Cross-references: UNIPARC:UPI000017AF6A; GB:AE002093; NID:g3236257; PIDN:AAC23645.1; C
C:Genetics:
A:Gene: F13M22.25; At2g37750
A:Map position: 2

Query Match      1.9%; Score 7; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          38 ASSTSTST 44
|||||
Db          45 ASSTSTST 51

RESULT 7
PC2221
ADP-ribosylated protein A8 - human (fragments)
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 31-Dec-2004
C:Accession: PC2221
R:Frabad, S.; Walent, J.; Dritschilo, A.
Biochem. Biophys. Res. Commun. 204, 772-779, 1994
A:Title: ADP-ribosylation of heterogeneous ribonucleoproteins in HeLa cells.
A:Reference number: PC2221; MUID:95071393; PMID:7980541
A:Accession: PC2221
A:Molecule type: protein
A:Residues: 1-75 <PRA>
A:Cross-references: UNIPROT:Q9UDG9; UNIPARC:UPI0000177218
C:Comment: This protein catalyzes the transfer of ADP-ribose from nicotinamide adenine
C:Superfamily: ribonucleoprotein repeat homology

Query Match      1.9%; Score 7; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          354 MASASSS 360

```

```
Db          48 MASASS 54
|||||||
Query Match      1.9%; Score 7; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSS 60
Db 10 SSSSSSS 16
|||||||

RESULT 9
T41800
ACNVPV orf55 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
C:Species: Bombyx mori nuclear polyhedrosis virus, BMSNPV
A:Variety: isolate T3
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41800
R:Gomi, S.; Majima, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A>Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A:Reference number: Z2020; MUID:99281911; PMID:10355780
A:Accession: T41800
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-77 <RAM>
A:Cross-references: UNIPROT:092421; UNIPARC:UPI00000F6480; EMBL:L333180; PIDN:AAC63729.1
A:Experimental source: isolate T3
C:Genetics:
A>Note: Orf_44

Query Match      1.9%; Score 7; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSS 60
Db 24 SSSSSSS 30
|||||||

RESULT 10
T27603
hypothetical protein ZC477.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27603
R:Du, Z.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid ZC477.
A:Reference number: Z20392
A:Accession: T27603
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-80 <DUZ>
A:Cross-references: UNIPROT:023341; UNIPARC:UPI0000082BF9; EMBL:U40802; PIDN:AAA81504.1;
```

```
C:Genetics:
A:Gene: CESP:ZC477.4

Query Match      1.9%; Score 7; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSS 60
Db 14 SSSSSSS 20
|||||||

RESULT 11
A86282
protein F1086.20 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: A86282
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.
Chin, C.W.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Ma, R.; Marziani
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86282
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-85 <STO>
A:Cross-references: UNIPROT:Q9LQV1; UNIPARC:UPI00000AAAF2E; GB:AE005172; NID:g8778231; P
C:Genetics:
A:Gene: F1086.20
A:Map position: 1

Query Match      1.9%; Score 7; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSS 60
Db 56 SSSSSSS 62
|||||||

RESULT 12
I60083
glycophorin A - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I60083
R:DuPont, B.R.; Grant, S.G.; Oto, S.H.; Bigbee, W.L.; Jensen, R.H.; Langlois, R.G.
Vox Sang. 68, 121-129, 1995
A>Title: Molecular characterization of glycophorin A transcripts in human erythroid cell
A:Reference number: I60083; MUID:95282423; PMID:7762218
A:Accession: I60083
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-25 <RES>
A:Cross-references: UNIPROT:Q9UM93; UNIPARC:UPI000006FDCF; GB:S77077; NID:g913054; PIDN
C:Genetics:
A:Gene: GDB:GYPA
A:Cross-references: GDB:118890; OMIM:111300
A:Map position: 4q28-q31
C:Superfamily: glycophorin

Query Match      1.6%; Score 6; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 TSTSSS 47
```

```
Db          20 TSTSS 25
|||||
Query Match      1.6%; Score 6; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      135 DEKVTD 140
Db       1 DEKVTD 6

RESULT 13
S68084
Probable RNA-binding protein RBD3 - fission yeast (Schizosaccharomyces pombe) (fragment)
C:Species: Schizosaccharomyces pombe
C>Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 05-Oct-2004
C:Accession: S68084
R:VanHoy, R.W.; Wise, J.A.
Curr. Genet. 29, 307-315, 1996
A:Title: Molecular analysis of a novel Schizosaccharomyces pombe gene containing two RNP
A:Reference number: S68083; MUID:96171513; PMID:8598051
A:Accession: S68084
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-34 <VAN>
A:Cross-references: UNIPARC:UPI000017A393

Query Match      1.6%; Score 6; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      135 DEKVTD 140
Db       1 DEKVTD 6

RESULT 14
C90523
Hypothetical protein MYPU_0910 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: C90523
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: C90523
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-39 <KUR>
A:Cross-references: UNIPROT:Q98RB8; UNIPARC:UPI00000C7FF4; GB:AL445566; PID:gl4089504; E
C:Genetics:
A:Gene: MYPU 0910
A:Genetic code: SGC3

Query Match      1.6%; Score 6; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      201 FVLVTS 206
Db       23 FVLVTS 28

RESULT 15
A29184
Vitellogenin - turkey (fragment)
N:Contains: phosvitin
C:Species: Meleagris gallopavo (common turkey)
C>Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 09-Jul-2004
C:Accession: A29184
R:Clark, R.C.
Int. J. Biochem. 17, 983-988, 1985
A:Title: The primary structure of avian phosvitins. Contributions through the Edman degr
A:Reference number: A91754; MUID:86056531; PMID:4065410
A:Accession: A29184
A:Molecule type: protein
A:Residues: 1-40 <CLA>
A:Cross-references: UNIPROT:P56531; UNIPARC:UPI0000138871
```

```
C:Superfamily: vitellogenin
C:Keywords: phosphoprotein
P:12,13,14,15,16,17,19,20,24,25,26,27,28,29,31,32/Binding site: phosphate (Ser) (covalen
Query Match      1.6%; Score 6; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      54 SSSSSS 59
Db       12 SSSSSS 17
```

Search completed: March 17, 2006, 23:17:21
Job time : 43 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:09:41 ; Search time 228 Seconds
(without alignments)
1141.842 Million cell updates/sec

Title: US-09-856-812B-1
Perfect score: 369
Sequence: 1 MPRAPKRCMPEDLQSQS.....DTTANASASSATGTSFSYPE 369

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0
Searched: 2166443 seqs, 705528306 residues

Word size : 0
Total number of hits satisfying chosen parameters: 283188

Minimum DB seq length: 0
Maximum DB-seq-length: 93

Post-processing: Listing first 45 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	10	2.7	47	2 Q76NT4 DICDI
2	10	2.7	54	2 Q85513 9GAMR
3	10	2.7	63	2 Q4YK11 PLABE
4	10	2.7	63	2 Q9M5P0 TOBAC
5	10	2.7	65	2 Q5TQAZ ANOGA
6	10	2.7	71	2 Q8VB36 WSSV
7	10	2.7	88	2 Q4YAE9 PLABE
8	9	2.4	42	2 Q52B1 DICDI
9	9	2.4	49	2 Q54NV6 DICDI
10	9	2.4	50	2 Q9NDB3 CRYPV
11	9	2.4	51	2 Q6PKF9 HUMAN
12	9	2.4	55	2 Q54EA9 DICDI
13	9	2.4	59	2 Q9NCR6 CRYPV
14	9	2.4	60	2 Q55B54 DICDI
15	9	2.4	62	2 Q55C53 DICDI
16	9	2.4	61	2 Q8TQ9 DICDI
17	9	2.4	61	2 Q8VB12 WSSV
18	9	2.4	63	2 Q6K7U4 ORYSA
19	9	2.4	64	2 Q4YVF8 PLABE
20	9	2.4	66	2 Q55G12 DICDI
21	9	2.4	68	2 Q9NCS0 CRYPV
22	9	2.4	69	2 Q86JP8 DICDI
23	9	2.4	69	2 Q8VAI3 WSSV
24	9	2.4	71	2 Q5UCV9 ORISA
25	9	2.4	71	2 Q8VBB9 WSSV
26	9	2.4	73	2 Q8MRV3 DROME
27	9	2.4	73	2 Q8IP81 DROME
28	9	2.4	74	2 Q58WZ9 ORENI
29	9	2.4	76	2 Q54W62 DICDI
30	9	2.4	80	2 Q8VXF7 LOTJA
31	9	2.4	80	2 Q8VBE8 WSSV

32 9 2.4 80 2 Q91LH8 WSSV Q91LH8 white spot
33 9 2.4 81 2 Q5CZQ3 BRARE Q5CZQ3 brachydanio
34 9 2.4 84 2 Q56S11 BOVIN Q56S11 bos taurus
35 9 2.4 84 2 Q5LY87 STRT1 Q5LY87 streptococc
36 9 2.4 86 2 Q8VAA3 WSSV Q8VAA3 white spot
37 9 2.4 87 2 Q5FR04 GLUOX Q5FR04 gluconobact
38 9 2.4 88 2 Q56YF5 ARATH Q56YF5 arabidopsis
39 9 2.4 91 2 Q4XC49 PLACH Q4XC49 plasmodium
40 8 2.2 52 2 Q9PTT4 CHICK Q9PTT4 gallus gall
41 8 2.2 54 2 Q24519 DIACA Q24519 dianthus ca
42 8 2.2 57 2 Q6YZT7 ORYSA Q6YZT7 oryza sativ
43 8 2.2 62 2 Q76PM1 VARV Q76PM1 variola min
44 8 2.2 62 2 Q80HU3 9POXV Q80HU3 vaccinia vi
45 8 2.2 62 2 Q89183 VARV Q89183 variola vir

ALIGNMENTS

RESULT 1
Q76NT4 DICDI PRELIMINARY; PRT; 47 AA.
AC Q76NT4;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J.A.,
RA Bankier A.T., Dear P.H., Lehmann R., Baumgart C., Parra G.,
RA Abril J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A.,
RA Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC117081; AAS38828.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 47 AA; 4489 MW; 3781AB1651807149 CRC64;

Query Match 2.7%; Score 10; DB 2; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSSSSSC 63
|||||
DB 29 SSSSSSSSSSC 38

RESULT 2
Q85513 9GAMR PRELIMINARY; PRT; 54 AA.
ID Q85513 9GAMR PRELIMINARY;
AC Q85513;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE (SM) v-fms 3' recombination site RNA. (Fragment).

OS Feline sarcoma virus.
OC Viruses; Retroid viruses; Retroviridae; Gammaretrovirus;
OC 1-Mammalian type C virus group.
OX NCBI_TaxID=11772;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86308237; PubMed=3018286;

RA Besmer P., Lader E., George P.C., Bergold P.J., Qiu F.-H.,
 RA Zuckerman E.E., Hardy W.D.;
 RT "A new acute transforming feline retrovirus with fms homology
 RT specifies a C-terminally truncated version of the c-fms protein that
 RT is different from SM-feline sarcoma virus v-fms protein.";
 RL J. Virol. 60:194-203(1986).
 RL EMBL; M14291; AAA43044.1; -; Genomic_RNA.
 FT NON TER 1
 FT 1
 SQ SEQUENCE 54 AA; 5583 MW; 7C116DDCAECFB93 CRC64;

Query Match 2.7%; Score 10; DB 2; Length 54;
 Best Local Similarity 100.0%; Pred. No. 0.32; Mismatches 0; Indels 0; Gaps
 Matches 10; Conservative 0;

QY 53 PSSSSSSSSSS 62
 |||||
 DB 22 PSSSSSSSSSS 31

RESULT 3
 Q4YK11_PLABE
 ID Q4YK11_PLABE PRELIMINARY; PRT; 63 AA.
 AC Q4YK11; 2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PB401632.00.0;
 OS Plasmodium berghei.
 OS Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5821;
 RN [1]

NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Koolij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Jancee C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RA "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses.";
 RL Science 307:82-86(2005).
 RL -/- EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; CAI01004200; CAI01481.1; -; Genomic_DNA.
 DR DR Hypothetical protein.
 KW FT NON TER 63
 FT 63
 SQ SEQUENCE 63 AA; 6394 MW; C3818213C161B03F CRC64;

Query Match 2.7%; Score 10; DB 2; Length 63;
 Best Local Similarity 100.0%; Pred. No. 0.37; Mismatches 0; Indels 0; Gaps
 Matches 10; Conservative 0;

QY 53 PSSSSSSSSSS 62
 |||||
 DB 35 PSSSSSSSSSS 44

RESULT 4
 Q9M5P0_TOBAC
 ID Q9M5P0_TOBAC PRELIMINARY; PRT; 63 AA.
 AC Q9M5P0;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 22, Last annotation update)
 DE Protoporphyrinogen oxidase (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterid
 OC lamids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]

DOI=10.1128/JVI.75.23.11811-11820.2001;
Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
"Complete genome sequence of the shrimp white spot bacilliform virus.";
J. Virol. 75:11811-11820(2001).
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Taiwan;
RC MEDLINE=20517548; PubMed=11062040; DOI=10.1006/viro.2000.0597;
RA Tsai M.F., Yu H.T., Tzeng H.F., Leu J.H., Chou C.M., Huang C.J.,
Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;
"Identification and characterization of a shrimp white spot syndrome virus (WSSV) gene that encodes a novel chimeric polypeptide of cellular-type thymidine kinase and thymidylate kinase.";
Virology 277:100-110(2000).
[3]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Taiwan;
RC MEDLINE=21844071; PubMed=11853398; DOI=10.1006/viro.2001.1273;
RA Chen L.L., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,
Lo C.F., Kou G.H.;
"Identification of a nucleocapsid protein (VP35) gene of shrimp white spot syndrome virus and characterization of the motif important for targeting VP35 to the nuclei of transfected insect cells.";
Virology 293:44-53(2002).
[4]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Taiwan;
RC PubMed=12202227; DOI=10.1006/viro.2002.1480;
RA Tzeng H.F., Chang Z.F., Peng S.E., Wang C.H., Lin J.Y., Kou G.H.,
Lo C.F.;
"Chimeric polypeptide of thymidine kinase and thymidylate kinase of shrimp white spot syndrome virus: thymidine kinase activity of the recombinant protein expressed in a baculovirus/insect cell system.";
Virology 299:248-255(2002).
[5]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Taiwan;
RC PubMed=12359454; DOI=10.1006/viro.2002.1536;
RA Chen L.L., Wang H.C., Huang C.J., Peng S.E., Chen Y.G., Lin S.J.,
Chen W.Y., Dai C.F., Yu H.T., Wang C.H., Lo C.F., Kou G.H.;
"Transcriptional analysis of the DNA polymerase gene of shrimp white spot syndrome virus.";
Virology 301:136-147(2002).
[6]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Taiwan;
RC PubMed=12504569; DOI=10.1006/viro.2002.1596;
RA Lin S.T., Chang Y.S., Wang H.C., Tzeng H.F., Chang Z.F., Lin J.Y.,
Wang C.H., Lo C.F., Kou G.H.;
"Ribonucleotide reductase of shrimp white spot syndrome virus (WSSV): expression and enzymatic activity in a baculovirus/insect cell system and WSSV-infected shrimp.";
Virology 304:282-290(2002).
[7]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Taiwan;
RC PubMed=15452257; DOI=10.1128/JVI.78.20.11360-11370.2004;
RA Tsai J.M., Wang H.C., Leu J.H., Hsiao H.H., Wang A.H., Kou G.H.,
Lo C.F.;
"Genomic and proteomic analysis of thirty-nine structural proteins of shrimp white spot syndrome virus.";
J. Virol. 78:11360-11370(2004).
[8]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Taiwan;
RC PubMed=15596810; DOI=10.1128/JVI.79.1.140-149.2005;
RA Leu J.H., Tsai J.M., Wang H.C., Wang A.H., Wang C.H., Kou G.H.,
Lo C.F.;
"The unique stacked rings in the nucleocapsid of the white spot syndrome virus virion are formed by the major structural protein VP66, the largest viral structural protein ever found.";
J. Virol. 79:140-149(2005).

[9]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Taiwan;
RA Lo C.F., Kou G.-H.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332093; AAL33166.1; -; Genomic_DNA.
DR EMBL; AF440570; AAL89086.1; -; Genomic_DNA.
SQ SEQUENCE 71 AA; 7313 MW; 0D57B06FEAB7DFB1 CRC64;
Query Match 2.7%; Score 10; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 49 PSSPSSSSSS 58
DB 53 PSSPSSSSSS 62
RESULT 7
QYAE9 PLABE PRELIMINARY; PRT; 88 AA.
AC QYAE9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB401576.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic, transcriptomic, and proteomic analyses.";
Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
CC EMBL; CAAI01007103; CAAI05267.1; -; Genomic_DNA.
DR Hypothetical protein.
FT NON_TER 1
FT NON_TER 88
SQ SEQUENCE 88 AA; 9007 MW; 4315F32B0C238BFD CRC64;
Query Match 2.7%; Score 10; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 53 PSSSSSSSSSS 62
DB 26 PSSSSSSSSSS 35
RESULT 8
Q552B1_DICDI
ID Q552B1_DICDI PRELIMINARY; PRT; 42 AA.
AC Q552B1;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DD0203491;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RN NUCLEOTIDE SEQUENCE.

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RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Pey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Farhournou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Karhorthou P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsey R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loulsegue H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzner M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Bartell B., Kuspa A.;
RA "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAFI01000032; EAL69388.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 42 AA; 4721 MW; 34A91177B08FA3E7 CRC64;

Query Match 2.4%; Score 9; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSSSSS 62
Db |||||||

RESULT 9
Q54NV6_DICDI PRELIMINARY; PRT; 49 AA.
AC Q54NV6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DPB0218656;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Pey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Farhournou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Karhorthou P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsey R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loulsegue H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzner M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Bartell B., Kuspa A.;
RA "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -!- CAUTION: The sequence shown here is derived from an
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```
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAFI010000116; EAL64994.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 49 AA; 4929 MW; AEE0CC0DC5C75BC CRC64;

Query Match 2.4%; Score 9; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSSSSS 62
Db |||||||

RESULT 10
Q9NDB3_CRYPV PRELIMINARY; PRT; 50 AA.
AC Q9NDB3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE 15 kDa glycoprotein gp15 (Fragment).
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Oocyst;
RX MEDLINE=20316040; PubMed=10858229;
RX DOI=10.1128/IAI.68.7.4117-4134.2000;
RA Strong W.B., Gut J., Nelson R.G.;
RT "Cloning and sequence analysis of a highly polymorphic Cryptosporidium
RT parvum gene encoding a 60-kilodalton glycoprotein and characterization
RT of its 15- and 45-kilodalton zoite surface antigen products.";
RL Infect. Immun. 68:4117-4134(2000).
DR EMBL; AF164508; AAF78362.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 50
FT NON_TER 50
SQ SEQUENCE 50 AA; 4705 MW; D87D5DFE8811C421 CRC64;

Query Match 2.4%; Score 9; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSSSSS 62
Db |||||||

RESULT 11
Q6PKF9_HUMAN PRELIMINARY; PRT; 51 AA.
AC Q6PKF9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DKFZP564J157 protein.
GN Name=DKFZP564J157;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
FAhey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC001464; AAH01464.2; -; mRNA.
SQ SEQUENCE 51 AA; 5793 MW; 757C3D5F4E1FA927 CRC64;

Query Match 2.4%; Score 9; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSSSSS 62
Db |||||
39 SSSSSSSSSS 47

RESULT 12
Q54EA9_DICDI PRELIMINARY; PRT; 55 AA.
AC Q54EA9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNames=DD0219883;
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Linday R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loulseghe H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitz E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox B.C.,
RA Chisholm R.L., Gibbs R., Loomis W.P., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0-0-0(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
DR EMBL; AAF101000257; EAL61829.1; -; Genomic_DNA.
KW Hypothetical protein.

SQ SEQUENCE 55 AA; 5490 MW; 817AFDFC0175766A CRC64;

Query Match 2.4%; Score 9; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSSSSS 62
Db |||||
18 SSSSSSSSSS 26

RESULT 13
Q9NCR6_CRYPV PRELIMINARY; PRT; 59 AA.
AC Q9NCR6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gp15 antigen (fragment).
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20316040; PubMed=10858229;
RX DOI=10.1128/IAI.68.7.4117-4134.2000;
RA Strong W.B., Gut J., Nelson R.G.;
RT "Cloning and sequence analysis of a highly polymorphic Cryptosporidium
RT parvum gene encoding a 60-kilodalton glycoprotein and characterization
RT of its 15- and 45-kilodalton zoite surface antigen products.";
RL Infect. Immun. 68:4117-4134(2000).
DR EMBL; AF178697; AAF81991.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 59
SQ SEQUENCE 59 AA; 5742 MW; D9173B91CB482AA3 CRC64;

Query Match 2.4%; Score 9; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 SSSSSSSSSS 62
Db |||||
30 SSSSSSSSSS 38

RESULT 14
Q55B54_DICDI PRELIMINARY; PRT; 60 AA.
AC Q55B54;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNames=DD0202750;
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Linday R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loulseghe H., Mungall K., Oliver K., Price C., Quail M.A.,

Search completed: March 17, 2006, 23:16:40
Job time : 237 secs

RA Urushihara H., Hernandez J., Rabbowitz E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shauly G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzner M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAF101000013; EAL71721.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 60 AA; 6281 MW; 06A10A0CBD5961B4 CRC64;

Query Match 2.4%; Score 9; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 SSSSSSSSS 62
DB 16 SSSSSSSSS 24

RESULT 15
Q55C53 DICDI
ID Q55C53_DICDI PRELIMINARY; PRT; 60 AA.
AC Q55C53;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DD0190889;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero P.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen C., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsey R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Louissege H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabbowitz E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shauly G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzner M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAF101000011; EAL72463.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 60 AA; 5821 MW; 2D9ADA4A25F011C6 CRC64;

Query Match 2.4%; Score 9; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 SSSSSSSSS 62
DB 13 SSSSSSSSS 21

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:41:49 ; Search time 186 Seconds
(without alignments)
21.260 Million cell updates/sec

Title: US-09-856-812B-57

Perfect score: 9

Sequence: 1 CLGLSYDGL 9

Scoring table: COLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003s.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	100.0	9	2	AAR79849 Test pept
2	9	100.0	9	2	AAR80908
3	9	100.0	9	2	AAR80908
4	9	100.0	9	2	AAR80908
5	9	100.0	9	4	AAR72011
6	9	100.0	9	6	AB99577
7	9	100.0	9	8	AD97901
8	9	100.0	9	8	AD97901
9	9	100.0	9	8	AD97901
10	9	100.0	9	8	AD97901
11	9	100.0	9	8	AD97901
12	9	100.0	9	8	AD97901
13	9	100.0	10	2	AAR80909
14	9	100.0	10	2	AAR80909
15	9	100.0	10	2	AAR80909
16	9	100.0	10	2	AAR80909
17	9	100.0	10	8	AD97910
18	9	100.0	10	8	AD97910
19	9	100.0	10	8	AD97910
20	9	100.0	10	8	AD97910
21	9	100.0	10	8	AD97910
22	9	100.0	11	2	AAR80934
23	9	100.0	11	2	AAR80934
24	9	100.0	11	8	ADK69481

25	9	100.0	11	8	ADQ11343	Adq11343 Homo sapi
26	9	100.0	11	8	ADQ11343	Adq11343 Homo sapi
27	9	100.0	13	2	AAy47298	AAy47298 Immunogen
28	9	100.0	13	8	AD98063	AD98063 Immunogen
29	9	100.0	15	3	AAy98995	AAy98995 HLA class
30	9	100.0	15	3	AAy98995	AAy98995 HLA class
31	9	100.0	15	4	AAy98995	AAy98995 HLA class
32	9	100.0	15	4	AAy98995	AAy98995 HLA class
33	9	100.0	15	4	AAy98995	AAy98995 HLA class
34	9	100.0	15	4	AAy98995	AAy98995 HLA class
35	9	100.0	15	4	AAy98995	AAy98995 HLA class
36	9	100.0	15	4	AAy98995	AAy98995 HLA class
37	9	100.0	15	4	AAy98995	AAy98995 HLA class
38	9	100.0	17	4	AAU72447	AAU72447
39	9	100.0	17	4	AAU72447	AAU72447
40	9	100.0	17	4	AAU72447	AAU72447
41	9	100.0	18	4	AAU72461	AAU72461
42	9	100.0	18	4	AAU72456	AAU72456
43	9	100.0	18	4	AAU72457	AAU72457
44	9	100.0	18	8	ADN65352	ADN65352 HLA bindi
45	9	100.0	20	4	AAU72444	AAU72444

ALIGNMENTS

RESULT 1
AAR79849
ID AAR79849 standard; peptide; 9 AA.
XX
AC AAR79849;
XX
DT 08-MAY-1996 (first entry)
XX
DE Test peptide #2 to determine HLA-2 stabilisation.
XX
KW Tumour rejection antigen; MAGS tumour rejection precursor; complex;
KW HLA-2; immunogen; antibody; cytolytic T cell clone.
XX
OS Synthetic.
XX
PN WO9525740-A1.
XX
PD 28-SEP-1995.
XX
PF 22-MAR-1995; 95WO-US003657.
XX
PR 24-MAR-1994; 94US-00217186.
PR 17-JUN-1994; 94US-00261160.
PR 15-AUG-1994; 94US-00290381.
XX
(LUDW-) LUDWIG INST CANCER RES.
PA (UYOX-) UNIV OXFORD.
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
Townsend A, Bastin J, Boon-Falleur T, Van Der Bruggen P, Coulie P;
Gajewski T, Melief CJ, Visseren MW, Kast WM;
WPI; 1995-344584/44.
XX
Isolated peptide(s) which complex with HLA-A2 - used as immunogens for
the prodn. of antibodies, or as targets for the generation of cytolytic T
cell clones.
XX
Example 1; Page 9; 44pp; English.
XX
The peptides given in AAR79848-52 represent peptides which were used in
an example of the invention to determine whether they acted to stabilise
HLA-2 and whether they were therefore displayed by HLA-2. These peptides
were based on sequences derived from tumour rejection antigens derived
from MAGS tumour rejection precursor. These peptides did not form a
complex with HLA-2. A peptide derived from influenza virus (see AAR79853)
was used as a control peptide as it is known to be presented by HLA-2.

CC Peptides which do form a strong complex with HLA-2 (see AAR79836-41) may
 CC be used diagnostically and as immunogens in the production of antibodies.
 CC They may also be used as targets for the generation of cytolytic T cell
 CC clones. This cytolytic T cell clone is used to treat a cancerous
 CC condition characterised by the fact that the cancer cells present the HLA
 CC -2/peptide complex on their surface

XX Sequence 9 AA;

Query Match 100.0%; Score 9; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9
 DB 1 CLGLSYDGL 9

RESULT 2
 AAR80908
 ID AAR80908 standard; peptide; 9 AA.

XX
 AC AAR80908;

XX 03-MAY-1996 (first entry)

XX MAGE-2 peptide (residues 181-189) with low HLA-A2.1 binding affinity.

XX Human melanoma-associated protein; MAGE-2; tumour rejection antigen;
 KW precursor; major histocompatibility complex; MHC; class 1; HLA-A2.1;
 KW binding; cytolytic T cell; CTL; induction.

XX Synthetic.

XX WO9525530-A1.

XX 28-SEP-1995.

XX 21-MAR-1995; 95WO-US003535.

XX 24-MAR-1994; 94US-00217188.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (UYLE-) RIJKSUNIV LEIDEN.

XX Melief CJM, Visseren MW, Kast WM, Van Der Bruggen P;

XX Boon-Falleur T;

XX WPI; 1995-344456/44.

XX New peptide(s) based on tumour rejection antigen precursor MAGE-2 - which
 PT bind HLA-A2 molecules to provoke cytolytic T cell prodn., used partic.
 PT for treating cancers.

XX Example 2; Page 29; 44pp; English.

XX All peptides of length 9-11 amino acids from the MAGE-2 sequence which
 CC fitted the HLA-A2.1 binding motif or the extended binding motif were
 CC synthesised. The peptides were tested for binding to HLA-A2.1 molecules
 CC expressed on the surface of 174CEM.T2 cells by measuring the fluorescence
 CC index (FI). The FI is a measure for the amount of upregulation of HLA-
 CC A2.1 molecules. The present sequence is that of a peptide that fits the
 CC HLA-A2.1 motif but which had an FI value of 65 mcg/ml, i.e. it is unable
 CC to bind to HLA-A2.1 with high affinity

XX Sequence 9 AA;

Query Match 100.0%; Score 9; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9
 DB 1 CLGLSYDGL 9

Db 1 CLGLSYDGL 9

RESULT 3

AAW36559

ID AAW36559 standard; peptide; 9 AA.

XX
 AC AAW36559;

XX 25-MAR-2003 (revised)

DT 09-MAR-1998 (first entry)

XX MAGE-2 peptide (residues 181-189).

XX Melanoma protein; MAGE-2; tumour rejection antigen precursor;
 KW binding motif; human leukocyte antigen; HLA-A2.1; cytolytic T cell; CTL;
 KW induce; production.

XX Homo sapiens.

XX US5686068-A.

XX 11-NOV-1997.

XX 25-JUL-1996; 96US-00687226.

XX 24-MAR-1994; 94US-00217188.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (UYLE-) RIJKSUNIV LEIDEN.

XX Boon-Falleur T, Van Der Bruggen P, Melief CJM, Visseren MW;

XX Van Der Burg S;

XX WPI; 1997-558084/51.

XX Induction of cytolytic T cell production in vivo - by administering MAGE-
 PT 2 peptide(s).

XX Example 2; Col 6; 24pp; English.

XX This peptide sequence represents part of the melanoma protein, MAGE-2, (a
 CC tumour rejection antigen precursor) and fits the binding motif for human
 CC leukocyte antigen (HLA) A2.1. Only peptides AAW36529-39 have the ability
 CC to bind to this HLA molecule with high affinity and are therefore the
 CC only candidates of the MAGE-2 protein to be recognised by human cytolytic
 CC T cells (CTL), because CTL recognise peptides only when bound to HLA
 CC molecules. Production of CTL in a subject can be induced by administering
 CC a MAGE-2 peptide (particularly AAW36531, AAW36533 and AAW36537) to a
 CC subject who presents HLA-A2 molecules on cells. The method can be used to
 CC treat subjects in need of additional CTL. (Updated on 25-MAR-2003 to
 CC correct PF field.)

XX Sequence 9 AA;

Query Match 100.0%; Score 9; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9

DB 1 CLGLSYDGL 9

RESULT 4

AAAY47136

ID AAAY47136 standard; peptide; 9 AA.

XX
 AC AAAY47136;

XX 01-DEC-1999 (first entry)

XX Immunogenic peptide having a human leukocyte antigen binding motif #1747.

XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW immune response; T cell activation; major histocompatibility complex;
XX cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW vaccine; immunisation.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9945954-A1.
XX
PD 16-SEP-1999.
XX
XX 13-MAR-1998; 98WO-US005039.
XX
XX 13-MAR-1998; 98WO-US005039.
XX
XX (EPIM-) EPIMUNE INC.
XX
XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
PI WPI; 1999-551214/46.
XX
DR
XX New immunogenic peptides with HLA binding motif, useful in treatment and
PT diagnosis of cancers and viral diseases.
XX
XX Claim 1; Page 95; 150pp; English.
XX
CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
CC having a human major histocompatibility complex (MHC) Class I (also known
CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
CC (CTLs) which destroy antigen-bearing cells are normally induced by an
CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
CC than the intact foreign antigen itself, and are particularly important in
CC tumour rejection and in fighting viral infections. The peptides are
CC therefore useful therapeutically to treat or prevent viral infections and
CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
CC elicit an immune response in individuals susceptible or otherwise at risk
CC of viral infection or cancer, or used to treat chronic or acute
CC conditions. They are also useful diagnostically, and can be used to
CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
CC patient. The polynucleotides encoding the immunogenic peptides are also
CC useful therapeutically and for immunisation as above
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CIGLSYDGL 9
DB 1 CIGLSYDGL 9
RESULT 5
AAU72011
ID AAU72011 standard; peptide; 9 AA.
XX
AC AAU72011;
XX
XX 26-FEB-2002 (first entry)
DT
XX MAGE-1 protein antigen #5.
DE
XX Melanoma antigen; MART-1; MAGE-1; gp100; cytostatic; immune response;
KW immunotherapeutic; heat shock protein; tyrosinase; BAGE; NYB01; GM2;
KW

KW tyrosinase related protein 1; tyrosinase related protein 2; vaccine;
KW javelin molecule; melanoma antigen recognised by T cells-1; human.
XX
OS Homo sapiens.
XX
PN WO200178655-A2.
XX
XX 25-OCT-2001.
XX
XX 17-APR-2001; 2001WO-US012449.
XX
XX 17-APR-2000; 2000US-0197462P.
XX
XX (HOUG/) HOUGHTON A.
PA (LIVI/) LIVINGSTON P.
PA (ALAW/) AL-AWQATI Q.
PA (MAYH/) MAYHEW M.
PA (HOEM/) HOE M.
XX
XX Houghton A, Livingston P, Al-Awqati Q, Mayhew M, Hoe M;
PI WPI; 2001-663092/76.
XX
DR
XX Anti cancer vaccine for the treatment of melanoma comprises a heat shock
PT protein and a melanoma antigen i.e. Tyrosinase.
XX
XX Claim 2; Page 13; 150pp; English.
XX
CC The invention relates to a method of induction of an immune response,
CC comprising administration of an immunotherapeutic composition, comprising
CC a heat shock protein, and a melanoma antigen, where the melanoma antigen
CC is selected from tyrosinase, tyrosinase related protein 1, tyrosinase
CC related protein 2, gp 100, MAGE antigens, BAGE antigens, NYB01, MART
CC antigens, GM2, antigenic portions and combinations of these. The melanoma
CC antigen is covalently bound to a javelin molecule, where the melanoma
CC antigen bound to the javelin molecule is non-covalently bound to the heat
CC shock protein. The composition is useful for inducing an immune response
CC for the treatment of melanoma. AAU71980-AAU72481 represent melanoma
CC antigen peptides of the invention
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CIGLSYDGL 9
DB 1 CIGLSYDGL 9
RESULT 6
ABB99577
ID ABB99577 standard; peptide; 9 AA.
XX
AC ABB99577;
XX
XX 28-MAR-2003 (first entry)
DT
XX Immunogenic peptide Mage A1 174 derived from MAGE-A1.
DE
XX Immunogen; MAGE-A1; immune response; cancer.
KW
XX Homo sapiens.
OS
XX WO200294859-A2.
PN
XX 28-NOV-2002.
XX
XX 22-MAY-2002; 2002WO-CA000743.
XX
XX 23-MAY-2001; 2001US-0292590P.
PR
XX 17-MAY-2002; 2002US-00150797.
PR

XX (AVET) AVENTIS PASTEUR LTD.
 PA Entage PCR, Karunakaran L, Pedyczak A, Barber B;
 XX N-PSDB; ABV77111.
 DR WPI; 2003-120784/11.
 DR N-PSDB; ABV77111.
 XX New immunogenic MAGE-A1 peptides useful for inducing an immune response
 PT in a patient, for treating or preventing cancer, or for use as reagents
 PT in drug screening assays.
 XX Claim 1; Page 40; 58pp; English.
 XX The present sequence represents an immunogenic peptide, derived from
 CC human MAGE-A1. The amino acid sequence of MAGE-A1 was assessed for
 CC sequences of 9 contiguous amino acids having specific anchor residues,
 CC leucine or methionine at position 2 and leucine or valine at position 9.
 CC Using this criteria, peptides ABB9574-600 were identified. Synthetic
 CC peptides based on these sequences were produced, and injected into HLA-
 CC A2kb transgenic mice in order to identify immunogenic peptides. The MAGE-
 CC A1 immunogenic peptides, polypeptides, and nucleic acids encoding the
 CC peptides are useful for inducing an immune response in a patient, or for
 CC treating or preventing cancer
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 9; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CLGLSYDGL 9
 Db |||||
 1 CLGLSYDGL 9
 RESULT 7
 ADE97901
 ID ADE97901 standard; peptide; 9 AA.
 XX
 AC ADE97901;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Immunogenic HLA-A2.1 binding peptide #383.
 XX
 KW cytostatic; anti-inflammatory; hepatotropic; virucide; anti-HIV;
 KW nephrotropic; neuroprotective; antiarthritic; antirheumatic;
 KW immunosuppressive; dermatological; muscular; nephrotropic; thyromimetic;
 KW haemostatic; antithyroid; antianaemic; anabolic; hypertensive;
 KW immunogenic peptide composition; immune response; prostate cancer;
 KW hepatitis B; hepatitis C; AIDS; renal carcinoma; cervical carcinoma;
 KW lymphoma; cytomegalovirus; CMV; condyloma acuminatum;
 KW autoimmune associated disorder; multiple sclerosis; rheumatoid arthritis;
 KW Sjogren syndrome; scleroderma; polymyositis; dermatomyositis;
 KW systemic lupus erythematosus; juvenile rheumatoid arthritis;
 KW ankylosing spondylitis; myasthenia gravis; MG; bullous pemphigoid;
 KW pemphigus; glomerulonephritis; Goodpasture's syndrome;
 KW autoimmune haemolytic anaemia; Hashimoto's disease; pernicious anaemia;
 KW idiopathic thrombocytopenic purpura; Grave's disease; Addison's disease;
 KW human leukocyte antigen A2.1; HLA A2.1;
 KW immunogenic HLA-A2.1 binding peptide.
 XX
 OS Synthetic.
 XX
 PN US2003185822-A1.
 XX
 XX 02-OCT-2003.
 PD
 XX
 XX 03-APR-2002; 2002US-00116557.
 PF
 XX
 XX 05-MAR-1993; 93US-00027146.
 PR
 PR 04-JUN-1993; 93US-00073205.

PR 29-NOV-1993; 93US-00159184.
 PR 02-DEC-1994; 94US-00349177.
 XX
 PA (GREY/) GREY H M.
 PA (SETT/) SETTE A.
 PA (SIDN/) SIDNEY J.
 XX
 PI Grey HM, Sette A, Sidney J;
 XX
 XX WPI; 2004-041186/04.
 DR
 XX
 XX Immunogenic peptide composition for preventing, treating or diagnosing
 PT pathological states, e.g. prostate cancer, hepatitis B and C, Acquired
 PT Immunodeficiency Syndrome, and renal carcinoma, includes conserved
 PT residues at specified positions.
 XX
 XX Example 11; Page 27; 38pp; English.
 XX The invention describes an immunogenic peptide composition comprising 9
 CC residues including a first conserved residue at a second position from N-
 CC terminus, and a second conserved residue at C-terminal position. The
 CC inventive peptide composition is used to elicit an immune response
 CC against a desired antigen for preventing, treating or diagnosing
 CC pathological states, e.g. prostate cancer, hepatitis B, hepatitis C,
 CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, cytomegalovirus
 CC (CMV), and condyloma acuminatum. It is also used to treat autoimmune
 CC associated disorders, e.g. multiple sclerosis, rheumatoid arthritis,
 CC Sjogren syndrome, scleroderma, polymyositis, dermatomyositis, systemic
 CC lupus erythematosus, juvenile rheumatoid arthritis, ankylosing
 CC spondylitis, myasthenia gravis (MG), bullous pemphigoid, pemphigus,
 CC glomerulonephritis, Goodpasture's syndrome, autoimmune hemolytic anemia,
 CC Hashimoto's disease, pernicious anaemia, idiopathic thrombocytopenic
 CC purpura, Grave's disease, and Addison's disease. The invention defines
 CC positions within a motif enabling the selection of the peptides, which
 CC will bind efficiently to human leukocyte antigen (HLA) A2.1. This is the
 CC amino acid sequence of an immunogenic HLA-A2.1 binding peptide.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 9; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CLGLSYDGL 9
 Db |||||
 1 CLGLSYDGL 9
 RESULT 8
 ADE97666
 ID ADE97666 standard; peptide; 9 AA.
 XX
 AC ADE97666;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Immunogenic HLA-A2.1 binding peptide #148.
 XX
 KW cytostatic; anti-inflammatory; hepatotropic; virucide; anti-HIV;
 KW nephrotropic; neuroprotective; antiarthritic; antirheumatic;
 KW immunosuppressive; dermatological; muscular; nephrotropic; thyromimetic;
 KW haemostatic; antithyroid; antianaemic; anabolic; hypertensive;
 KW immunogenic peptide composition; immune response; prostate cancer;
 KW hepatitis B; hepatitis C; AIDS; renal carcinoma; cervical carcinoma;
 KW lymphoma; cytomegalovirus; CMV; condyloma acuminatum;
 KW autoimmune associated disorder; multiple sclerosis; rheumatoid arthritis;
 KW Sjogren syndrome; scleroderma; polymyositis; dermatomyositis;
 KW systemic lupus erythematosus; juvenile rheumatoid arthritis;
 KW ankylosing spondylitis; myasthenia gravis; MG; bullous pemphigoid;
 KW pemphigus; glomerulonephritis; Goodpasture's syndrome;
 KW autoimmune haemolytic anaemia; Hashimoto's disease; pernicious anaemia;
 KW idiopathic thrombocytopenic purpura; Grave's disease; Addison's disease;
 KW human leukocyte antigen A2.1; HLA A2.1;
 KW immunogenic HLA-A2.1 binding peptide.

KW immunogenic HLA-A2.1 binding peptide.

XX Synthetic.

XX US2003185822-A1.

XX 02-OCT-2003.

XX 03-APR-2002; 2002US-00116557.

XX 05-MAR-1993; 93US-00027146.

XX 04-JUN-1993; 93US-00073205.

XX 29-NOV-1993; 93US-00159184.

XX 02-DEC-1994; 94US-00349177.

XX (GREY/) GREY H M.

XX (SETT/) SETTE A.

XX (SIDN/) SIDNEY J.

XX Grey HM, Sette A, Sidney J;

XX WPI; 2004-041186/04.

XX Immunogenic peptide composition for preventing, treating or diagnosing

XX pathological states, e.g. prostate cancer, hepatitis B and C, Acquired

XX Immunodeficiency Syndrome, and renal carcinoma, includes conserved

XX residues at specified positions.

XX Example 11; Page 24; 38pp; English.

XX The invention describes an immunogenic peptide composition comprising 9

XX residues including a first conserved residue at a second position from N-

XX terminus, and a second conserved residue at C-terminal position. The

XX inventive peptide composition is used to elicit an immune response

XX against a desired antigen for preventing, treating or diagnosing

XX pathological states, e.g. prostate cancer, hepatitis B, hepatitis C,

XX AIDS, renal carcinoma, cervical carcinoma, lymphoma, cytomegalovirus

XX (CMV), and condyloma acuminatum. It is also used to treat autoimmune

XX associated disorders, e.g. multiple sclerosis, rheumatoid arthritis,

XX Sjogren syndrome, scleroderma, polymyositis, dermatomyositis, systemic

XX lupus erythematosus, juvenile rheumatoid arthritis, ankylosing

XX spondylitis, myasthenia gravis (MG), bullous pemphigoid, pemphigus,

XX glomerulonephritis, Goodpasture's syndrome, autoimmune hemolytic anemia,

XX Hashimoto's disease, pernicious anaemia, idiopathic thrombocytopenic

XX purpura, Grave's disease, and Addison's disease. The invention defines

XX positions within a motif enabling the selection of the peptides, which

XX will bind efficiently to human leukocyte antigen (HLA) A2.1. This is the

XX amino acid sequence of an immunogenic HLA-A2.1 binding peptide.

XX Sequence 9 AA;

Query Match

Best Local Similarity 100.0%; Score 9; DB 8; Length 9;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CIGLSYDGL 9

Db 1 CIGLSYDGL 9

RESULT 9

ADI47236

ID ADI47236 standard; peptide; 9 AA.

XX AC ADI47236;

XX 22-APR-2004 (first entry)

DE Anti-cancer HLA-A2 complex associated peptide seq id 3.

XX cytostatic; gene therapy; cancer; cytolytic T cell; HLA-A2.

XX Unidentified.

XX US6682731-B1.

XX 27-JAN-2004.

XX 23-MAR-2000; 2000US-00533499.

XX 24-MAR-1994; 94US-00217186.

XX 17-JUN-1994; 94US-00261160.

XX 15-AUG-1994; 94US-00290381.

XX 06-FEB-1997; 97US-00722115.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (UYOX-) UNIV OXFORD.

XX (UYLE-) RIJKSUNIV LEIDEN.

XX Townsend A, Bastin J, Boon-Falleur T, Van Der Bruggen P, Coullie P;

XX Gajewski T, Mellief CUM, Visseren MJW, Kast MW;

XX WPI; 2004-118569/12.

XX Treating a subject with a cancerous condition by administering cytolytic

XX T cells specific for the complexes to lyse the cancer cells.

XX Example 1; SEQ ID NO 3; 27pp; English.

XX The invention describes a method of treating a subject with a cancerous

XX condition comprising administering cytolytic T cells specific for the

XX complexes to lyse the cancer cells of the subject. The cancer cells

XX present complexes of HLA-A2 molecules and a peptide with a fully defined

XX sequence comprising 9 amino acids. The method is useful for treating a

XX subject with a cancerous condition. This is the amino acid sequence of a

XX HLA-A2 complex associated peptide.

XX Sequence 9 AA;

Query Match

Best Local Similarity 100.0%; Score 9; DB 8; Length 9;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CIGLSYDGL 9

Db 1 CIGLSYDGL 9

RESULT 10

ADK69455

ID ADK69455 standard; peptide; 9 AA.

XX AC ADK69455;

XX 06-MAY-2004 (first entry)

DE Epitope liberation-related peptide #818.

XX epitope liberation; substrate; proteasome; cytostatic; antibacterial;

XX protozoacide; fungicide; T-cell activator; vaccine; housekeeping epitope;

XX cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell;

XX virus; bacterium; protozoan; fungus; housekeeping proteasome system;

XX Homo sapiens.

XX US2003228634-A1.

XX 11-DEC-2003.

XX 07-NOV-2002; 2002US-00292413.

XX 07-NOV-2001; 2001US-0336968P.

XX (SIMA/) SIMARD J J L.

XX (SIMA/) SIMARD J J L.
PA (DIAM/) DIAMOND D C.
PA (QIUZ/) QIU Z.
PA (LEIX/) LEI X.
XX
PI Simard J J L, Diamond DC, Qiu Z, Lei X;
XX
XX WPI; 2004-746974/73.
XX
XX Novel isolated nucleic acid comprising reading frame having first
PT sequence that encodes segments of tumor-associated antigen NY-ESO, useful
PT in designing recombinant vaccines against tumors such as fibro sarcoma,
PT or breast cancer.
XX
XX Disclosure; SEQ ID NO 882; 259pp; English.
XX
XX The invention describes an isolated nucleic acid (I) comprising a reading
CC frame comprising a first sequence, where the first sequence encodes one
CC or more segments of tumour-associated antigen NY-ESO having a fully
CC defined sequence of 180 amino acids (S1) as given in the specification,
CC where the first sequence does not encode the complete NY-ESO antigen, and
CC where each segment comprises an epitope cluster, the cluster comprising
CC or encoding at least two amino acid sequences having a known or predicted
CC affinity for a same major histocompatibility complex (MHC) receptor
CC peptide binding cleft. Also described are: an isolated polypeptide (II)
CC comprising the amino acid sequence encoded in the reading frame of (S1);
CC and an immunogenic composition comprising (I) or (II). The following are
CC disclosed: epitope clusters identified in the tumour-associated antigen
CC NY-ESO; expression cassettes for use in vaccine vectors; vectors
CC including house-keeping epitope; and activating T-cell using the vector.
CC (I) is useful in designing recombinant vaccines against tumours such as
CC human sarcoma, fibro sarcoma, osteogenic sarcoma, breast cancer, ovarian
CC cancer, prostate cancer, chronic leukaemia, Hodgkin's disease, non-
CC Hodgkin's disease, multiple myeloma, Waldenstrom's macroglobulinaemia, or
CC against cells infected with virus, bacteria, protozoa or fungi. (I)
CC enables to manufacture a recombinant vaccine economically and rapidly, by
CC a simple process. The vaccine is highly safe as it consists of only a
CC fragment of the antigen rather than the whole protein. This is the amino
CC acid sequence of a tumour-associated antigen epitope useful in the
CC methods, therapies and composition discussed in the invention.
XX
XX Sequence 9 AA;
SQ

Query Match 100.0%; Score 9; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9
|||
DB 1 CLGLSYDGL 9

RESULT 13
AAR61627
ID AAR61627 standard; peptide; 10 AA.
XX
AC AAR61627;
XX
XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 12-MAY-1995 (first entry)
XX
XX Peptide fragment (1.0643) of MAGE binds HLA-A2.1.
XX
XX antigen; epitope; immunogenic target protein; PSA; HBVc; EBV; HIV1;
KW plasma specific antigen; hepatitis B virus; Epstein Barr;
KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MAGE-1;
KW melanoma antigen-1; core antigen; surface antigen;
KW pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic;
KW MHC class I molecule; major histocompatibility complex; HLA-A2.1; 9mer;
XX 10mer; anchor; human leukocyte antigen.
PI

OS Unidentified.
XX
PN WO9420127-A1.
XX
PD 15-SEP-1994.
XX
XX 04-MAR-1994; 94WO-US002353.
XX
XX 05-MAR-1993; 93US-00027146.
PR 04-JUN-1993; 93US-00073205.
PR 29-NOV-1993; 93US-00159184.
XX
XX (CYTE-) CYTEL CORP.
XX
XX Grey HM, Sette A, Sidney J, Kast W;
PI WPI; 1994-302678/37.
XX
XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for
PT treatment or prophylaxis of cancer, virus infection or autoimmune
PT diseases.
XX
XX Example 5; Page 111; 138pp; English.
XX
XX AAR59496-R61666 are immunogenic 10mer peptides that contain a HLA-A2.1
CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity
CC of at least 1% as compared to a reference peptide (AAR71293). AAR61627
CC occurs at position 174 in the melanoma antigen. The peptides of the
CC invention can induce cytotoxic T lymphocytes which can react with target
CC cells. They can be used for the treatment or prophylaxis of cancer, eg.
CC prostate cancer or lymphoma, etc. (Updated on 25-MAR-2003 to correct PN
CC field.) (Updated on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 10 AA;
SQ

Query Match 100.0%; Score 9; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9
|||
DB 1 CLGLSYDGL 9

RESULT 14
AAR80909
ID AAR80909 standard; peptide; 10 AA.
XX
AC AAR80909;
XX
XX 03-MAY-1996 (first entry)
DT
XX
XX MAGE-2 peptide (residues 181-190) with low HLA-A2.1 binding affinity.
XX
XX Human melanoma-associated protein; MAGE-2; tumour rejection antigen;
KW precursor; major histocompatibility complex; MHC; class 1; HLA-A2.1;
KW binding; cytolytic T cell; CTL; induction.
XX
XX Synthetic.
XX
XX WO9525530-A1.
PN
XX
XX 28-SEP-1995.
PD
XX
XX 21-MAR-1995; 95WO-US003535.
PF
XX
XX 24-MAR-1994; 94US-00217188.
PR
XX (LUDW-) LUDWIG INST CANCER RES.
PA (UYLE-) RIJCKSUNIV LEIDEN.
XX
XX Melief CJM, Visseren MW, Kast WM, Van Der Bruggen P;
PI Boon-Falleur T;

XX WPI; 1995-344456/44.

XX New peptide(s) based on tumour rejection antigen precursor MAGE-2 - which

XX bind HLA-A2 molecules to provoke cytolytic T cell prodn., used partic.

XX for treating cancers.

XX

XX Example 2; Page 29; 44pp; English.

XX

XX All peptides of length 9-11 amino acids from the MAGE-2 sequence which

XX fitted the HLA-A2.1 binding motif or the extended binding motif were

XX synthesised. The peptides were tested for binding to HLA-A2.1 molecules

XX expressed on the surface of 174CEM.T2 cells by measuring the fluorescence

XX index (FI). The FI is a measure for the amount of upregulation of HLA-

XX A2.1 molecules. The present sequence is that of a peptide that fits the

XX HLA-A2.1 motif but which had an FI value of more than 100 mcg/ml, i.e. it

XX is unable to bind to HLA-A2.1 with high affinity

XX

XX Sequence 10 AA;

SQ

Query Match 100.0%; Score 9; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9

Db |||||

1 CLGLSYDGL 9

RESULT 15

AAW36560

ID AAW36560 standard; peptide; 10 AA.

XX

XX AC AAW36560;

XX

XX 25-MAR-2003 (revised)

DT 09-MAR-1998 (first entry)

XX

XX MAGE-2 peptide (residues 181-190).

XX

XX Melanoma protein; MAGE-2; tumour rejection antigen precursor;

KW binding motif; human leukocyte antigen; HLA-A2.1; cytolytic T cell; CTL;

KW induce; production.

XX

XX Homo sapiens.

XX

XX US5686068-A.

PN

XX

XX 11-NOV-1997.

PD

XX

XX 25-JUL-1996; 96US-00687226.

PF

XX

XX 24-MAR-1994; 94US-00217188.

PR

XX

XX (LUDW-) LUDWIG INST CANCER RES.

PA (UYLE-) RIJKSUNIV LEIDEN.

PA

XX

XX Boon-Falleur T, Van Der Bruggen P, Melief CJM, Visseren MW;

PI Van Der Burg S;

PI

XX

XX WPI; 1997-558084/51.

DR

XX

XX Induction of cytolytic T cell production in vivo - by administering MAGE-

PT 2 peptide(s).

PT

XX

XX Example 2; Col 6; 24pp; English.

PS

XX

XX This peptide sequence represents part of the melanoma protein, MAGE-2, (a

CC tumour rejection antigen precursor) and fits the binding motif for human

CC leukocyte antigen (HLA) A2.1. Only peptides AAW36529-39 have the ability

CC to bind to this HLA molecule with high affinity and are therefore the

CC only candidates of the MAGE-2 protein to be recognised by human cytolytic

CC T cells (CTL), because CTL recognise peptides only when bound to HLA

CC molecules. Production of CTL in a subject can be induced by administering

CC a MAGE-2 peptide (particularly AAW36531, AAW36533 and AAW36537) to a

CC subject who presents HLA-A2 molecules on cells. The method can be used to

CC treat subjects in need of additional CTL. (Updated on 25-MAR-2003 to

CC correct PF field.)

XX

XX Sequence 10 AA;

SQ

Query Match 100.0%; Score 9; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9

Db |||||

1 CLGLSYDGL 9

Search completed: March 17, 2006, 23:45:14

Job time : 189 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:50:08 ; Search time 163 Seconds
(without alignments)
23.070 Million cell updates/sec

Title: US-09-856-812B-57

Perfect score: 9

Sequence: 1 CIGLSYDGL 9

Scoring table: QLIIGO>

Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database : Published Applications AA Main:*
- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
 - 4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	100.0	9	4	US-10-150-797-4
2	9	100.0	9	4	US-10-149-135-95
3	9	100.0	9	4	US-10-149-135-294
4	9	100.0	9	4	US-10-149-135-533
5	9	100.0	9	4	US-10-149-135-661
6	9	100.0	9	4	US-10-258-144-32
7	9	100.0	9	4	US-10-777-053-882
8	9	100.0	9	4	US-10-837-217-882
9	9	100.0	10	4	US-10-149-135-96
10	9	100.0	10	4	US-10-149-135-295
11	9	100.0	10	4	US-10-149-135-534
12	9	100.0	10	4	US-10-149-135-662
13	9	100.0	10	4	US-10-777-053-883
14	9	100.0	10	4	US-10-837-217-883
15	9	100.0	11	4	US-10-149-135-260
16	9	100.0	11	4	US-10-149-135-291
17	9	100.0	11	4	US-10-149-135-645
18	9	100.0	11	4	US-10-149-135-660
19	9	100.0	11	4	US-10-149-135-987
20	9	100.0	11	4	US-10-149-135-1003
21	9	100.0	11	4	US-10-777-053-908
22	9	100.0	11	4	US-10-837-217-908
23	9	100.0	15	4	US-10-149-135-1914
24	9	100.0	15	4	US-10-149-135-1963
25	9	100.0	15	4	US-10-149-135-1970
26	9	100.0	15	4	US-10-149-135-2019
27	9	100.0	15	4	US-10-149-135-2029

28	9	100.0	15	4	US-10-149-135-2413	Sequence 2413, Ap
29	9	100.0	15	4	US-10-149-135-2426	Sequence 2426, Ap
30	9	100.0	17	4	US-10-258-144-467	Sequence 467, App
31	9	100.0	17	4	US-10-258-144-468	Sequence 468, App
32	9	100.0	17	4	US-10-258-144-472	Sequence 472, App
33	9	100.0	18	4	US-10-258-144-477	Sequence 477, App
34	9	100.0	18	4	US-10-258-144-478	Sequence 478, App
35	9	100.0	20	4	US-10-258-144-482	Sequence 482, App
36	9	100.0	20	4	US-10-258-144-464	Sequence 464, App
37	9	100.0	20	4	US-10-258-144-465	Sequence 465, App
38	9	100.0	20	4	US-10-258-144-470	Sequence 470, App
39	9	100.0	21	4	US-10-258-144-474	Sequence 474, App
40	9	100.0	21	4	US-10-258-144-475	Sequence 475, App
41	9	100.0	21	4	US-10-258-144-480	Sequence 480, App
42	9	100.0	25	4	US-10-258-144-469	Sequence 469, App
43	9	100.0	25	4	US-10-258-144-473	Sequence 473, App
44	9	100.0	26	4	US-10-258-144-479	Sequence 479, App
45	9	100.0	26	4	US-10-258-144-483	Sequence 483, App

ALIGNMENTS

RESULT 1
US-10-150-797-4
; Sequence 4, Application US/10150797
; Publication NO. US20030148973A1
; GENERAL INFORMATION:
; APPLICANT: Emage, Peter
; APPLICANT: Karunakaran, Liza
; APPLICANT: Pedyczak, Artur
; APPLICANT: Barber, Brian H.
; TITLE OF INVENTION: MAGE-A1 Peptides for Treating or Preventing Cancer
; FILE REFERENCE: 001-022
; CURRENT APPLICATION NUMBER: US/10/150,797
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/292,590
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-150-797-4

Query Match 100.0%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CIGLSYDGL	9
Db	1	CIGLSYDGL	9

RESULT 2
US-10-149-135-95
; Sequence 95, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Cheanut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Eilissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545

; PRIOR FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: US 09/458,298
 ; PRIOR FILING DATE: 1993-12-10
 ; PRIOR APPLICATION NUMBER: US 09/189,702
 ; PRIOR FILING DATE: 1998-11-10
 ; PRIOR APPLICATION NUMBER: US 08/205,713
 ; PRIOR FILING DATE: 1994-03-04
 ; PRIOR APPLICATION NUMBER: US 08/159,184
 ; PRIOR FILING DATE: 1993-11-29
 ; PRIOR APPLICATION NUMBER: US 08/073,205
 ; PRIOR FILING DATE: 1993-06-04
 ; PRIOR APPLICATION NUMBER: US 08/027,146
 ; PRIOR FILING DATE: 1993-03-05
 ; NUMBER OF SEQ ID NOS: 2479
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 95
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial Peptide
 US-10-149-135-95

Query Match 100.0%; Score 9; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CIGLSYDGL 9
 |||||
 Db 1 CIGLSYDGL 9

RESULT 3
 US-10-149-135-294
 ; Sequence 294, Application US/10149135
 ; Publication No. US20040053822A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fikes, John
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Chesnut, Robert
 ; APPLICANT: Celis, Esteban
 ; APPLICANT: Keogh, Elissa
 ; TITLE OF INVENTION: Inducing Cellular Immune Responses to
 ; FILE REFERENCE: 2060.0130001
 ; CURRENT FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: PCT/US00/33545
 ; PRIOR FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: US 09/458,298
 ; PRIOR FILING DATE: 1999-12-10
 ; PRIOR APPLICATION NUMBER: US 09/189,702
 ; PRIOR FILING DATE: 1998-11-10
 ; PRIOR APPLICATION NUMBER: US 08/205,713
 ; PRIOR FILING DATE: 1994-03-04
 ; PRIOR APPLICATION NUMBER: US 08/159,184
 ; PRIOR FILING DATE: 1993-11-29
 ; PRIOR APPLICATION NUMBER: US 08/073,205
 ; PRIOR FILING DATE: 1993-06-04
 ; PRIOR APPLICATION NUMBER: US 08/027,146
 ; PRIOR FILING DATE: 1993-03-05
 ; NUMBER OF SEQ ID NOS: 2479
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 294
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial Peptide
 US-10-149-135-294

Query Match 100.0%; Score 9; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CIGLSYDGL 9
 |||||
 Db 1 CIGLSYDGL 9

RESULT 4
 US-10-149-135-533
 ; Sequence 533, Application US/10149135
 ; Publication No. US20040053822A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fikes, John
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Chesnut, Robert
 ; APPLICANT: Celis, Esteban
 ; APPLICANT: Keogh, Elissa
 ; TITLE OF INVENTION: Inducing Cellular Immune Responses to
 ; FILE REFERENCE: 2060.0130001
 ; CURRENT FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: PCT/US00/33545
 ; PRIOR FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: US 09/458,298
 ; PRIOR FILING DATE: 1999-12-10
 ; PRIOR APPLICATION NUMBER: US 09/189,702
 ; PRIOR FILING DATE: 1998-11-10
 ; PRIOR APPLICATION NUMBER: US 08/205,713
 ; PRIOR FILING DATE: 1994-03-04
 ; PRIOR APPLICATION NUMBER: US 08/159,184
 ; PRIOR FILING DATE: 1993-11-29
 ; PRIOR APPLICATION NUMBER: US 08/073,205
 ; PRIOR FILING DATE: 1993-06-04
 ; PRIOR APPLICATION NUMBER: US 08/027,146
 ; PRIOR FILING DATE: 1993-03-05
 ; NUMBER OF SEQ ID NOS: 2479
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 533
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial Peptide
 US-10-149-135-533

Query Match 100.0%; Score 9; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CIGLSYDGL 9
 |||||
 Db 1 CIGLSYDGL 9

RESULT 5
 US-10-149-135-661
 ; Sequence 661, Application US/10149135
 ; Publication No. US20040053822A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fikes, John
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Chesnut, Robert
 ; APPLICANT: Celis, Esteban
 ; APPLICANT: Keogh, Elissa
 ; TITLE OF INVENTION: Inducing Cellular Immune Responses to
 ; FILE REFERENCE: 2060.0130001
 ; CURRENT FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: PCT/US00/33545
 ; PRIOR FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: US 09/458,298
 ; PRIOR FILING DATE: 1999-12-10
 ; PRIOR APPLICATION NUMBER: US 09/189,702
 ; PRIOR FILING DATE: 1998-11-10
 ; PRIOR APPLICATION NUMBER: US 08/205,713
 ; PRIOR FILING DATE: 1994-03-04
 ; PRIOR APPLICATION NUMBER: US 08/159,184
 ; PRIOR FILING DATE: 1993-11-29
 ; PRIOR APPLICATION NUMBER: US 08/073,205
 ; PRIOR FILING DATE: 1993-06-04
 ; PRIOR APPLICATION NUMBER: US 08/027,146
 ; PRIOR FILING DATE: 1993-03-05
 ; NUMBER OF SEQ ID NOS: 2479
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 661
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial Peptide
 US-10-149-135-661

FILE REFERENCE: 2060.0130001
CURRENT APPLICATION NUMBER: US/10/149,135
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: PCT/US00/33545
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,298
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: Patent in version 3.1
SEQ ID NO 661
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-149-135-661

Query Match 100.0%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9
Db 1 CLGLSYDGL 9

RESULT 6
US-10-258-144-32
Sequence 32, Application US/10258144
Publication No. US20040101532A1
GENERAL INFORMATION:
APPLICANT: Houghton, Alan
APPLICANT: Livingston, Phil
APPLICANT: Al-Awqati, Qais
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HEAT SHOCK
FILE REFERENCE: 11746/46401
CURRENT APPLICATION NUMBER: US/10/258,144
PRIOR FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: 60/197,642
PRIOR FILING DATE: 2000-04-17
NUMBER OF SEQ ID NOS: 502
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-258-144-32

Query Match 100.0%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9
Db 1 CLGLSYDGL 9

RESULT 7
US-10-777-053-882
Sequence 882, Application US/10777053

Publication No. US20040132088A1
GENERAL INFORMATION:
APPLICANT: Simard, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Qiu, Zhiyong
APPLICANT: Lei, Xiang-Dong
TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
FILE REFERENCE: MANNK.022C1
CURRENT APPLICATION NUMBER: US/10/777,053
CURRENT FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: 10/292,413
PRIOR FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: 60/336,968
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 979
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 882
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapien
US-10-777-053-882

Query Match 100.0%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9
Db 1 CLGLSYDGL 9

RESULT 8
US-10-837-217-882
Sequence 882, Application US/10837217
Publication No. US20040203051A1
GENERAL INFORMATION:
APPLICANT: Simard, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Qiu, Zhiyong
APPLICANT: Lei, Xiang-Dong
TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
FILE REFERENCE: MANNK.022C2
CURRENT APPLICATION NUMBER: US/10/837,217
CURRENT FILING DATE: 2004-04-30
PRIOR APPLICATION NUMBER: 10/292,413
PRIOR FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: 60/336,968
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 979
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 882
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapien
US-10-837-217-882

Query Match 100.0%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9
Db 1 CLGLSYDGL 9

RESULT 9
US-10-149-135-96
Sequence 96, Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
APPLICANT: Fikes, John

```
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 96
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-96

Query Match          100.0%; Score 9; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CIGLSYDGL 9
Db      1  CIGLSYDGL 9

RESULT 10
US-10-149-135-295
; Sequence 295, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 96
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-295

Query Match          100.0%; Score 9; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CIGLSYDGL 9
Db      1  CIGLSYDGL 9

RESULT 10
US-10-149-135-295
; Sequence 295, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
```

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; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 295
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-295

Query Match          100.0%; Score 9; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CIGLSYDGL 9
Db      1  CIGLSYDGL 9

RESULT 11
US-10-149-135-534
; Sequence 534, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 534
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-534

Query Match          100.0%; Score 9; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CIGLSYDGL 9
Db      1  CIGLSYDGL 9

RESULT 12
US-10-149-135-662
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; Sequence 662, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cellis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 662
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
; US-10-149-135-662

Query Match      100.0%; Score 9; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CIGLSYDGL 9
Db      1  CIGLSYDGL 9

RESULT 13
US-10-777-053-883
; Sequence 883, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; MAGE2/3 USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: MANNK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 883
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-777-053-883
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Query Match      100.0%; Score 9; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CIGLSYDGL 9
Db      1  CIGLSYDGL 9

RESULT 14
US-10-837-217-883
; Sequence 883, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; MAGE2/3 USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: MANNK.022C2
; CURRENT APPLICATION NUMBER: US/10/837,217
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 883
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-837-217-883

Query Match      100.0%; Score 9; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CIGLSYDGL 9
Db      1  CIGLSYDGL 9

RESULT 15
US-10-149-135-260
; Sequence 260, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cellis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
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; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 260
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-260
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Query Match      100.0%; Score 9; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CLGLSYDGL 9
   |||||
Db 3 CLGLSYDGL 11
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Search completed: March 17, 2006, 23:53:33
Job time : 163 secs
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:50:59 ; Search time 22 Seconds
(without alignments)
11.709 Million cell updates/sec

Title: US-09-856-812B-57

Perfect score: 9

Sequence: 1 CIGLSYDGL 9

Scoring table: {OLIGO}

Gapop 60.0 , Gapext 60.0

Searched: 169630 seqs, 28622889 residues

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Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA_New.*

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- 2: /cgn2_6/protdata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/protdata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/protdata/1/pubpaa/PCT_NEW_PUB.pep.*
- 5: /cgn2_6/protdata/1/pubpaa/US05_NEW_PUB.pep.*
- 6: /cgn2_6/protdata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/protdata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/protdata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	100.0	309	7 US-11-155-288-5	Sequence 5, Appli
2	9	100.0	314	6 US-10-510-101-69	Sequence 69, Appl
3	9	100.0	314	7 US-11-155-288-6	Sequence 6, Appli
4	8	88.9	260	7 US-11-245-400-43	Sequence 43, Appl
5	6	66.7	159	7 US-11-096-568A-29761	Sequence 29761, A
6	6	66.7	343	7 US-11-096-568A-6853	Sequence 6853, Ap
7	6	66.7	440	6 US-10-467-657-7664	Sequence 7664, Ap
8	6	66.7	470	6 US-10-467-657-8420	Sequence 8420, Ap
9	6	66.7	482	6 US-10-467-657-7660	Sequence 7660, Ap
10	6	66.7	809	6 US-10-858-730-210	Sequence 210, App
11	5	55.6	8	6 US-10-510-101-145	Sequence 145, App
12	5	55.6	59	6 US-10-667-295-170	Sequence 170, App
13	5	55.6	121	6 US-10-821-234-1160	Sequence 1160, Ap
14	5	55.6	163	6 US-10-965-694-21	Sequence 21, Appl
15	5	55.6	177	7 US-11-072-512-3347	Sequence 3347, Ap
16	5	55.6	184	6 US-10-742-634-9	Sequence 9, Appli
17	5	55.6	184	6 US-10-967-527A-8	Sequence 8, Appli
18	5	55.6	184	7 US-11-242-294-27	Sequence 27, Appl
19	5	55.6	185	6 US-10-967-527A-10	Sequence 10, Appl
20	5	55.6	216	7 US-11-096-568A-6860	Sequence 6860, Ap
21	5	55.6	228	7 US-11-096-568A-6859	Sequence 6859, Ap
22	5	55.6	231	7 US-11-096-568A-25374	Sequence 25374, A
23	5	55.6	235	6 US-10-873-528-58	Sequence 58, Appl
24	5	55.6	235	6 US-10-873-528-59	Sequence 59, Appl
25	5	55.6	254	7 US-11-054-515-881	Sequence 881, App

ALIGNMENTS

RESULT 1

US-11-155-288-5
; Sequence 5, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.050A
; CURRENT APPLICATION NUMBER: US/11/155,288
; PRIOR FILING DATE: 2003-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-5

Query Match 100.0%; Score 9; DB 7; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CIGLSYDGL 9

Db 174 CIGLSYDGL 182

RESULT 2

US-10-510-101-69
; Sequence 69, Application US/10510101
; Publication No. US20060018915A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Ishioka, Glenn
; APPLICANT: Pikes, John
; APPLICANT: Tangri, Shabnam
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
; FILE REFERENCE: 2060.009PC05
; CURRENT APPLICATION NUMBER: US/10/510,101
; PRIOR FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: US 60/413,471
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 10/116,118

; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-510-101-69

Query Match 100.0%; Score 9; DB 6; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9
||| |||||
Db 181 CLGLSYDGL 189

RESULT 3
US-11-155-288-6
; Sequence 6, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.050A
; CURRENT APPLICATION NUMBER: US/11/155,288
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-6

Query Match 100.0%; Score 9; DB 7; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9
||| |||||
Db 181 CLGLSYDGL 189

RESULT 4
US-11-245-400-43
; Sequence 43, Application US/11245400
; Publication No. US20060040357A1
; GENERAL INFORMATION:
; APPLICANT: Bandaru, Rajasekhkar
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Encoding Melanoma
; TITLE OF INVENTION: Associated Antigen Molecules, Aminotransferase
; TITLE OF INVENTION: Associated Molecules, ATPase Molecules, Acyltransferase Molecules,
; TITLE OF INVENTION: Pyridoxal-Phosphate Dependant Enzyme Molecules and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/247400
; CURRENT APPLICATION NUMBER: US/11/245,400
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US/10/164,966
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 10/034,864
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/258,517
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 09/996,194

; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/250,348
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/250,073
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/253,878
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,338
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/908,928
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/220,465
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MAGE family PFAM consensus domain
US-11-245-400-43

Query Match 88.9%; Score 8; DB 7; Length 260;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGLSYDGL 9
||| |||||
Db 211 LGLSYDGL 218

RESULT 5
US-11-096-568A-29761
; Sequence 29761, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 29761
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(159)
; OTHER INFORMATION: Ceres Seq. ID no. 4929187
US-11-096-568A-29761

Query Match 66.7%; Score 6; DB 7; Length 159;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSYDGL 9
||| |||||
Db 148 LSYDGL 153

RESULT 6
US-11-096-568A-6853
; Sequence 6853, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2

; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6853
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(343)
; OTHER INFORMATION: Ceres Seq. ID no. 15168501
US-11-096-568A-6853

Query Match 66.7%; Score 6; DB 7; Length 343;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSYDGL 9
|||||
DB 332 LSYDGL 337

RESULT 7
US-10-467-657-7664
; Sequence 7664, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7664
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7664

Query Match 66.7%; Score 6; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGLSYD 7
|||||
DB 166 LGLSYD 171

RESULT 8
US-10-467-657-8420
; Sequence 8420, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

; SEQ ID NO 8420
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8420

Query Match 66.7%; Score 6; DB 6; Length 470;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGLSYD 7
|||||
DB 196 LGLSYD 201

RESULT 9
US-10-467-657-7660
; Sequence 7660, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7660
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7660

Query Match 66.7%; Score 6; DB 6; Length 482;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGLSYD 7
|||||
DB 208 LGLSYD 213

RESULT 10
US-10-858-730-210
; Sequence 210, Application US/10858730
; Publication No. US2005025568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-858-730-210

Query Match 66.7%; Score 6; DB 6; Length 809;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSYDGL 9
|||||
Db 504 LSYDGL 509

RESULT 11
US-10-510-101-145
; Sequence 145, Application US/10510101
; Publication No. US20060018915A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Ishioka, Glenn
; APPLICANT: Fikes, John
; APPLICANT: Tangri, Shabnam
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Heterocyclic Analogs and Related Methods
; FILE REFERENCE: 2060.009PC05
; CURRENT APPLICATION NUMBER: US/10/510,101
; CURRENT FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: US 60/413,471
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 10/116,118
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 145
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide derived from Homo sapiens melanoma antigens
US-10-510-101-145

Query Match 55.6%; Score 5; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGLSY 6
|||||
Db 4 LGLSY 8

RESULT 12
US-10-667-295-170
; Sequence 170, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 170
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: VARIANT

; LOCATION: (1)...(59)
; OTHER INFORMATION: Ceres Seq. ID no. 12443606
US-10-667-295-170

Query Match 55.6%; Score 5; DB 6; Length 59;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CIGLS 5
|||||
Db 39 CIGLS 43

RESULT 13
US-10-821-234-1160
; Sequence 1160, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1160
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1160

Query Match 55.6%; Score 5; DB 6; Length 121;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CIGLS 5
|||||
Db 32 CIGLS 36

RESULT 14
US-10-965-694-21
; Sequence 21, Application US/10965694
; Publication No. US20050271644A1
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Johannes
; APPLICANT: Muller-Reible, Clemens
; APPLICANT: Fregin, Andreas
; APPLICANT: Rost, Simone
; APPLICANT: Strom, Tim
; TITLE OF INVENTION: VITAMIN K EPOXID RECYCLING POLYPEPTIDE VKORC1, A THERAPEUTIC TARGET
; TITLE OF INVENTION: OF COUMARIN AND THEIR DERIVATIVES
; FILE REFERENCE: MBP-025XX
; CURRENT APPLICATION NUMBER: US/10/965,694
; CURRENT FILING DATE: 2004-10-14
; PRIOR APPLICATION NUMBER: US 60/511,041
; PRIOR FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Fugu rubripes
US-10-965-694-21

Query Match 55.6%; Score 5; DB 6; Length 163;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLGSL 5
|
|
|
|
Db 92 CLGSL 96

RESULT 15

US-11-072-512-3347
; Sequence 3347, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cdna
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3347
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3347

Query Match 55.6%; Score 5; DB 7; Length 177;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLGSL 5
|
|
|
|
Db 54 CLGSL 58

Search completed: March 17, 2006, 23:54:03
Job time : 23 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:45:33 ; Search time 38 Seconds
(without alignments)
22.788 Million cell updates/sec

Title: US-09-856-812B-57

Perfect score: 9

Sequence: 1 CLGLSYDGL 9

Scoring table: ~~FASTA~~
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	9	100.0	234	2 I38667	melanoma antigen M
2	9	100.0	280	2 JC2358	melanoma antigen M
3	9	100.0	314	2 JC2360	melanoma antigen M
4	9	100.0	314	2 I68889	melanoma antigen M
5	9	100.0	314	2 JC2361	melanoma antigen M
6	9	100.0	317	2 I38661	melanoma antigen M
7	7	77.8	823	2 T08092	plus fringe glycop
8	6	66.7	111	2 B70401	hypothetical prote
9	6	66.7	129	2 H86673	single-strand bind
10	6	66.7	168	2 D91227	hypothetical prote
11	6	66.7	168	2 C86074	hypothetical prote
12	6	66.7	169	2 S40811	hypothetical 19.1k
13	6	66.7	171	2 AE0950	conserved hypothet
14	6	66.7	288	2 S44630	f22b7.9 protein -
15	6	66.7	314	2 I54519	melanoma antigen M
16	6	66.7	468	2 S21172	glutamate-tRNA lig
17	6	66.7	482	2 E81248	6-phosphogluconate
18	6	66.7	482	2 B82021	phosphogluconate d
19	6	66.7	506	2 S58150	hypothetical prote
20	6	66.7	516	2 T05940	cytochrome P450 83
21	6	66.7	528	2 S26948	cytochrome-c oxida
22	6	66.7	567	1 ODAS1	cytochrome-c oxida
23	6	66.7	577	2 D91239	membrane protein l
24	6	66.7	577	2 A86087	hypothetical prote
25	6	66.7	577	2 F65202	hypothetical 66.6
26	6	66.7	579	2 JC7629	membrane-type friz
27	6	66.7	614	2 B96656	unknown protein, 4
28	6	66.7	705	2 T30521	surface protein -
29	6	66.7	779	2 S64680	exoribonuclease 10

30	6	66.7	807	2 E90523	leucyl-trna synthe
31	6	66.7	810	1 DECK2	metL bifunctional
32	6	66.7	810	2 AB6085	aspartokinase II /
33	6	66.7	810	2 E91237	aspartokinase II /
34	6	66.7	811	2 AB0015	aspartate kinase (
35	6	66.7	879	2 S23006	shed acute-phase a
36	6	66.7	968	2 T29532	hypothetical prote
37	6	66.7	1052	2 AF2959	conserved hypothet
38	6	66.7	1162	2 JH0557	exo-alpha-sialidas
39	6	66.7	1341	2 H98323	hypothetical prote
40	6	66.7	1432	2 S58819	antiviral protein
41	6	66.7	1434	2 C82923	DNA-directed RNA p
42	5	55.6	109	2 AI2029	hypothetical prote
43	5	55.6	111	2 E83462	hypothetical prote
44	5	55.6	122	2 S78167	NADH2 dehydrogenas
45	5	55.6	136	2 H75197	yhcV homolog PAB22

ALIGNMENTS

RESULT 1

I38667

melanoma antigen MAGE-8 - human

C:Species: Homo sapiens (man)

C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004

C:Accession: I38667

R:De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; B

oon, T.

Immunogenetics 40, 360-369, 1994

A:Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fa

A:Reference number: I38659; MUID:95012457; PMID:7927540

A:Accession: I38667

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-234 <RES>

A:Cross-references: UNIPROT:P43361; UNIPARC:UPI00000335D6; EMBL:U10693; MID:g533525; PI

C:Genetics:

A:Gene: GDB:MAGEA8; MAGE8

A:Cross-references: GDB:331123

A:Map position: Xq28-Xq28

A:Introns: #status absent

C:Superfamily: tumor associated protein MAGE

Query Match 100.0%; Score 9; DB 2; Length 234;

Best Local Similarity 100.0%; Pred. No. 0.012;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9

Db 184 CLGLSYDGL 192

RESULT 2

JC2358

melanoma antigen MAGE-1 - human

C:Species: Homo sapiens (man)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 18-Feb-2000

C:Accession: JC2358

R:Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.

Biochem. Biophys. Res. Commun. 202, 549-555, 1994

A:Title: Cloning and analysis of MAGE-1-related genes.

A:Reference number: JC2358; MUID:94311935; PMID:8037761

A:Accession: JC2358

A:Molecule type: mRNA

A:Residues: 1-280 <DIN>

A:Cross-references: UNIPARC:UPI0000178982

A:Experimental source: melanoma cell line DM150

C:Genetics:

A:Gene: MAGE

C:Superfamily: tumor associated protein MAGE

F161-169/Region: HLA-A1 binding #status predicted

Query Match 100.0%; Score 9; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 0.014; 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

QY 1 CIGLSYDGL 9
DB 174 CIGLSYDGL 182
|||||

RESULT 3
JC2360
melanoma antigen MAGE-6 - human
N:Alternate names: tumor-associated antigen, MAGE-3b
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: JC2360; PH1301; I38665; G01445
R: Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
Biochem. Biophys. Res. Commun. 202, 549-555, 1994
A:Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic
A:Reference number: JC2358; MUID:94311935; PMID:8037761
A:Accession: JC2360
A:Molecule type: mRNA
A:Residues: 1-314 <DIN>
A:Cross-references: UNIPROT:P43360; UNIPARC:UPI000000D9B0
A:Experimental source: melanoma cell line DM150
R: Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,
J. Exp. Med. 176, 1453-1457, 1992
A:Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic
A:Reference number: PH1294; MUID:93018875; PMID:1402688
A:Accession: PH1301
A:Molecule type: DNA
A:Residues: 168-176 <TRA>
A:Cross-references: UNIPARC:UPI0000042625
R: De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Boon, T.
Immunogenetics 40, 360-369, 1994
A:Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fam
A:Reference number: I38659; MUID:95012457; PMID:7927540
A:Accession: I38665
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-314 <RES>
A:Cross-references: UNIPARC:UPI00000D9B0; EMBL:U10691; NID:G533522; PIDN:AAA68875.1; PI
R: Fenton, R.G.
submitted to the EMBL Data Library, June 1994
A:Reference number: G07126
A:Accession: G01445
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-314 <FEN>
A:Cross-references: UNIPARC:UPI00000D9B0; EMBL:U10339; NID:G499121; PIDN:AAA19006.1; PI
C:Genetics:
A:Gene: GDB:MAGEA6; MAGE6
A:Cross-references: GDB:I31121
A:Map position: Xq28-Xq28
A:Introns: #status absent
C:Superfamily: tumor associated protein MAGE
F:168-176/Region: HLA-A1 binding #status predicted

Query Match 100.0%; Score 9; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CIGLSYDGL 9
DB 181 CIGLSYDGL 189
|||||

RESULT 4
I6889
melanoma antigen MAGE-2 - human
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004

C:Accession: I6889; PH1294
R:De Smet, C.; Lurquin, C.; van der Bruggen, P.; De Plaen, E.; Brasseur, F.; Boon, T.
Immunogenetics 39, 121-129, 1994
A:Title: Sequence and expression pattern of the human MAGE2 gene.
A:Reference number: I54519; MUID:94102805; PMID:8276455
A:Accession: I6889
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-314 <RES>
A:Cross-references: UNIPROT:P43356; UNIPARC:UPI000012EB28; GB:U18920; NID:G436180; PIDN:
R:Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,
J. Exp. Med. 176, 1453-1457, 1992
A:Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic
A:Reference number: PH1294; MUID:93018875; PMID:1402688
A:Accession: PH1294
A:Molecule type: DNA
A:Residues: 168-176 <TRA>
A:Cross-references: UNIPARC:UPI000004262C
C:Genetics:
A:Gene: GDB:MAGEA2; MAGE2
A:Cross-references: GDB:273684
A:Map position: Xq28-Xq28
C:Superfamily: tumor associated protein MAGE

Query Match 100.0%; Score 9; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CIGLSYDGL 9
DB 181 CIGLSYDGL 189
|||||

RESULT 5
JC2361
melanoma antigen MAGE-3 - human
N:Alternate names: MAGE 3 protein
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: JC2361; PH1296; I38438
R: Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
Biochem. Biophys. Res. Commun. 202, 549-555, 1994
A:Title: Cloning and analysis of MAGE-1-related genes.
A:Reference number: JC2358; MUID:94311935; PMID:8037761
A:Accession: JC2361
A:Molecule type: mRNA
A:Residues: 1-314 <DIN>
A:Cross-references: UNIPROT:P43357; UNIPARC:UPI0000062194
A:Experimental source: melanoma cell line DM150
R: Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,
J. Exp. Med. 176, 1453-1457, 1992
A:Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic
A:Reference number: PH1294; MUID:93018875; PMID:1402688
A:Accession: PH1296
A:Molecule type: DNA
A:Residues: 168-176 <TRA>
A:Cross-references: UNIPARC:UPI000002F152
R: Gaugler, B.; Van den Eynde, B.; van der Bruggen, P.; Romero, P.; Gaforio, J.J.; De Pla
J. Exp. Med. 179, 921-930, 1994
A:Title: Human gene MAGE-3 codes for an antigen recognized on a melanoma by autologous
A:Reference number: I38438; MUID:94157413; PMID:8113684
A:Accession: I38438
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-314 <RES>
A:Cross-references: UNIPARC:UPI0000062194; EMBL:U03735; NID:G468825; PIDN:AAA17446.1; PI
C:Genetics:
A:Gene: MAGE-3
C:Superfamily: tumor associated protein MAGE
F:168-176/Region: HLA-A1 binding #status predicted

Query Match 100.0%; Score 9; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.016;

A:Molecule type: DNA
A:Residues: 1-129 <STO>
A:Cross-references: UNIPROT:Q9CIG8; UNIPARC:UPI00000C681C; GB:AE005176; PID:gl2723265; F
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: ssbA
C:Superfamily: single-strand binding protein

Query Match 66.7%; Score 6; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGLSYD 7
|||||
DB 95 LGLSYD 100

RESULT 10
D91227
hypothetical protein ECs4788 [imported] - Escherichia coli (strain O157:H7, substrain R1
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: D91227
R:Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Iehii, K.; Yokoyama, K.; Han, C.G.
sasawara, N.; Yaeunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: D91227
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-168 <HAY>
A:Cross-references: UNIPROT:Q9X8G9; UNIPARC:UPI00000D0933; GB:BA000007; PIDN:BA038211.1;
A:Experimental source: strain O157:H7, substrain R1MD 050952
C:Genetics:
A:Gene: ECs4788

Query Match 66.7%; Score 6; DB 2; Length 168;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGLSYD 7
|||||
DB 142 LGLSYD 147

RESULT 11
C86074
hypothetical protein yihI [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: C86074
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: C86074
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-168 <STO>
A:Cross-references: UNIPROT:Q9X8G9; UNIPARC:UPI00000D0933; GB:AE005174; NID:gl2518745; F
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yihI

Query Match 66.7%; Score 6; DB 2; Length 168;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGLSYD 7
|||||
DB 142 LGLSYD 147

RESULT 12

S40811
hypothetical 19.1k protein (pola-hemN intergenic region) - Escherichia coli (strain K-12
N)Alternate names: hypothetical protein o169
C:Species: Escherichia coli
C:Date: 19-May-1994 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S40811; E65191
R:Plunkett III, G.; Burland, V.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 21, 3391-3398, 1993
A:Title: Analysis of the Escherichia coli genome. III. DNA sequence of the region from
A:Reference number: S40802; MUID:93347969; PMID:8346018
A:Accession: S40811
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-169 <PLU>
A:Cross-references: UNIPROT:P32130; UNIPARC:UPI000013B3F7; EMBL:L19201; NID:g304961; PFI
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1993
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: E65191
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-169 <BLAT>
A:Cross-references: UNIPARC:UPI000013B3F7; GB:AE0000462; GB:U000096; NID:gl790295; PIDN:A
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: yihI

Query Match 66.7%; Score 6; DB 2; Length 169;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGLSYD 7
|||||
DB 143 LGLSYD 148

RESULT 13

AE0950
conserved hypothetical protein STY3878 [imported] - Salmonella enterica subsp. enterica
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AE0950
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AE0950
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-171 <PAR>
A:Cross-references: UNIPARC:UPI000005A660; GB:AL513382; PIDN:CAD03097.1; PID:gl6504734;
C:Genetics:
A:Gene: STY3878

Query Match 66.7%; Score 6; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGLSYD 7
|||||
DB 143 LGLSYD 148

```
RESULT 14
S44630
I22b7.9 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Sep-1997
C:Accession: S44630
R.Anderson, K.
submitted to the EMBL Data Library, March 1993
A:Description: Sequence of the C. elegans cosmid F22B7.
A:Reference number: S44628
A:Accession: S44630
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-288 <AND>
A:Cross-References: UNIPARC:UPI000017B6BE; EMBL:L12018; NID:G156298; PID:G156301
A:Genetics:
A:Introns: 54/1; 189/2

Query Match 66.7%; Score 6; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GLSYDG 8
Db 182 GLSYDG 187

RESULT 15
I54519
melanoma antigen MAGE-12 - human
N:Alternate names: MAGE 21 protein
C:Species: Homo sapiens (man)
C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C:Accession: I54519; J02362; PH1295
R:De Smet, C.; Lurquin, C.; van der Bruggen, P.; De Plaen, E.; Brasseur, F.; Boon, T.
Immunogenetics 39; 121-129, 1994
A:Title: Sequence and expression pattern of the human MAGE2 gene.
A:Reference number: I54519; MUID:94102805; PMID:8276455
A:Accession: I54519
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-314 <DES>
A:Cross-References: UNIPROT:P43365; UNIPARC:UPI0000039F48; GB:L18877; NID:G499345; PIDN:
R: Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
Biochem. Biophys. Res. Commun. 202, 549-555, 1994
A:Title: Cloning and analysis of MAGE-1-related genes.
A:Reference number: J02358; MUID:94311935; PMID:8037761
A:Accession: J02362
A:Molecule type: mRNA
A:Residues: 1-9,'S',11-186,'D',188-299,'S',301-314 <DIN>
A:Cross-References: UNIPARC:UPI0000178981
A:Experimental source: melanoma cell line DM150; MAGE-12f
R: Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,
J. Exp. Med. 176, 1453-1457, 1992
A:Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic
A:Reference number: PH1294; MUID:93018875; PMID:1402688
A:Accession: PH1295
A:Molecule type: DNA
A:Residues: 168-176 <TRA>
A:Cross-References: UNIPARC:UPI0000039F49
A:Experimental source: MAGE-21
C:Genetics:
A:Gene: GDB:MAGEA12; MAGE12; MAGE-12f
A:Cross-References: GDB:331129
A:Map position: Xq28-Xq28
C:Superfamily: tumor associated protein MAGE
F:168-176/Region: HLA-A1 binding #status predicted

Query Match 66.7%; Score 6; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSY 6
```

Db 181 CLGLSY 186

Search completed: March 17, 2006, 23:49:57
Job time : 43 secs

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GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:42:18 ; Search time 231 Seconds
(without alignments)
27.488 Million cell updates/sec

Title: US-09-856-812B-57

Perfect score: 9

Sequence: 1 CIGLSYDGL 9

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	9	100.0	234	1	MAG88_HUMAN	P43361 homo sapien
2	9	100.0	309	1	MAG81_HUMAN	P43355 homo sapien
3	9	100.0	314	1	MAG82_HUMAN	P43356 homo sapien
4	9	100.0	314	1	MAG83_HUMAN	P43357 homo sapien
5	9	100.0	314	1	MAG86_HUMAN	P43360 homo sapien
6	9	100.0	314	1	MAG8C_HUMAN	P43365 homo sapien
7	9	100.0	314	2	Q6FGT7_HUMAN	Q6fgt7 homo sapien
8	9	100.0	314	2	Q6FHH5_HUMAN	Q6fhh5 homo sapien
9	9	100.0	314	2	Q6FHH8_HUMAN	Q6fhh8 homo sapien
10	9	100.0	314	2	Q53EX0_HUMAN	Q53ex0 homo sapien
11	9	100.0	314	2	Q9SE03_HUMAN	Q9se03 homo sapien
12	9	100.0	314	2	Q6P448_HUMAN	Q6p448 homo sapien
13	9	100.0	314	2	Q6FHH6_HUMAN	Q6fhh6 homo sapien
14	9	100.0	314	2	Q6NW44_HUMAN	Q6nw44 homo sapien
15	9	100.0	314	2	Q4R400_MACFA	Q4r400 macaca fasc
16	9	100.0	316	2	Q8WWH6_HUMAN	Q8wwh6 homo sapien
17	9	100.0	317	1	MAG84_HUMAN	P43358 homo sapien
18	9	100.0	317	2	Q14798_HUMAN	Q14798 homo sapien
19	9	100.0	318	2	Q9BUN9_HUMAN	Q9bun9 homo sapien
20	7	77.8	823	2	Q39594_CHLRE	Q39594 chlamydomon
21	6	66.7	93	2	Q5QZQ8_IDILO	Q5qzq8 idiomarina
22	6	66.7	111	1	Y1176_AQUAE	Q67237 aquifex aeo
23	6	66.7	129	2	Q8XR33_LACIC	Q8xr33 lactococcus
24	6	66.7	129	2	Q9CIG8_LACIA	Q9cig8 lactococcus
25	6	66.7	167	2	Q5PKC4_SALPA	Q5pkc4 salmonella
26	6	66.7	168	1	YIHI_ECO57	Q8x8g9 escherichia
27	6	66.7	169	1	YIHI_ECOL6	Q8fbg9 escherichia
28	6	66.7	169	1	YIHI_ECOLI	P08ah6 escherichia
29	6	66.7	169	1	YIHI_SHIFL	P08ah7 shigella fl
30	6	66.7	171	1	YIHI_SALTI	P0a2n9 salmonella
31	6	66.7	171	1	YIHI_SALTY	P0a2n8 salmonella

32	6	66.7	171	2	Q57HL1_SALCH	Q57hl1 salmonella
33	6	66.7	174	2	Q88P96_PSEPK	Q88p96 pseudomonas
34	6	66.7	186	2	Q8F5C7_LEPPI	Q8f5c7 leptospira
35	6	66.7	189	2	Q7ME49_VIBVY	Q7me49 vibrio vuln
36	6	66.7	218	2	Q9SK56_MACFA	Q9sk56 macaca fasc
37	6	66.7	224	1	EPDR1_HUMAN	Q9um22 homo sapien
38	6	66.7	224	1	EPDR1_MACFA	Q9umc7 macaca fasc
39	6	66.7	224	2	Q99M77_MOUSE	Q99m77 mus musculus
40	6	66.7	227	2	Q9SK54_MACFA	Q9sk54 macaca fasc
41	6	66.7	227	2	Q9SK77_MACFA	Q9sk77 macaca fasc
42	6	66.7	227	2	Q84X11_MANES	Q84x11 manihot esc
43	6	66.7	243	1	YLW9_CAEEL	P34412 caenorhabdi
44	6	66.7	244	2	Q6OMZ8_CAEER	Q6omz8 caenorhabdi
45	6	66.7	262	2	Q4Y6T5_PLACH	Q4y6t5 plasmodium

ALIGNMENTS

RESULT 1
MAG88_HUMAN STANDARD; PRT; 234 AA.
AC P43361:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Melanoma-associated antigen 8 (MAGE-8 antigen).
GN Name=MAGE8; Synonym=MAGE8;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95012457; PubMed=7927540;
RA de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,
RA de Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C.,
RA Brasseur R., Chomez P., de Backer O., Cavenee W., Boon T.;
RT "Structure, chromosomal localization, and expression of 12 genes of
the MAGE family.";
RL Immunogenetics 40:360-369(1994).
CC -!- FUNCTION: Not known, though may play a role in embryonal
development and tumor transformation or aspects of tumor
progression.
CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
such as melanoma, head and neck squamous cell carcinoma, lung
carcinoma and breast carcinoma, but not in normal tissues except
for testes and placenta.
CC -!- SIMILARITY: Contains 1 MAGE domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
CC EMBL: U10693; AAA68876.1; -, Genomic_DNA.
DR PIR: I38667; I38667.
DR Ensembl: ENSG00000156009; Homo sapiens.
DR HGNC: HGNC:6806; MAGE8.
DR MIM: 300341; -.
DR InterPro: IPR002190; MAGE.
DR PANTHER: PTHR11736; MAGE; 1.
DR Pfam: PF01454; MAGE; 1.
DR PROSITE: PS50838; MAGE; 1.
DR Antigen: Multigene family; Tumor antigen.
FT DOMAIN 112 234 MAGE.
SQ COMPBIAS 40 43 Poly-Ser.
SQ SEQUENCE 234 AA; 25197 MW; 058A92EE6003A982 CRC64;
Query Match 100.0%; Score 9; DB 1; Length 234;
Best Local Similarity 100.0%; Score No. 0.12;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CIGLSYDGL 9
 DB 184 CIGLSYDGL 192

RESULT 2
 MAGAL_HUMAN STANDARD; PRT; 309 AA.
 AC P43355; O00346;
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Melanoma-associated antigen 1 (MAGE-1 antigen) (Antigen M22-E).
 GN Name=MAGE1; Synonyms=MAGE1, MAGE1A;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92086861; PubMed=1840703;
 RA van der Bruggen P., Traversari C., Chomez P., Lurquin C., de Plaen E.,
 RA van den Eynde B., Knuth A., Boon T.;
 RT "A gene encoding an antigen recognized by cytolytic T lymphocytes on a
 human melanoma.";
 RL Science 254:1643-1647(1991).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Skin;
 RX MEDLINE=94311935; PubMed=8037761;
 RA Ding M., Beck R.J., Keller C.J., Fenton R.G.;
 RT "Cloning and analysis of MAGE-1-related genes.";
 RL Biochem. Biophys. Res. Commun. 202:549-555(1994).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20314869; PubMed=10854409; DOI=10.1101/gr.10.6.758;
 RA Mallon A.-M., Platzter M., Bate R., Gloeckner G., Botcherby M.R.M.,
 RA Nordiek G., Strivens M.A., Kioschis P., Dangel A., Cunningham D.,
 RA Straw R.N.A., Weston P., Gilbert M., Fernando S., Goodall K.,
 RA Hunter G., Greystrong J.S., Clarke D., Kimberley C., Goerdes M.,
 RA Blechschmidt K., Rump A., Hinzmann B., Mundy C.R., Miller W.,
 RA Poustka A., Herman G.E., Rhodes M., Denny P., Rosenthal A.,
 RA Brown S.D.N.;
 RT "Comparative genome sequence analysis of the Bpa/Str region in mouse
 and man.";
 RL Genome Res. 10:758-775(2000).
 RN [4]
 RP NUCLEOTIDE SEQUENCE, AND VARIANT ALA-32.
 RA Chen H., Wang L., Mei M., Qin L., Cong X., Xu J., Wei L., Wang Y.,
 RA Chen W.;
 RT "The polymorphism of MAGE-1 gene in Chinese people.";
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT ALA-32.
 RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
 RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
 RA Phelan M., Farmer A.;
 RT "Cloning of human full-length CDSs in BD Creator(TM) system donor
 vector.";
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT ALA-32.
 RC TISSUE=Skin;
 RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP MUTAGENESIS.
 RC TISSUE=Blood;
 RX MEDLINE=94157413; PubMed=8113684; DOI=10.1094/jem.179.3.921;
 RA Gaugler B., van den Eynde B., van der Bruggen P., Romero P.,
 RA Gaforio J.J., de Plaen E., Lethe B., Brasseur F., Boon T.;
 RT "Human gene MAGE-3 codes for an antigen recognized on a melanoma by
 autologous cytolytic T lymphocytes.";
 RL J. Exp. Med. 179:921-930(1994).
 RN [8]
 RP SUBCELLULAR LOCATION.
 RX MEDLINE=95012905; PubMed=7927954;
 RA Schultz-Thater E., Juretic A., Dellabona P., Luscher U., Siegrist W.,
 RA Harder F., Heberer M., Zuber M., Spagnoli G.C.;
 RT "MAGE-1 gene product is a cytoplasmic protein.";
 RL Int. J. Cancer 59:435-439(1994).
 CC -!- FUNCTION: Not known, though may play a role in embryonal
 development and tumor transformation or aspects of tumor
 progression. Antigen recognized on a melanoma by autologous
 cytolytic T lymphocytes.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
 such as melanoma, head and neck squamous cell carcinoma, lung
 carcinoma and breast carcinoma, but not in normal tissues except
 for testes. Never expressed in kidney tumors, leukemias and
 lymphomas.
 CC -!- SIMILARITY: Contains 1 MAGE domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC EMBL; M77481; AAA03229.1; -; Unassigned DNA.
 CC EMBL; U82670; -; NOT ANNOTATED CDS; Genomic_DNA.
 CC EMBL; AY148486; AAN62752.1; -; mRNA.
 CC EMBL; BT009789; AAP88791.1; -; mRNA.
 CC EMBL; BC017555; AAH17555.1; -; mRNA.
 CC PDB; 1W72; X-ray; C/F=161-169.
 CC Ensembl; ENSG00000126977; Homo sapiens.
 CC HGNC; HGNC:6796; MAGEA1.
 CC H-InvDB; HIX0017126; -.
 CC MIM; 300036; -.
 CC GO; GO:0005886; C:plasma membrane; TAS.
 CC InterPro; IPR002190; MAGE.
 CC PANTHER; PTHR11736; MAGE; 1.
 CC Pfam; PF01454; MAGE; 1.
 CC PROSITE; PS50838; MAGE; 1.
 CC 3D-structure; Antigen; Multigene family; Polymorphism; Tumor antigen.
 KW DOMAIN 102 301
 FT COMPBIAS 33 36
 FT VARIANT 32 32
 FT T -> A (probable polymorphism).
 FT R -> Q (in dbSNP:2008144).
 FT /FTID=VAR 004283.
 FT R -> Q (in dbSNP:2008144).
 FT /FTID=VAR 011737.
 FT D -> A: Abolishes HLA-A1 binding.
 FT Y -> A: Abolishes HLA-A1 binding.
 FT MUTAGEN 163 163
 FT MUTAGEN 169 169
 FT SEQUENCE 309 AA; 34342 MW; 544EEB1F9F4E9D33 CRC64;
 SQ

Query Match 100.0%; Score 9; DB 1; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9
DB 174 CLGLSYDGL 182

RESULT 3
MAGE2 HUMAN
ID MAGE2 HUMAN STANDARD; PRT; 314 AA.
AC P43356;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Melanoma-associated antigen 2 (MAGE-2 antigen).
GN Name=MAGE2A2; Synonyms=MAGE2, MAGEA2;
and
GN Name=MAGEA2B; Synonyms=MAGE2, MAGEA2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94102805; PubMed=8276455;
RA de Smet C., Lurquin C., van der Bruggen P., de Plaen E., Brasseur F.,
RA Boon T.;
RT "Sequence and expression pattern of the human MAGE2 gene.";
RL Immunogenetics 39:121-129(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=20314869; PubMed=10854409; DOI=10.1101/gr.10.6.758;
RA Mallon A.-M., Platzer M., Bate R., Gloeckner G., Botcherby M.R.M.,
RA Nordsiek G., Strivens M.A., Kioschis P., Dangel A., Cunningham D.,
RA Straw R.N.A., Weston P., Gilbert M., Fernando S., Goodall K.,
RA Hunter G., Greystrom J.S., Clarke D., Kimberley C., Goerdes M.,
RA Blechschmidt K., Rump A., Hinzmann B., Mundy C.R., Miller W.,
RA Poustka A., Herman G.E., Rhodes M., Denny P., Rosenthal A.,
RA Brown S.D.M.;
RT "Comparative genome sequence analysis of the Bpa/Str region in mouse
RT and man.";
RL Genome Res. 10:758-775(2000).
RN [3]
RP MUTAGENESIS.
RC TISSUE=Blood;
RX MEDLINE=94157413; PubMed=8113684; DOI=10.1084/jem.179.3.921;
RA Gaugler B., van den Eynde B., van der Bruggen P., Romero P.,
RA Gaforio J.J., de Plaen E., Lethe B., Brasseur F., Boon T.;
RT "Human gene MAGE-3 codes for an antigen recognized on a melanoma by
RT autologous cytolytic T lymphocytes.";
RL J. Exp. Med. 179:921-930(1994).
RN [4]
RP FUNCTION: Not known, though may play a role in embryonal
RP development and tumor transformation or aspects of tumor
RP progression. Antigen recognized on a melanoma by autologous
RP cytolytic T lymphocytes.
CC -! TISSUE SPECIFICITY: Expressed in many tumors of several types,
CC such as melanoma, head and neck squamous cell carcinoma, lung
CC carcinoma and breast carcinoma, but not in normal tissues except
CC for testes.
CC -! SIMILARITY: Contains 1 MAGE domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; L18920; AAA17729.1; -; Unassigned DNA.
DR EMBL; U82671; -; NOT_ANNOTATED_CDS; Genomic_DNA.

DR PIR; I68889; I68889.
DR HGNC; HGNC:6800; MAGEA2.
DR HGNC; HGNC:19340; MAGEA2B.
DR H-InvDB; HIX0017118; -.
DR MIM; 300173; -.
DR InterPro; IPR002190; MAGE.
DR PANTHER; PTHR11736; MAGE; 1.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
DR KW Antigen; Multigene family; Tumor antigen.
FT DOMAIN 109 308
FT COMPBIAS 40 43 Poly-Ser.
FT MUTAGEN 170 170 V->D: Improves ability to bind to HLA-A1.
SQ SEQUENCE 314 AA; 35055 MW; 844F16335A2BCE7 CRC64;
Query Match 100.0%; Score 9; DB 1; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9
DB 181 CLGLSYDGL 189

RESULT 4
MAGE3 HUMAN
ID MAGE3 HUMAN STANDARD; PRT; 314 AA.
AC P43357;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Melanoma-associated antigen 3 (MAGE-3 antigen) (Antigen M22-D).
GN Name=MAGEA3; Synonyms=MAGE3;
and
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND MUTAGENESIS.
RC TISSUE=Blood;
RX MEDLINE=94157413; PubMed=8113684; DOI=10.1084/jem.179.3.921;
RA Gaugler B., van den Eynde B., van der Bruggen P., Romero P.,
RA Gaforio J.J., de Plaen E., Lethe B., Brasseur F., Boon T.;
RT "Human gene MAGE-3 codes for an antigen recognized on a melanoma by
RT autologous cytolytic T lymphocytes.";
RL J. Exp. Med. 179:921-930(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=94311935; PubMed=8037761;
RA Ding M., Beck R.J., Keller C.J., Fenton R.G.;
RT "Cloning and analysis of MAGE-1-related genes.";
RL Biochem. Biophys. Res. Commun. 202:549-555(1994).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=20314869; PubMed=10854409; DOI=10.1101/gr.10.6.758;
RA Mallon A.-M., Platzer M., Bate R., Gloeckner G., Botcherby M.R.M.,
RA Nordsiek G., Strivens M.A., Kioschis P., Dangel A., Cunningham D.,
RA Straw R.N.A., Weston P., Gilbert M., Fernando S., Goodall K.,
RA Hunter G., Greystrom J.S., Clarke D., Kimberley C., Goerdes M.,
RA Blechschmidt K., Rump A., Hinzmann B., Mundy C.R., Miller W.,
RA Poustka A., Herman G.E., Rhodes M., Denny P., Rosenthal A.,
RA Brown S.D.M.;
RT "Comparative genome sequence analysis of the Bpa/Str region in mouse
RT and man.";
RL Genome Res. 10:758-775(2000).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX TISSUE=Bone marrow, Lung, Prostate, and Skin;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Not known, though may play a role in embryonal
CC development and tumor transformation or aspects of tumor
CC progression. Antigen recognized on a melanoma by autologous
CC cytolytic T lymphocytes.
CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
CC such as melanoma, head and neck squamous cell carcinoma, lung
CC carcinoma and breast carcinoma, but not in normal tissues except
CC for testes and placenta. Never expressed in kidney tumors,
CC leukemias and lymphomas.
CC -!- SIMILARITY: Contains 1 MAGE domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
DR EMBL; U03735; AAA17446.1; -; Unassigned DNA.
DR EMBL; U82671; -; NOT ANNOTATED CDS; Genomic_DNA.
DR EMBL; BC003040; AAH0340.1; -; mRNA.
DR EMBL; BC005963; AAH05963.1; -; mRNA.
DR EMBL; BC011744; AAH11744.1; -; mRNA.
DR EMBL; BC016803; AAH16803.1; -; mRNA.
DR EMBL; BC017389; AAH17389.1; -; mRNA.
DR PIR; JC2361; JC2361
DR Ensembl; ENSG00000197172; Homo sapiens.
DR HGNC; HGNC:6801; MAGEA3.
DR H-InvDB; HIX0017120; -.
DR MIM; 300174; -.
DR InterPro; IPR002190; MAGE.
DR PANTHER; PTHR11736; MAGE; 1.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
KW Antigen; Multigene family; Tumor antigen.
FT DOMAIN 109 308
FT COMPBIAS 40 43 Poly-Ser.
FT MUTAGEN 170 170 D->A: Abolishes HLA-A1 binding.
FT MUTAGEN 176 176 Y->A: Abolishes HLA-A1 binding.
SQ SEQUENCE 314 AA; 34747 MW; 3F5EB13D1C9946A1 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

QY 1 CIGLSYDGL 9
DB 181 CIGLSYDGL 189

RESULT 5
MAGE6_HUMAN
ID MAGEA6_HUMAN STANDARD; PRT; 314 AA.
AC P43360;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Melanoma-associated antigen 6 (MAGE-6 antigen) (MAGE3B).
GN Name=MAGEA6; Synonyms=MAGE6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95012457; PubMed=7927540;
RA de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,
RA de Smet C., Brasseur F., van der Brugge P., Lethe B., Lurquin C.,
RA Brasseur R., Chomez P., de Backer O., Cavenee W., Boon T.;
RT "Structure, chromosomal localization, and expression of 12 genes of
RT the MAGE family.";
RL Immunogenetics 40:360-369(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Skin;
MEDLINE=94311935; PubMed=8037761;
Ding M., Beck R.J., Keller C.J., Fenton R.G.;
RT "Cloning and analysis of MAGE-1-related genes.";
RL Biochem. Biophys. Res. Commun. 202:549-555(1994).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95369706; PubMed=7642112; DOI=10.1016/0378-1119(94)00680-Q;
RA Imai Y., Shichiyo S., Yamada A., Katayama T., Yano H., Itoh K.;
RT "Sequence analysis of the MAGE gene family encoding human tumor-
RT rejection antigens.";
RL Gene 160:287-290(1995).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX TISSUE=Oesophageal carcinoma;
RG The German cDNA consortium;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berger J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Not known, though may play a role in tumor or aspects of
CC tumor progression.
CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
CC such as melanoma, head and neck squamous cell carcinoma, lung
CC carcinoma and breast carcinoma, but not in normal tissues except
CC for testes.
CC -!- SIMILARITY: Contains 1 MAGE domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.


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CC -----
DR EMBL; U10691; AAC68975.1; -; Genomic_DNA.
DR EMBL; U10339; AAA19006.1; -; mRNA.
DR EMBL; D32076; BAA06842.1; -; mRNA.
DR EMBL; BX640600; CAE45706.1; -; mRNA.
DR EMBL; BC041599; AAH41599.1; -; mRNA.
DR PIR; JC2360; JC2360.
DR Ensembl; ENSG00000183305; Homo sapiens.
DR HGNC; HGNC:6804; MAGEA6.
DR MIM; 300176; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
DR Antigen; Multigene family; Tumor antigen.
KW DOMAIN 109 308
FT COMPBIAS 40 43 Poly-Ser.
SQ SEQUENCE 314 AA; 34891 MW; 29B83C7FA6E50263 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9
DB 181 CLGLSYDGL 189

RESULT 6
MAGAC HUMAN STANDARD; PRT; 314 AA.
AC P43365; Q9NSD3;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Melanoma-associated antigen 12 (MAGE-12 antigen) (MAGE12F).
GN Name=MAGE12; Synonyms=MAGE12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94102805; PubMed=8276455;
RA de Smet C., Lurquin C., van der Bruggen P., de Plaen E., Brasseur F.,
RA Boon T.;
RT "Sequence and expression pattern of the human MAGE2 gene.";
RL Immunogenetics 39:121-129(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Skin;
RX MEDLINE=94311935; PubMed=8037761;
RA Ding M., Beck R.J., Keller C.J., Fenton R.G.;
RT "Cloning and analysis of MAGE-1-related genes.";
RL Biochem. Biophys. Res. Commun. 202:549-555(1994).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=203114869; PubMed=10854409; DOI=10.1101/gr.10.6.758;
RA Mallon A.M., Platzer M., Bate R., Gloeckner G., Botcherby M.R.M.,
RA Nordstiek G., Strivens M.A., Kioschis P., Dangel A., Cunningham D.,
RA Straw R.N.A., Weston P., Gilbert M., Fernando S., Goodall K.,
RA Hunter G., Greystrong J.S., Clarke D., Kimberley C., Goerdall K.,
RA Blechschmidt K., Rump A., Hinzmann B., Mundy C.R., Miller W.,
RA Poustka A., Herman G.E., Rhodes M., Denny P., Rosenthal A.,
RA Brown S.D.M.;
RT "Comparative genome sequence analysis of the Bpa/Str region in mouse
and man.";
RL Genome Res. 10:758-775(2000).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley J., LaBaer J., Lin Y.,

```

```

RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) system donor
vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Not known, though may play a role in tumor
CC transformation or aspects of tumor progression.
CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
CC such as melanoma, head and neck squamous cell carcinoma, lung
CC carcinoma and breast carcinoma, but not in normal tissues except
CC for testes.
CC -!- SIMILARITY: Contains 1 MAGE domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U18877; AAA19023.1; -; Unassigned DNA.
DR EMBL; U82671; -; NOT ANNOTATED CDS; Genomic_DNA.
DR EMBL; BT007108; AAP35772.1; -; mRNA.
DR EMBL; BC003408; AAH03408.1; -; mRNA.
DR PIR; I54519; I54519.
DR Ensembl; ENSG00000147381; Homo sapiens.
DR HGNC; HGNC:6799; MAGEA12.
DR H-InvDB; HIX0020426; -.
DR MIM; 300177; -.
DR InterPro; IPR002190; MAGE.
DR PANTHER; PTHR11736; MAGE; 1.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
KW Antigen; Multigene family; Tumor antigen.
FT DOMAIN 109 308 MAGE.
FT COMPBIAS 40 43 Poly-Ser.
FT CONFLICT 10 10 C -> S (in Ref. 2).
FT CONFLICT 187 187 D -> A (in Ref. 1).
FT CONFLICT 300 300 S -> P (in Ref. 1).
SQ SEQUENCE 314 AA; 34836 MW; 7E00F7CECD8F6568 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9
DB 181 CLGLSYDGL 189

RESULT 7

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Q6FGT7 HUMAN
ID Q6FGT7_HUMAN PRELIMINARY; PRT; 314 AA.
AC Q6FGT7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MAGA6 protein (Fragment).
DE MAGA6 protein (Fragment).
GN Name=MAGEA6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR541766; CAG4567.1; -; mRNA.
FT NON_TER 314
SQ SEQUENCE 314 AA; 34842 MW; 69562C7FA6E50275 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CIGLSYDGL 9
DB 181 CIGLSYDGL 189

RESULT 8
Q6FH5 HUMAN
ID Q6FH5_HUMAN PRELIMINARY; PRT; 314 AA.
AC Q6FH5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MAGA6 protein.
GN Name=MAGEA6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR541766; CAG4567.1; -; mRNA.
FT NON_TER 314
SQ SEQUENCE 314 AA; 34925 MW; 29B83C7FA6EBE263 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CIGLSYDGL 9
DB 181 CIGLSYDGL 189

RESULT 9
Q6FHH8 HUMAN
ID Q6FHH8_HUMAN PRELIMINARY; PRT; 314 AA.

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AC Q6FHH8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE MAGA12 protein (Fragment).
GN Name=MAGEA12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR541775; CAG46574.1; -; mRNA.
FT NON_TER 314
SQ SEQUENCE 314 AA; 34836 MW; 7E00F7CECD8F6568 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CIGLSYDGL 9
DB 181 CIGLSYDGL 189

RESULT 10
Q53EX0 HUMAN
ID Q53EX0_HUMAN PRELIMINARY; PRT; 314 AA.
AC Q53EX0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Melanoma antigen, family A, 3 variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RA Maruyama K., Sugano S.;
RT "Oligo-capping: a simple method to replace the cap structure of
RT eucaryotic mRNAs with oligoribonucleotides.";
RL Gene 138:171-174 (1994).
RN [2]_
RP NUCLEOTIDE SEQUENCE.
RA Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
RT "Construction and characterization of a full length-enriched and a 5'-
RT end-enriched cDNA library.";
RL Gene 200:149-156 (1997).
RN [3]_
RP NUCLEOTIDE SEQUENCE.
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK223519; BAD97239.1; -; mRNA.
FT NON_TER 1
SQ SEQUENCE 314 AA; 34807 MW; F89866E66C84F073 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CIGLSYDGL 9
DB 181 CIGLSYDGL 189

RESULT 11

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Q95E03 HUMAN
ID Q95E03 HUMAN PRELIMINARY; PRT; 314 AA.
AC Q95E03;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Melanoma antigen family A, 2B.
GN Name=MAGEA2B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Adrenal cortex;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Young A.A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Breast;
RX Director MGC Project;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063681; AAH63681.1; -, mRNA.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
SQ SEQUENCE 314 AA; 35026 MW; 28810BE358FA3FE6 CRC64;
Query Match 100.0%; Score 9; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CIGLSYDGL 9
DB 181 CIGLSYDGL 189
RESULT 12
Q6P448 HUMAN
ID Q6P448 HUMAN PRELIMINARY; PRT; 314 AA.
AC Q6P448;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Melanoma antigen family A, 2.
GN Name=MAGEA2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Adrenal cortex;
RX Director MGC Project;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013098; AAH13098.1; -, mRNA.
DR HGNC; HGNC:19340; MAGEA2B.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
SQ SEQUENCE 314 AA; 35024 MW; A94F16247D1BFBC0 CRC64;
Query Match 100.0%; Score 9; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CIGLSYDGL 9
DB 181 CIGLSYDGL 189
RESULT 13
Q6FHI6 HUMAN
ID Q6FHI6 HUMAN PRELIMINARY; PRT; 314 AA.
AC Q6FHI6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE MAGRA3 protein.
GN Name=MAGEA3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Schrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR541767; CAG46566.1; -, mRNA.
DR EMBL; CR541774; CAG46573.1; -, mRNA.
SQ SEQUENCE 314 AA; 34747 MW; 3F5EB13D1C9946A1 CRC64;
Query Match 100.0%; Score 9; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CIGLSYDGL 9
DB 181 CIGLSYDGL 189
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RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Breast;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Young A.A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Breast;
RX Director MGC Project;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063681; AAH63681.1; -, mRNA.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
SQ SEQUENCE 314 AA; 35026 MW; 28810BE358FA3FE6 CRC64;
Query Match 100.0%; Score 9; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CIGLSYDGL 9
DB 181 CIGLSYDGL 189
RESULT 13
Q6FHI6 HUMAN
ID Q6FHI6 HUMAN PRELIMINARY; PRT; 314 AA.
AC Q6FHI6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE MAGRA3 protein.
GN Name=MAGEA3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Schrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR541767; CAG46566.1; -, mRNA.
DR EMBL; CR541774; CAG46573.1; -, mRNA.
SQ SEQUENCE 314 AA; 34747 MW; 3F5EB13D1C9946A1 CRC64;
Query Match 100.0%; Score 9; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CIGLSYDGL 9
DB 181 CIGLSYDGL 189
```

```
Db 181 CLGLSYDGL 189

RESULT 14
Q6NW44 HUMAN PRELIMINARY; PRT; 314 AA.
AC Q6NW44
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Melanoma antigen family A, 6.
GN Name=MAGEA6;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE-Testis;
RG NIH MGC Project;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC067731; AAH67731.1; -; mRNA.
DR Ensembl; ENSG00000183305; Homo sapiens.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
SQ SEQUENCE 314 AA; 34918 MW; 3484C62E0A684983 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9
Db 181 CLGLSYDGL 189

Search completed: March 17, 2006, 23:49:11
Job time : 235 secs

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheciidae; Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA International consortium for macaque cDNA sequencing, analysis;
RT "DNA sequences of macaque genes expressed in brain or testis and its
evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
RT "Substitution rate and structural divergence of 5'UTR evolution:
Comparative analysis between human and cynomolgus monkey cDNAs.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
RT "Substitution rate and structural divergence of 5'UTR evolution:
Comparative analysis between human and cynomolgus monkey cDNAs.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB179115; BAE02166.1; -; mRNA.
DR EMBL; AB168565; BAE00679.1; -; mRNA.
SQ SEQUENCE 314 AA; 35132 MW; 40AEB13FB2BB5359 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLGLSYDGL 9
Db 181 CLGLSYDGL 189

Search completed: March 17, 2006, 23:49:11
Job time : 235 secs

RESULT 15
Q4R400 MACFA PRELIMINARY; PRT; 314 AA.
AC Q4R400;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Testis cDNA clone: Q4R4-13065, similar to human melanoma antigen,
family A, 2, copy b (MAGEA2b).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 18, 2006, 00:12:30 ; Search time 189 Seconds
(without alignments)
20.923 Million cell updates/sec

Title: US-09-856-812b-1_COPY_254_262

Perfect score: 9

Sequence: 1 GLYDGMHL 9

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	9	100.0	9	3	AAY71487	Human MAG
2	9	100.0	9	4	AAB31323	Exemplary
3	9	100.0	9	5	AA017088	Human mag
4	9	100.0	9	6	ABJ19876	MHC bindi
5	9	100.0	9	8	ADG89586	Class I H
6	9	100.0	9	8	ADJ19869	Human HLA
7	9	100.0	9	8	ADI19026	Human HLA
8	9	100.0	9	8	ADJ58374	Peptide p
9	9	100.0	9	8	ADL26560	Melanoma
10	9	100.0	9	8	ADR69760	Novel hyb
11	9	100.0	9	9	ADK08536	Class I H
12	9	100.0	9	9	AEB01337	Melanoma
13	9	100.0	10	3	AAY71489	Human MAG
14	9	100.0	20	8	ADR69766	Novel hyb
15	9	100.0	20	8	ADU08506	Hybrid an
16	9	100.0	369	3	AAY71485	Human MAG
17	9	100.0	369	4	AAB80297	Human pro
18	9	100.0	369	6	ABR48215	Human bla
19	9	100.0	369	6	ABU56516	Lung canc
20	9	100.0	383	8	ABO58424	Human gen
21	6	66.7	6	5	ABG79151	Human MAG
22	6	66.7	184	8	ADT60907	Plant pol
23	6	66.7	185	8	ADY12435	Plant ful
24	6	66.7	190	8	ADT60905	Plant pol

25	6	66.7	192	8	ADT60906	Plant pol
26	6	66.7	234	6	ABM67109	Photorhab
27	6	66.7	241	4	AAU38355	Salmonell
28	6	66.7	248	4	AAU34654	E. coli c
29	6	66.7	372	8	ADX91227	Plant ful
30	6	66.7	383	8	ADX96477	Plant ful
31	6	66.7	398	2	AAW24252	Ammonifex
32	6	66.7	398	6	ABU57355	A. degens
33	6	66.7	471	6	ABR44018	E. coli t
34	6	66.7	476	4	AAU29351	Novel mar
35	6	66.7	567	8	ADY24045	Plant ful
36	6	66.7	953	4	ABG15730	Novel hum
37	6	66.7	3835	8	ADX56095	Streptomy
38	5	55.6	9	2	AAY46489	Immunogen
39	5	55.6	9	2	AAY46037	Immunogen
40	5	55.6	9	2	AAY46435	Immunogen
41	5	55.6	9	3	AAY71488	Human MAG
42	5	55.6	9	4	AAG88669	HER2/NEU
43	5	55.6	9	4	AAG88319	HER2/NEU
44	5	55.6	9	9	ADW95463	Amino aci
45	5	55.6	10	2	AAR61556	Peptide f

ALIGNMENTS

RESULT 1

AAAY71487
ID AAY71487 standard; peptide; 9 AA.
XX
AC AAY71487;

DT 12-OCT-2000 (first entry)

DE Human MAG-A10 nonapeptide-1.

XX
KW MAG-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
KW immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
KW cancer; TNF; tumour necrosis factor; vaccine; cytostatic.

OS Homo sapiens.

XX WO200032769-A2.

XX 08-JUN-2000.

PF 26-NOV-1999; 99WO-IB002018.

XX 27-NOV-1998; 98GB-00026143.

PA (LUDW-) LUDWIG INST CANCER RES.

PI Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;

XX WPI; 2000-412317/35.

PT Novel polypeptides expressed in tumor cells useful for treating cancers
PT have an ability to complex with a major histocompatibility complex
PT molecule and comprises a specific unbroken amino acid sequence.

XX Claim 8; Page 36; 80pp; English.

CC The patent discloses MAG-A10 and MAG-A8 polypeptide, nonapeptide and
CC decapeptide sequences, that function as tumour rejection antigens (TRAe).
CC These peptides are capable of forming a complex with major
CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
CC Antigen), that are recognised by T-lymphocytes and elicit an immune
CC response from cytolytic T-lymphocytes (CTL). They function as an immune
CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
CC therapy and diagnosis of tumours and are effective in controlling or
CC preventing tumour growth. The present peptide sequence is the human MAG-A10
CC nonapeptide-1, that corresponds to residues 254-262 of the MAG-A10

CC protein. This peptide can serve as a tumour rejection antigen (TRA) and
CC in combination with adjuvants, can produce vaccines useful for treating a
CC variety of tumours that express MAGE-A10
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMGHEHL 9
|||
Db 1 GLYDGMGHEHL 9

RESULT 2

AAB31323
ID AAB31323 standard; peptide; 9 AA.

XX
AC AAB31323;

XX 20-APR-2001 (first entry)

XX Exemplary antigen characteristic of tumours and derived from MAGE-A10.

XX MAGE-A1; HLA; human leukocyte antigen; CD4+ T lymphocyte; cancer;

KW MAGE-A1 HLA class II-binding protein; vaccine.

XX Homo sapiens.

XX WO200078806-A1.

XX 28-DEC-2000.

XX 14-JUN-2000; 2000WO-US016287.

XX 18-JUN-1999; 99US-00336091.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Van Snick J, Lethe B, Chaux P, Boon-Falleur T, Van Der Bruggen P;

XX WPI; 2001-102698/11.

XX Novel MAGE-A1 human leukocyte antigen class II peptides which bind to and
PT are presented to the class II molecules, useful for inducing immune
PT response and treating cancers characterized by expression of MAGE-A1.
XX Disclosure; Page 32; 78pp; English.

XX AAB31302-59 represent exemplary antigens which are characteristic of

CC tumours. They can be used to enhance the immune response of vaccines

CC comprising peptides derived from human MAGE-A1 HLA (human leukocyte
CC antigen) class II-binding protein. Peptides derived from the MAGE-A1 HLA
CC binding protein stimulate the activity and proliferation of CD4+ T
CC lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic

CC agent for diagnosing a disorder characterized by expression of MAGE-A1.

CC The protein is used for treating a disorder characterized by expression

CC of MAGE-A1 such as cancers e.g. melanoma, squamous cell carcinomas,

CC colorectal carcinomas, osteosarcomas, and lymphocytic leukemias. Peptides

CC derived from the MAGE-A1 HLA binding protein are useful in the production

CC of anti-tumour vaccines

XX Sequence 9 AA;

Query Match 100.0%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMGHEHL 9
|||
Db 1 GLYDGMGHEHL 9

RESULT 3

AAO17088
ID AAO17088 standard; peptide; 9 AA.

XX
AC AAO17088;

XX 06-JUN-2002 (first entry)

XX Human mage-A10 protein antigen SEQ ID NO: 8.

XX Cryopreserved mature dendritic cell; antigen; vaccine; cytostatic;
KW virucide; cancer; hepatitis B virus.

XX Homo sapiens.

XX WO200216560-A1.

XX 28-FEB-2002.

XX 24-AUG-2001; 2001WO-EP009790.

XX 24-AUG-2000; 2000DE-01041515.

XX (SCHU/) SCHULER G.

XX Schuler G, Schuler-Thurner B;

XX WPI; 2002-292062/33.

XX Preparation of cryopreserved, mature dendritic cells, useful in vaccines,
PT comprises culturing immature cells on medium containing cocktail of
PT maturation factors, then freezing.

XX Disclosure; Fig 28; 87pp; German.

XX The present invention relates to a method for the preparation of ready-
CC for-use, cryopreserved, mature dendritic cells comprising growing
CC immature dendritic cells in a culture medium that includes a 'maturation
CC cocktail' of one or more maturation stimuli and freezing the resulting
CC matured cells in a freezing medium that does not contain heterologous
CC serum. When loaded with antigens, the dendritic cells can be used as
CC vaccines, e.g. against tumours and hepatitis B virus. The present
CC sequence is an antigen described in the invention

XX Sequence 9 AA;

Query Match 100.0%; Score 9; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMGHEHL 9

Db 1 GLYDGMGHEHL 9

RESULT 4

ABU19876
ID ABU19876 standard; peptide; 9 AA.

XX
AC ABU19876;

XX 10-APR-2003 (first entry)

XX MHC binding peptide SEQ ID No 39.

XX Antirheumatic; antiallergic; antiarthritic; nootropic; neuroprotective;
KW antiinflammatory; major histocompatibility complex; MHC;

KW autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;

KW rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;

KW inflammation; gene therapy; MHC binding peptide.

XX Synthetic.

XX WO200294981-A2.
XX
XX PD 28-NOV-2002.
XX
XX PF 16-MAY-2002; 2002WO-IL000383.
XX
XX PR 16-MAY-2001; 2001US-0290958P.
XX PR 29-MAY-2001; 2001US-00865548.
XX
XX PA (TECR) TECHNION RES & DEV FOUND LTD.
XX
XX PI Barnea E, Beer I, Ziv T, Admon A, Dassau L, Buchsbaum S;
XX
XX DR WPI; 2003-210043/20.
XX
XX PT Identifying peptides that are capable of binding to major
PT histocompatibility complex (MHC) molecules of a particular haplotype by
PT analyzing peptides bound to the soluble and secreted form of the MHC
PT molecules of the particular haplotype.
XX
XX PS Example; Fig 5D; 238pp; English.
XX
XX CC The invention relates to a novel method for identifying peptides
CC originating from a particular cell type, which are capable of binding to
CC major histocompatibility complex (MHC) molecules of a particular
CC haplotype. The method comprises analysing peptides bound to the soluble
CC and secreted form of the MHC molecules of the particular haplotype. The
CC method is useful for identifying peptides for treating an autoimmune
CC disease, such as T or B cell and/or allergic disease or condition,
CC rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,
CC e.g. Alzheimer's disease, or diseases associated with inflammation. The
CC sequences of the invention may be used in a gene therapy application.
CC This sequence represents a peptide relating to the method for identifying
CC MHC binding peptides of the invention
XX
XX SQ Sequence 9 AA;

Query Match 100.0%; Score 9; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 GLYDGMGHEHL 9
Db 1 GLYDGMGHEHL 9
|||||||
RESULT 5
ADG89586
ID ADG89586 standard; peptide; 9 AA.
XX
XX AC ADG89586;
XX
XX DT 11-MAR-2004 (first entry)
XX
XX DE Class I HLA-restricted testis cancer antigen #21.
XX
XX KW metastatic cancer cell differentiation; mutated fibronectin;
KW metastatic cancer; Class I HLA-restricted; testis; cancer antigen.
XX
XX OS Unidentified.
XX
XX PN WO2003100027-A2.
XX
XX PD 04-DEC-2003.
XX
XX PF 28-MAY-2003; 2003WO-US016736.
XX
XX PR 28-MAY-2002; 2002US-0383530P.
XX
XX PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
XX PI Wang R;

Query Match 100.0%; Score 9; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 GLYDGMGHEHL 9
Db 1 GLYDGMGHEHL 9
|||||||
RESULT 6
AD119869
ID AD119869 standard; peptide; 9 AA.
XX
XX AC AD119869;
XX
XX DT 22-APR-2004 (first entry)
XX
XX DE Human HLA-B18 binding WAGE-3 peptide #11.
XX
XX KW HLA; human leucocyte antigen; melanoma; lung cancer; head cancer;
KW neck cancer; WAGE-3; human.
XX
XX OS Homo sapiens.
XX
XX PN US2003228325-A1.
XX
XX PD 11-DEC-2003.
XX
XX PF 05-JUN-2002; 2002US-00164078.
XX
XX PR 05-JUN-2002; 2002US-00164078.
XX
XX PA (BILS/) BILSBOROUGH J.
PA (SCHU/) SCHULTZ E.
PA (PANI/) PANICHELLI C.
PA (BOON/) BOON-FALLEUR T.
PA (BRUG/) BRUGGEN P V D.
XX
XX PI Bilborough J, Schultz E, Panichelli C, Boon-Falleur T;
PI Bruggen PVD;
XX
XX DR WPI; 2004-042211/04.
XX
XX PT Treating subject with pathological condition having human leucocyte
PT antigen-B18 molecules presented on cell surface by administering peptides
PT to subject for generating immunologically active response against cells.
XX
XX PS Claim 22; SEQ ID NO 12; 15pp; English.
XX
XX CC The present invention relates to a peptide which binds HLA (human
CC leucocyte antigen)-B18 to form T-cell epitope. The invention is useful
CC for treating a pathological conditions such as melanoma, lung cancer and
CC head and neck cancer. The present sequence is human HLA-B18 binding WAGE-
CC 3 peptide.
XX
XX SQ Sequence 9 AA;

XX WPI; 2004-035134/03.
XX
XX PT Identifying a cell that differentiates into a metastatic cancer cell,
PT useful for preventing metastatic cancer, comprises identifying a mutated
PT fibronectin in the cell.
XX
XX PS Disclosure; SEQ ID NO 29; 137pp; English.
XX
XX CC The invention comprises a method for identifying a cell that will
CC differentiate into a metastatic cancer cell, the method involves
CC identifying a mutated fibronectin in the cell. The method of the
CC invention is useful for preventing metastatic cancer. The present amino
CC acid sequence represents a Class I HLA-restricted testis cancer antigen.
XX
XX SQ Sequence 9 AA;

Query Match 100.0%; Score 9; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 GLYDGMGHEHL 9
Db 1 GLYDGMGHEHL 9
|||||||
RESULT 6
AD119869
ID AD119869 standard; peptide; 9 AA.
XX
XX AC AD119869;
XX
XX DT 22-APR-2004 (first entry)
XX
XX DE Human HLA-B18 binding WAGE-3 peptide #11.
XX
XX KW HLA; human leucocyte antigen; melanoma; lung cancer; head cancer;
KW neck cancer; WAGE-3; human.
XX
XX OS Homo sapiens.
XX
XX PN US2003228325-A1.
XX
XX PD 11-DEC-2003.
XX
XX PF 05-JUN-2002; 2002US-00164078.
XX
XX PR 05-JUN-2002; 2002US-00164078.
XX
XX PA (BILS/) BILSBOROUGH J.
PA (SCHU/) SCHULTZ E.
PA (PANI/) PANICHELLI C.
PA (BOON/) BOON-FALLEUR T.
PA (BRUG/) BRUGGEN P V D.
XX
XX PI Bilborough J, Schultz E, Panichelli C, Boon-Falleur T;
PI Bruggen PVD;
XX
XX DR WPI; 2004-042211/04.
XX
XX PT Treating subject with pathological condition having human leucocyte
PT antigen-B18 molecules presented on cell surface by administering peptides
PT to subject for generating immunologically active response against cells.
XX
XX PS Claim 22; SEQ ID NO 12; 15pp; English.
XX
XX CC The present invention relates to a peptide which binds HLA (human
CC leucocyte antigen)-B18 to form T-cell epitope. The invention is useful
CC for treating a pathological conditions such as melanoma, lung cancer and
CC head and neck cancer. The present sequence is human HLA-B18 binding WAGE-
CC 3 peptide.
XX
XX SQ Sequence 9 AA;

Query Match 100.0%; Score 9; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMGHEHL 9
DB 1 GLYDGMGHEHL 9

RESULT 7
ADI19026
ID ADI19026 standard; peptide; 9 AA.
XX
AC ADI19026;
XX
DT 22-APR-2004 (first entry)
XX
XX Human HLA-Cw6 binding MAGE-1 peptide #11.
DE
XX MHC; major histocompatibility; therapy; cancer; melanoma; HLA-Cw6; human;
KW MAGE-1; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003228308-A1.
XX
PD 11-DEC-2003.
XX
XX 05-JUN-2002; 2002US-00164121.
XX
XX 05-JUN-2002; 2002US-00164121.
XX
XX (ZHAN/) ZHANG Y.
PA (TRAV/) TRAVERSARI C.
PA (BOON/) BOON-FALLEUR T.
PA (BRUG/) BRUGGEN P V D.
XX
XX Zhang Y, Traversari C, Boon-Falleur T, Bruggen PVD;
PI WPI; 2004-042210/04.
XX
DR Treating subject with pathological condition having human leukocyte
XX antigen-Cw6 molecules presented on cell surface by administering peptides
PT to subject for generating immunologically active response against cells.
XX
PS Example 7; SEQ ID NO 13; 15pp; English.
XX
XX The present invention relates to peptides which form immunologically
CC active complexes with MHC molecules. The invention is useful for treating
CC a subject with pathological condition such as cancer which is melanoma by
CC presenting HLA-Cw6 molecules on the cell surface. The present sequence is
CC human HLA-Cw6 binding MAGE-1 peptide.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 9; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMGHEHL 9
DB 1 GLYDGMGHEHL 9

RESULT 8
ADJ58374
ID ADJ58374 standard; peptide; 9 AA.
XX
AC ADJ58374;
XX
DT 06-MAY-2004 (first entry)
XX
XX

DE Peptide predicted to bind to HLA-A2 #34.
XX
KW major histocompatibility complex; MHC; cytolytic T-cell; HLA-A2;
KW Cytostatic; cancer.
XX
OS Synthetic.
XX
PN WO2004011483-A2.
XX
PD 05-FEB-2004.
XX
XX 23-JUL-2003; 2003WO-US023306.
XX
XX 31-JUL-2002; 2002US-0400076P.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
PA (TORR-) TORREY PINES INST MOLECULAR STUDIES.
XX
XX Valmori D, Ayyoub M, Pinilla C;
PI WPI; 2004-143815/14.
XX
DR New isolated SSX-2 and SSX-2-related peptides that bind to human
XX leukocyte antigen (HLA) molecules, useful for diagnosing or treating
PT cancer, particularly melanoma.
PT
XX Example 8; SEQ ID NO 34; 20pp; English.
XX
XX The present invention relates to an isolated peptide which binds to a
CC major histocompatibility complex (MHC) molecule to form a complex that is
CC recognized by a cytolytic T-cell which recognizes and lyses cells
CC presenting complexes of HLA-A2 molecules comprising a sequence of 9 amino
CC acids fully defined in the specification, with the proviso that the
CC peptide is not the peptide of S17 itself. Specifically claimed is an HLA-
CC binding peptide comprising a sequence of 9 amino acids fully defined in
CC the specification. The composition and methods are useful for diagnosing
CC or treating cancer, particularly melanoma. The present sequence
CC represents a peptide predicted to bind to HLA-A2.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 9; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMGHEHL 9
DB 1 GLYDGMGHEHL 9

RESULT 9
ADL26560
ID ADL26560 standard; peptide; 9 AA.
XX
AC ADL26560;
XX
XX 03-JUN-2004 (first entry)
XX
XX Melanoma cell line MAGE gene encoded HLA-A2 peptide.
DE
XX cytostatic; gene therapy; vaccine; cancer; immune response.
KW
XX Homo sapiens.
XX
XX WO2004019886-A2.
PN
XX 11-MAR-2004.
PD
XX 29-AUG-2003; 2003WO-US027125.
XX
XX 29-AUG-2002; 2002US-0407492P.
XX
XX (CYTO-) CYTOCURE LLC.
PA

XX Durda PJ, Kurnick JT, Dunn IS;
XX WPI; 2004-239114/22.
XX Increasing an immune response against a tumor cell comprises
XX administering to a subject with a tumor an amount of IFN-beta receptor
XX agonist and tumor associated antigen (TAA).
XX Example 7; Page 47; 80pp; English.
XX The present invention relates to a method of increasing an immune
XX response against a tumour cell, comprising administering to a subject
XX with a tumour an amount of IFN-beta receptor agonist and tumour
XX associated antigen (TAA). The method is useful for increasing an immune
XX response against a tumour cell. The present sequence is a peptide used in
XX the exemplification of the invention.
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 9; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLYDGMHL 9
DB 1 GLYDGMHL 9
RESULT 10
ID ADR69760 standard; peptide; 9 AA.
XX ADR69760;
XX 18-NOV-2004 (first entry)
XX Unidentified.
XX WO2004071457-A2.
XX 26-AUG-2004.
XX 13-FEB-2004; 2004WO-US004340.
XX 13-FEB-2003; 2003US-0447142P.
XX 11-APR-2003; 2003US-0462469P.
XX 18-APR-2003; 2003US-0463746P.
XX 16-SEP-2003; 2003US-0503417P.
XX 12-FEB-2004; 2004US-00776521.
XX (MOJA-) MOJAVE THERAPEUTICS INC.
XX Fletcher J, Prince-Cohane K, Mehta S, Slusarewicz P, Andjelic S;
XX Barber B;
XX WPI; 2004-625768/60.
XX New hybrid antigens comprising an antigenic domain and improved heat
XX shock protein-binding domains, useful for preventing or treating
XX infectious diseases or cancer.
XX Example 11; Page 44; 56pp; English.
XX This invention relates to a novel hybrid antigen which comprises at least
XX one antigenic domain of an infectious agent or tumour antigen and a
XX binding domain that non-covalently binds to a heat shock protein. The

CC invention may be useful for the production of compounds with an
CC antimicrobial or cytostatic activity. In addition, the invention may
CC prove useful for the production of a vaccine or for gene therapy. The
CC composition and methods disclosed are useful for preventing or treating
CC infectious diseases or cancer. The present sequence is that of a peptide
CC which was used in the exemplification of the invention.
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 9; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLYDGMHL 9
DB 1 GLYDGMHL 9
RESULT 11
ADX08536
ID ADR08536 standard; peptide; 9 AA.
XX ADR08536;
XX 21-APR-2005 (first entry)
XX Class I HLA-restricted cancer/testis antigen peptide #21.
XX vaccine; infection; viral infections; virucide; bacterial infection;
XX antibacterial; yeast infection; fungicide; fungal infection;
XX protozoal infection; protozoicide; cancer; cytostatic; melanoma;
XX lung tumor; colon tumor; breast tumor; leukemia; autoimmune disease;
XX multiple sclerosis; neuroprotective; rheumatoid arthritis; antiarthritic;
XX antirheumatic; systemic lupus erythematosus; antiinflammatory;
XX dermatological; immunosuppressive.
XX Unidentified.
XX WO2005011730-A1.
XX 10-FEB-2005.
XX 30-JUL-2004; 2004WO-GB003285.
XX 01-AUG-2003; 2003GB-00018096.
XX (UNLO) QUEEN MARY & WESTFIELD COLLEGE.
XX Wang P, Li S;
XX WPI; 2005-152360/16.
XX New vaccine composition comprises inverted microsomes from animal cells
XX with an externally disposed peptide antigen and a protein of the Major
XX Histocompatibility Complex (MHC), useful for treating or preventing, e.g.
XX cancer.
XX Disclosure; Page 47; 83pp; English.
XX The invention comprises a vaccine composition that consists of isolated
XX inverted microsomes from an animal cell (or its membrane fragments), in
XX association with an externally disposed peptide antigen and a protein of
XX the MHC. The vaccine composition of the invention is useful for the
XX prophylaxis or treatment of: infection (e.g. viral, bacterial, yeast,
XX fungal or protozoal), cancer (e.g. melanoma, lung adenocarcinoma, colon
XX cancer, breast cancer or leukemia), autoimmune disease (e.g. multiple
XX sclerosis, rheumatoid arthritis or systemic lupus erythematosus). The
XX present amino acid sequence represents a class I HLA-restricted cancer
XX antigen which was found to be expressed by normal spermatocytes and/or
XX spermatogonia of testis.
XX Sequence 9 AA;
SQ

```

Query Match      100.0%; Score 9; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLYDGMHEHL 9
DB      1 GLYDGMHEHL 9
|||||||

RESULT 12
ID AEB01337 standard; peptide; 9 AA.
XX
AC AEB01337;
XX
XX 25-AUG-2005 (first entry)
XX
DE Melanoma protein Mage 10 peptide, SEQ ID 11.
XX
KW Cytostatic; Vaccine; immunotherapy; tumor-associated antigen; cancer.
XX
OS Unidentified.
XX
XX WO2005053738-A1.
XX
PD 16-JUN-2005.
XX
XX 19-NOV-2004; 2004WO-BP014086.
XX
XX 21-NOV-2003; 2003US-0523632P.
XX
XX (INSP ) INST PASTEUR.
XX
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PA (CNRS ) CENT NAT RECH SCI.
XX
XX Dadaglio G, Leclerc C, Ladant D, Van Den Eynde B, Morel S;
XX Bauche C;
XX WPI; 2005-425294/43.
XX
XX Immunogenic composition useful for treating cancer comprises recombinant
XX protein or vector expressing the recombinant protein that has Bordetella
XX adenyate cyclase and peptide corresponding to tumor antigen.
XX
XX Example 5; SEQ ID NO 11; 56pp; English.
XX
XX The present invention relates to a novel immunogenic composition
XX comprising a recombinant protein or vector expressing the recombinant
XX protein, where the recombinant protein comprises Bordetella adenyate
XX cyclase (CyaA) (a), or its fragment, and a peptide (p) that corresponds
XX to a tumor antigen. The Bordetella CyaA is derived from B. pertussis, B.
XX paraptussis or B. bronchiseptica and the tumor antigen is an HLA*0201
XX epitope e.g. AEB01327 or AEB01330. The composition is useful in an
XX immunotherapy for inducing T cell response e.g. cytotoxic T lymphocytic
XX (CTL) response during treatment of cancer e.g. melanoma. The present
XX sequence was used to illustrate the invention.
XX
XX Sequence 9 AA;

Query Match      100.0%; Score 9; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLYDGMHEHL 9
DB      1 GLYDGMHEHL 9
|||||||

RESULT 13
AAY71489
ID AAY71489 standard; peptide; 10 AA.
XX
XX AAY71489;
XX
XX 12-OCT-2000 (first entry)
XX
XX Human MAGE-A10 decapeptide-1.
XX
XX MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
XX HLA; Major Histocompatibility Complex; MHC; Cytolytic T-lymphocyte; CTL;
XX immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
XX cancer; TNF; tumour necrosis factor; vaccine; cytostatic.
XX
XX Homo sapiens.
XX
XX WO200032769-A2.
XX
XX 08-JUN-2000.
XX
XX 26-NOV-1999; 99WO-IB002018.
XX
XX 27-NOV-1998; 98GB-00026143.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
XX WPI; 2000-412317/35.
XX
XX Novel polypeptides expressed in tumor cells useful for treating cancers
XX have an ability to complex with a major histocompatibility complex
XX molecule and comprises a specific unbroken amino acid sequence.
XX
XX Claim 9; Page 37; 80pp; English.
XX
XX The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
XX decapeptide sequences, that function as tumour rejection antigens (TRA).
XX These peptides are capable of forming a complex with major
XX histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
XX Antigen), that are recognised by T-lymphocytes and elicit an immune
XX response from cytolytic T-lymphocytes (CTL). They function as an immune
XX response stimulator. Tumour rejection antigens are useful in prophylaxis,
XX therapy and diagnosis of tumours and are effective in controlling or
XX preventing tumour growth. The present peptide sequence is the human MAGE-
XX A10 decapeptide-1, that corresponds to residues 254-263 of the MAGE-A10
XX protein. This peptide can serve as a tumour rejection antigen (TRA) and
XX in combination with adjuvants, can produce vaccines useful for treating a
XX variety of tumours that express MAGE-A10
XX
XX Sequence 10 AA;

Query Match      100.0%; Score 9; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLYDGMHEHL 9
DB      1 GLYDGMHEHL 9
|||||||

RESULT 14
ADR69766
ID ADR69766 standard; peptide; 20 AA.
XX
XX ADR69766;
XX
XX 18-NOV-2004 (first entry)
XX
XX Novel hybrid antigen-related peptide #1346.
XX
XX hybrid antigen; antigenic domain; infectious agent; tumour antigen;
XX binding domain; heat shock protein; antimicrobial; cytostatic; vaccine;
XX gene therapy; infectious disease; cancer.
XX
XX Unidentified.

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OM protein - protein search, using sw model

Run on: March 18, 2006, 00:21:00 ; Search time 164 Seconds
(without alignments)
22.930 Million call updates/sec

Title: US-09-856-812B-1_COPY_254_262

Perfect score: 9

Sequence: 1 GLYDGMHL 9

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

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Word size : 0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	100.0	9	3	US-09-865-548A-39
2	9	100.0	9	4	US-10-164-121A-13
3	9	100.0	9	4	US-10-164-078A-12
4	9	100.0	9	4	US-10-447-161-29
5	9	100.0	9	5	US-10-651-616-24
6	9	100.0	9	5	US-10-362-715-8
7	9	100.0	9	5	US-10-705-459-39
8	9	100.0	9	5	US-10-776-521B-392
9	9	100.0	9	5	US-10-941-150A-13
10	9	100.0	20	5	US-10-776-521B-398
11	9	100.0	20	5	US-10-820-067A-896
12	9	100.0	369	4	US-10-036-542-84
13	9	100.0	369	4	US-10-188-832-149
14	9	100.0	369	5	US-10-658-884-4
15	9	100.0	369	5	US-10-756-149-4721
16	9	100.0	383	4	US-10-029-386-32058
17	6	66.7	96	4	US-10-767-701-58318
18	6	66.7	122	4	US-10-437-963-182171
19	6	66.7	184	5	US-10-739-930-10984
20	6	66.7	185	4	US-10-425-114-68250
21	6	66.7	190	5	US-10-739-930-10982
22	6	66.7	192	5	US-10-739-930-10983
23	6	66.7	194	4	US-10-425-115-304865
24	6	66.7	241	3	US-09-815-242-13948
25	6	66.7	248	3	US-09-815-242-10247
26	6	66.7	372	4	US-10-425-114-53891
27	6	66.7	383	4	US-10-425-114-59141

28	6	66.7	395	4	US-10-425-115-304870	Sequence 304870,
29	6	66.7	398	3	US-09-905-173-29	Sequence 29, Appl
30	6	66.7	398	4	US-10-060-432-29	Sequence 29, Appl
31	6	66.7	415	4	US-10-437-963-173687	Sequence 173687,
32	6	66.7	471	4	US-10-254-763-12	Sequence 12, Appl
33	6	66.7	476	5	US-10-893-671-43	Sequence 43, Appl
34	6	66.7	562	4	US-10-425-115-352403	Sequence 352403,
35	6	66.7	567	4	US-10-425-114-71829	Sequence 71829, A
36	6	66.7	953	5	US-10-450-763-46089	Sequence 46089, A
37	5	55.6	8	4	US-10-149-138-338	Sequence 338, App
38	5	55.6	8	4	US-10-149-138-901	Sequence 901, App
39	5	55.6	8	4	US-10-149-138-2092	Sequence 2092, Ap
40	5	55.6	8	4	US-10-149-138-2681	Sequence 2681, Ap
41	5	55.6	8	4	US-10-149-138-3329	Sequence 3329, App
42	5	55.6	8	4	US-10-149-138-338	Sequence 338, App
43	5	55.6	8	4	US-10-149-138-901	Sequence 901, App
44	5	55.6	8	4	US-10-149-138-2092	Sequence 2092, Ap
45	5	55.6	8	4	US-10-149-138-2681	Sequence 2681, Ap

ALIGNMENTS

RESULT 1

US-09-865-548A-39
; Sequence 39, Application US/09865548A
; Publication No. US20030096298A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamir
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECUL
; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-39

Query Match 100.0%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GLYDGMHL	9
DB	1	GLYDGMHL	9

RESULT 2

US-10-164-121A-13
; Sequence 13, Application US/10164121A
; Publication No. US20030228308A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Boon, Thierry
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Traversari, Catra
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-Cw6 Molecules And Uses There
; FILE REFERENCE: LUD-5771
; CURRENT APPLICATION NUMBER: US/10/164,121A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 13

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; LENGTH: 9
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-121A-13

Query Match      100.0%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMHGL 9
Db 1 GLYDGMHGL 9

RESULT 3
US-10-164-078A-12
; Sequence 12, Application US/10164078A
; Publication No. US20030228325A1
; GENERAL INFORMATION:
; APPLICANT: Bilsborough, Janine
; APPLICANT: Schultz, Erwin
; APPLICANT: Panichelli, Christophe
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Boon, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B18 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5756
; CURRENT APPLICATION NUMBER: US/10/164,078A
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-078A-12

Query Match      100.0%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMHGL 9
Db 1 GLYDGMHGL 9

RESULT 4
US-10-447-161-29
; Sequence 29, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-29

Query Match      100.0%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMHGL 9

us-09-856-812b-1_copy_254_262.olig.rapbm

Db 1 GLYDGMHGL 9

RESULT 5
US-10-651-616-24
; Sequence 24, Application US/10651616
; Publication No. US20040253235A1
; GENERAL INFORMATION:
; APPLICANT: CytoCure, LLC
; APPLICANT: DURDA, PAUL
; APPLICANT: KURNICK, JAMES T.
; TITLE OF INVENTION: METHODS FOR UP-REGULATING ANTIGEN EXPRESSION IN TUMORS
; FILE REFERENCE: 027823-0305578
; CURRENT APPLICATION NUMBER: US/10/651,616
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 60/407,492
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapien artificial
US-10-651-616-24

Query Match      100.0%; Score 9; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMHGL 9
Db 1 GLYDGMHGL 9

RESULT 6
US-10-362-715-8
; Sequence 8, Application US/10362715
; Publication No. US20040253574A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: Schuler-Thurner, Beatrice
; TITLE OF INVENTION: METHOD FOR READY-TO-USE, ANTIGEN LOADED OR UNLOADED,
; FILE REFERENCE: 1430/12
; CURRENT APPLICATION NUMBER: US/10/362,715
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-715-8

Query Match      100.0%; Score 9; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMHGL 9
Db 1 GLYDGMHGL 9

RESULT 7
US-10-705-459-39
; Sequence 39, Application US/10705459
; Publication No. US20050053918A1
; GENERAL INFORMATION:
; APPLICANT: Barnea , Eilon
```

; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; APPLICANT: Dasseau, Lior
; APPLICANT: Buchsbaum, Samuel
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
; FILE REFERENCE: 26884
; CURRENT APPLICATION NUMBER: US/10/705,459
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 372
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-705-459-39

Query Match 100.0%; Score 9; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHHL 9
Db 1 GLYDGMHHL 9

RESULT 8

US-10-776-521B-392
; Sequence 392, Application US/10776521B
; Publication No. US200502033A1
; GENERAL INFORMATION:
; APPLICANT: Fletchner, Jessica
; APPLICANT: Mehta, Sunil
; APPLICANT: Slusarewicz, Paul
; APPLICANT: Andjelic, Sofija
; APPLICANT: Barber, Brian
; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED VACCINES AND
; TITLE OF INVENTION: IMMUNOTHERAPIES
; FILE REFERENCE: 8449-405-999
; CURRENT APPLICATION NUMBER: US/10/776,521B
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 60/503,417
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/463,746
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/462,469
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/447,142
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 392
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heat shock protein binding domain
US-10-776-521B-392

Query Match 100.0%; Score 9; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHHL 9
Db 1 GLYDGMHHL 9

RESULT 9

US-10-941-150A-13
; Sequence 13, Application US/10941150A
; Publication No. US20050226881A1
; GENERAL INFORMATION:
; APPLICANT: VAN DER BRUGEN, Pierre
; APPLICANT: BOON-FALLEUR, Thierry
; APPLICANT: BRECKPOT, Karine
; APPLICANT: THIELEMAN, Kris
; TITLE OF INVENTION: ISOLATED PEPTIDE WHICH BINDS TO HLA-CW*07 AND USES THEREOF
; FILE REFERENCE: LUD-5853-US (10411307)
; CURRENT APPLICATION NUMBER: US/10/941,150A
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: US 60/504,874
; PRIOR FILING DATE: 2003-09-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from MAGEA10
US-10-941-150A-13

Query Match 100.0%; Score 9; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHHL 9
Db 1 GLYDGMHHL 9

RESULT 10

US-10-776-521B-398
; Sequence 398, Application US/10776521B
; Publication No. US200502033A1
; GENERAL INFORMATION:
; APPLICANT: Fletchner, Jessica
; APPLICANT: Prince-Cohane, Kenya
; APPLICANT: Mehta, Sunil
; APPLICANT: Slusarewicz, Paul
; APPLICANT: Andjelic, Sofija
; APPLICANT: Barber, Brian
; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED VACCINES AND
; TITLE OF INVENTION: IMMUNOTHERAPIES
; FILE REFERENCE: 8449-405-999
; CURRENT APPLICATION NUMBER: US/10/776,521B
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 60/503,417
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/463,746
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/462,469
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/447,142
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 398
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid antigen
US-10-776-521B-398

Query Match 100.0%; Score 9; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGMHHL 9
Db 1 GLYDGMHHL 9

Db 1 GLYDGMHL 9

RESULT 11

US-10-820-067A-896
; Sequence 896, Application US/10820067A
; Publication No. US20050214312A1
; GENERAL INFORMATION:
; APPLICANT: Fletcher, J.
; APPLICANT: Prince-Cohane, K.
; APPLICANT: Mehta, S.
; APPLICANT: Slusarewicz, P.
; APPLICANT: Andjelic, S.
; APPLICANT: Barber, B.
; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED
; TITLE OF INVENTION: VACCINES AND IMMUNOTHERAPIES
; FILE REFERENCE: 8449-406-999
; CURRENT APPLICATION NUMBER: US/10/820,067A
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: 60/462,469
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/463,746
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/503,417
; PRIOR FILING DATE: 2003-09-16
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 896
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid antigen
US-10-820-067A-896

Query Match 100.0%; Score 9; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMHL 9

Db 1 GLYDGMHL 9

RESULT 12

US-10-036-542-84
; Sequence 84, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: PA002P1
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-036-542-84

Query Match 100.0%; Score 9; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMHL 9

Db 254 GLYDGMHL 262

RESULT 13

US-10-188-832-149
; Sequence 149, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-0023300S
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 149
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-149

Query Match 100.0%; Score 9; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMHL 9

Db 254 GLYDGMHL 262

RESULT 14

US-10-658-884-4
; Sequence 4, Application US/10658884
; Publication No. US20050019304A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: NOVEL HUMAN MAGE-LIKE PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 317A Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/658,884
FILING DATE: 09-Sep-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/773,870
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0179 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 533511
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-658-884-4

Query Match 100.0%; Score 9; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.017; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGM EHL 9
|||
Db 254 GLYDGM EHL 262

RESULT 15

US-10-756-149-4721
Sequence 4721, Application US/10756149
Publication No. US20050181375A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
FILE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4721
LENGTH: 369
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-756-149-4721

Query Match 100.0%; Score 9; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.017; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGM EHL 9
|||
Db 254 GLYDGM EHL 262

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Job time : 165 secs

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OM protein - protein search, using sw model

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11.200 Million cell updates/sec

Title: US-09-856-812B-1_COPY_254_262

Perfect score: 9

Sequence: 1 GLYDGMHL 9

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- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	100.0	9	US-10-994-204-11	Sequence 11, Appl
2	9	100.0	9	US-11-032-498-14	Sequence 14, Appl
3	6	66.7	191	US-11-096-568A-574	Sequence 574, App
4	6	66.7	247	US-11-096-568A-573	Sequence 573, App
5	5	55.6	70	US-11-140-024-10	Sequence 10, Appl
6	5	55.6	70	US-11-165-963-10	Sequence 10, Appl
7	5	55.6	118	US-11-098-686-67	Sequence 67, Appl
8	5	55.6	169	US-11-182-908-21	Sequence 21, Appl
9	5	55.6	213	US-11-096-568A-6142	Sequence 6142, Ap
10	5	55.6	216	US-11-098-686-10735	Sequence 10735, A
11	5	55.6	227	US-11-022-562-230	Sequence 230, App
12	5	55.6	235	US-11-130-935-2	Sequence 2, Appli
13	5	55.6	235	US-11-096-568A-6141	Sequence 6141, Ap
14	5	55.6	241	US-10-993-143-14	Sequence 14, Appl
15	5	55.6	245	US-11-096-568A-6140	Sequence 6140, Ap
16	5	55.6	262	US-11-087-099-6500	Sequence 6500, Ap
17	5	55.6	285	US-11-096-568A-21144	Sequence 21144, A
18	5	55.6	295	US-11-096-568A-21143	Sequence 21143, A
19	5	55.6	296	US-11-096-568A-7787	Sequence 7787, Ap
20	5	55.6	301	US-11-096-568A-7786	Sequence 7786, Ap
21	5	55.6	306	US-11-096-568A-7785	Sequence 7785, Ap
22	5	55.6	336	US-11-096-568A-21142	Sequence 21142, A
23	5	55.6	365	US-10-454-437-394	Sequence 394, App
24	5	55.6	376	US-11-096-568A-6980	Sequence 6980, Ap
25	5	55.6	377	US-11-096-568A-6979	Sequence 6979, Ap

26	5	55.6	398	6	US-10-873-528-61	Sequence 61, Appl
27	5	55.6	412	7	US-11-093-808-9	Sequence 9, Appl
28	5	55.6	412	7	US-11-093-808-11	Sequence 11, Appl
29	5	55.6	412	7	US-11-093-808-12	Sequence 12, Appl
30	5	55.6	412	7	US-11-093-808-13	Sequence 13, Appl
31	5	55.6	412	7	US-11-093-808-14	Sequence 14, Appl
32	5	55.6	426	7	US-11-174-150-44	Sequence 44, Appl
33	5	55.6	435	7	US-11-096-568A-6978	Sequence 6978, Ap
34	5	55.6	459	7	US-11-024-959-299	Sequence 299, App
35	5	55.6	475	7	US-11-087-099-1870	Sequence 1870, Ap
36	5	55.6	475	7	US-11-087-099-7571	Sequence 7571, Ap
37	5	55.6	482	7	US-11-087-099-4146	Sequence 4146, Ap
38	5	55.6	525	7	US-11-102-120-13	Sequence 13, Appl
39	5	55.6	530	7	US-11-028-800-2	Sequence 2, Appli
40	5	55.6	577	7	US-11-072-512-3148	Sequence 3148, Ap
41	5	55.6	624	7	US-11-053-100-48	Sequence 48, Appl
42	5	55.6	645	7	US-11-154-337-13	Sequence 13, Appl
43	5	55.6	645	7	US-11-223-361-13	Sequence 13, Appl
44	5	55.6	645	7	US-11-213-557-1	Sequence 1, Appli
45	5	55.6	774	7	US-11-053-100-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-10-994-204-11
; Sequence 11, Application US/10994204
; Publication No. US20050271679A1
; GENERAL INFORMATION:
; APPLICANT: DADAGLIO, GILLES
; APPLICANT: LECLERC, CLAUDE
; APPLICANT: LADANT, DANIEL
; APPLICANT: VAN DEN EYNDE, BENOIT
; APPLICANT: MOREL, SANDRA
; APPLICANT: BAUCHE, CECILE
; TITLE OF INVENTION: RECOMBINANT ADENYLATE CYCLASE TOXIN OF BORDETELLA
; FILE REFERENCE: INDUCES T CELL RESPONSES AGAINST TUMORAL ANTIGENS
; FILE REFERENCE: 03495.0327
; CURRENT APPLICATION NUMBER: US/10/994,204
; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: 60/523,632
; PRIOR FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-994-204-11

Query Match 100.0%; Score 9; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMHL 9

Db 1 GLYDGMHL 9

RESULT 2

US-11-032-498-14
; Sequence 14, Application US/11032498
; Publication No. US20050249743A1
; GENERAL INFORMATION:
; APPLICANT: Boon-Faller, Thierry
; APPLICANT: Van der Bruggen, Pierre
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-A24 Molecule and Uses Thereof;
; FILE REFERENCE: LUD 5881
; CURRENT APPLICATION NUMBER: US/11/032,498

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; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: US 60/535,751
; PRIOR FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MAGE-A10 peptide
US-11-032-498-14

Query Match          100.0%; Score 9; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLYDGMHEHL 9
Db      1 GLYDGMHEHL 9

RESULT 3
US-11-096-568A-574
; Sequence 574, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 574
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(191)
; OTHER INFORMATION: Ceres Seq. ID no. 12634482
US-11-096-568A-574

Query Match          66.7%; Score 6; DB 7; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 YDGMHEH 8
Db      49 YDGMHEH 54

RESULT 4
US-11-096-568A-573
; Sequence 573, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 573
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(247)
; OTHER INFORMATION: Ceres Seq. ID no. 12634481
```

```
US-11-096-568A-573

Query Match          66.7%; Score 6; DB 7; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 YDGMHEH 8
Db      105 YDGMHEH 110

RESULT 5
US-11-140-024-10
; Sequence 10, Application US/11140024
; Publication No. US20060025340A1
; GENERAL INFORMATION:
; APPLICANT: Knopf, John
; TITLE OF INVENTION: CERBERUS/COCO DERIVATIVES AND USES
; FILE REFERENCE: PHPH-P01-005
; CURRENT APPLICATION NUMBER: US/11/140,024
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/575,062
; PRIOR FILING DATE: 2004-05-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-140-024-10

Query Match          55.6%; Score 5; DB 7; Length 70;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 DGMHEH 8
Db      30 DGMHEH 34

RESULT 6
US-11-165-963-10
; Sequence 10, Application US/11165963
; Publication No. US20060030520A1
; GENERAL INFORMATION:
; APPLICANT: Knopf, John
; TITLE OF INVENTION: GDF3 PROPEPTIDES AND RELATED METHODS
; FILE REFERENCE: PHPH-P01-008
; CURRENT APPLICATION NUMBER: US/11/165,963
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: US 60/583,073
; PRIOR FILING DATE: 2004-06-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-165-963-10

Query Match          55.6%; Score 5; DB 7; Length 70;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 DGMHEH 8
Db      30 DGMHEH 34

RESULT 7
```

US-11-098-686-67
; Sequence 67, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(118)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-11-098-686-67

Query Match 55.6%; Score 5; DB 7; Length 118;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDG 5
|||||
DB 58 GLYDG 62

RESULT 8
US-11-182-908-21
; Sequence 21, Application US/11182908
; Publication No. US20060018899A1
; GENERAL INFORMATION:
; APPLICANT: KAO, YUNG-HSIANG
; APPLICANT: VANDERLAAN, MARTIN
; TITLE OF INVENTION: HER2 ANTIBODY COMPOSITIONS
; FILE REFERENCE: P2105R1
; CURRENT APPLICATION NUMBER: US/11/182,908
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 60/590,202
; PRIOR FILING DATE: 2004-07-22
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 21
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-908-21

Query Match 55.6%; Score 5; DB 7; Length 169;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GMEHL 9
|||||
DB 5 GMEHL 9

RESULT 9
US-11-096-568A-6142
; Sequence 6142, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Theryby
; FILE REFERENCE: 2750-1592PUS2

; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6142
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(213)
; OTHER INFORMATION: Ceres Seq. ID no. 14313962
US-11-096-568A-6142

Query Match 55.6%; Score 5; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDG 5
|||||
DB 26 GLYDG 30

RESULT 10
US-11-098-686-10735
; Sequence 10735, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10735
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10735

Query Match 55.6%; Score 5; DB 7; Length 216;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YDGME 7
|||||
DB 146 YDGME 150

RESULT 11
US-11-022-562-230
; Sequence 230, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DEN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 230

```
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Bordetella pertussis
US-11-022-562-230

Query Match          55.6%; Score 5; DB 7; Length 227;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDG 5
Db 84 GLYDG 88

RESULT 12
US-11-130-935-2
; Sequence 2, Application US/11130935
; Publication No. US20050256048A1
; GENERAL INFORMATION:
; APPLICANT: Salvati, Mark
; APPLICANT: Attar, Ricardo M
; APPLICANT: Gottardis, Marco M
; APPLICANT: Kryatek, Stanley R
; APPLICANT: Sack, John S
; TITLE OF INVENTION: SELECTIVE ANDROGEN RECEPTOR MODULATORS AND METHODS FOR THEIR
; TITLE OF INVENTION: IDENTIFICATION, DESIGN AND USE
; FILE REFERENCE: LD0250 Div 1
; CURRENT APPLICATION NUMBER: US/11/130,935
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 09/885,827
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/214,392
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/233,519
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/284,617
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/284,438
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/284,730
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-130-935-2

Query Match          55.6%; Score 5; DB 7; Length 235;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GMEHL 9
Db 208 GMEHL 212

RESULT 13
US-11-096-568A-6141
; Sequence 6141, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6141
; LENGTH: 235
; TYPE: PRT
```

```
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(235)
; OTHER INFORMATION: Ceres Seq. ID no. 14313961
US-11-096-568A-6141

Query Match          55.6%; Score 5; DB 7; Length 235;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDG 5
Db 48 GLYDG 52

RESULT 14
US-10-993-143-14
; Sequence 14, Application US/10993143
; Publication No. US20060036374A1
; GENERAL INFORMATION:
; APPLICANT: California Institute of Technology
; APPLICANT: Debe, Derek A.
; APPLICANT: Goddard III, William A.
; TITLE OF INVENTION: METHOD FOR DETERMINING THREE-DIMENSIONAL PROTEIN STRUCTURE FROM
; TITLE OF INVENTION: PRIMARY PROTEIN SEQUENCE
; FILE REFERENCE: 54318, 8001, US02
; CURRENT APPLICATION NUMBER: US/10/993,143
; CURRENT FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: 60/218,016
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 09/905,176
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-993-143-14

Query Match          55.6%; Score 5; DB 6; Length 241;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GMEHL 9
Db 212 GMEHL 216

RESULT 15
US-11-096-568A-6140
; Sequence 6140, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6140
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(245)
; OTHER INFORMATION: Ceres Seq. ID no. 14313960
US-11-096-568A-6140

Query Match          55.6%; Score 5; DB 7; Length 245;
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Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDG 5
|||
Db 58 GLYDG 62

Search completed: March 18, 2006, 00:24:55
Job time : 24 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 18, 2006, 00:16:25 ; Search time 39 Seconds
(without alignments)
22.204 Million cell updates/sec

Title: US-09-856-812B-1_COPY_254_262

Perfect score: 9

Sequence: 1 GLYDGMHEHL 9

Scoring table: OLIGO)
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- 1: pir1.*
- 2: pir2.*
- 3: pir3.*
- 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	100.0	369	2 I38659	melanoma antigen MAGE-10 - human
2	6	66.7	241	2 AF0818	conserved hypothetical protein STY2737 [imported] - Salmonella enterica subsp. enterica
3	6	66.7	242	2 D40590	transcription init
4	6	66.7	248	2 G65025	probable DNA repli
5	6	66.7	248	2 B85893	probable DNA repli
6	6	66.7	248	2 F91048	probable DNA repli
7	6	66.7	374	2 T06276	benzothiadiazole-i
8	6	66.7	472	2 B82492	tryptophanase VCA0
9	6	66.7	476	1 WZEC	tryptophanase (EC
10	6	66.7	476	2 E91209	tryptophanase [imp
11	6	66.7	476	2 B86055	estrogen receptor
12	5	55.6	80	2 PW0044	ribosomal protein
13	5	55.6	81	2 T02717	ribosomal protein
14	5	55.6	81	2 T03945	ribosomal protein
15	5	55.6	82	2 S33357	ribosomal protein
16	5	55.6	87	2 AH1445	hypothetical prote
17	5	55.6	106	2 D20553	cobyrinic acid a,c
18	5	55.6	145	2 G81094	hypothetical prote
19	5	55.6	152	2 T36058	hypothetical prote
20	5	55.6	169	2 F84259	hypothetical prote
21	5	55.6	173	2 A82935	type I restriction
22	5	55.6	180	2 S27944	ADP-ribosylation f
23	5	55.6	180	2 A23741	ADP-ribosylation f
24	5	55.6	180	2 JC4949	ADP-ribosylation f
25	5	55.6	208	2 H87592	hypothetical prote
26	5	55.6	227	1 F25973	pertussis toxin ch
27	5	55.6	227	1 WEBR31	pertussis toxin ch
28	5	55.6	227	2 E25973	pertussis toxin ch
29	5	55.6	237	2 S64718	formin-binding pro

30	5	55.6	238	2 B97265	alpha-acetolactate
31	5	55.6	266	2 H71521	probable metal dep
32	5	55.6	270	2 C72073	metal dependent hy
33	5	55.6	270	2 C86550	metal dependent hy
34	5	55.6	281	2 AH1327	nicotinate-nucleot
35	5	55.6	281	2 AB1699	nicotinate-nucleot
36	5	55.6	289	2 G89663	nicotinate-nucleot
37	5	55.6	303	2 F95866	probable pyrroloqu
38	5	55.6	304	1 B69449	conserved hypothet
39	5	55.6	305	2 C83687	hypothetical prote
40	5	55.6	316	2 F82320	glutaminase family
41	5	55.6	329	1 IMBKBB	immunogenic protei
42	5	55.6	329	2 AF3351	31K immunogenic pr
43	5	55.6	337	2 A96911	ketol-acid reducto
44	5	55.6	341	2 S72649	sucrose-phosphate
45	5	55.6	341	2 E84156	hypothetical prote

ALIGNMENTS

RESULT 1

I38659

melanoma antigen MAGE-10 - human

C:Species: Homo sapiens (man)

C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004

C:Accession: I38659

R:De Plaen, B.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; B...

con, T.

Immunogenetics 40, 360-369, 1994

A:Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fam

A:Reference number: I38659; MUID:95012457; PMID:7927540

A:Accession: I38659

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-369 <RES>

A:Cross-references: UNIPROT:P43363; UNIPARC:UPI00000000C57; EMBL:U10685; NID:G533510; PI

C:Genetics:

A:Gene: GDB:MAGEA10; MAGE10

A:Cross-references: GDB:331126

A:Map position: Xq28-Xq28

A:Introns: #status absent

C:Superfamily: tumor associated protein MAGE

Query Match 100.0%; Score 9; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGMHEHL 9

DB 254 GLYDGMHEHL 262

RESULT 2

AF0818

conserved hypothetical protein STY2737 [imported] - Salmonella enterica subsp. enterica

C:Species: Salmonella enterica subsp. enterica serovar Typhi

A>Note: this species has also been called Salmonella typhi

C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C:Accession: AF0818

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AF0818

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-241 <PAR>

A:Cross-references: UNIPARC:UPI00000059ABA; GB:AL513382; PIDN:CAD02698.1; PID:G16503714; C:Genetics:

```

A:Gene: STY2737
Query Match          66.7%; Score 6; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGMEHL 9
|||||
Db 99 DGMEHL 104

RESULT 3
D40590
transcription initiation factor sigma, flagellar-specific - Vibrio parahaemolyticus
C:Species: Vibrio parahaemolyticus
C:Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
C:Accession: D40590
R:McCarter, L.L.; Wright, M.E.
J. Bacteriol. 175, 3361-3371, 1993
A:Title: Identification of genes encoding components of the swarmer cell flagellar motor
A:Reference number: A40590; MUID:93273702; PMID:8501040
A:Accession: D40590
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-242 <MCC>
A:Cross-references: UNIPROT:Q03474; UNIPARC:UPI000000A999; GB:U20541; GB:L06177; NID:967
C:Genetics:
A:Gene: lafs
C:Superfamily: transcription initiation factor sigma; transcription initiation factor sigma
C:Keywords: DNA binding; sigma factor; transcription initiation

Query Match          66.7%; Score 6; DB 2; Length 242;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YDGM EH 8
|||||
Db 174 YDGM EH 179

RESULT 4
G65025
probable DNA replication factor b2496 [similarity] - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: G65025
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen,
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: G65025
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-248 <BLAT>
A:Cross-references: UNIPROT:P76570; UNIPARC:UPI000013AE7A; GB:AE0000336; GB:U00096; NID:9
A:Experimental source: strain K-12, substrain MG1655

Query Match          66.7%; Score 6; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGMEHL 9
|||||
Db 106 DGMEHL 111

RESULT 5
B85893
probable DNA replication factor 23759 [imported] - Escherichia coli (strain O157:H7, sub
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: B85893

```

```

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousia, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: B85893
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-248 <STO>
A:Cross-references: UNIPROT:P76570; UNIPARC:UPI000013AE7A; GB:AE0005174; NID:gl2516884; F
A:Experimental source: strain O157:H7, substrain EDU933
C:Genetics:
A:Gene: 23759

Query Match          66.7%; Score 6; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGMEHL 9
|||||
Db 106 DGMEHL 111

RESULT 6
F91048
probable DNA replication factor [imported] - Escherichia coli (strain O157:H7, substrain
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: F91048
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F91048
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-248 <HAV>
A:Cross-references: UNIPROT:P76570; UNIPARC:UPI000013AE7A; GB:BA000007; PIDN:BA036781.1;
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECs3358

Query Match          66.7%; Score 6; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGMEHL 9
|||||
Db 106 DGMEHL 111

RESULT 7
T06276
benzothiadiazole-induced protein (clone WCI-4) - wheat
C:Species: Triticum aestivum (common wheat)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06276
R:Gorlach, J.; Volrath, S.; Knauf-Beiter, G.; Hengy, G.; Beckhove, U.; Kogel, K.H.; Oost
Plant Cell 8, 629-643, 1996
A:Title: Benzothiadiazole, a novel class of inducers of systemic acquired resistance, a
A:Reference number: Z15582; MUID:96206814; PMID:8624439
A:Accession: T06276
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-374 <GOR>
A:Cross-references: UNIPROT:Q41522; UNIPARC:UPI00000A5EB9; EMBL:U52430; NID:gl3232747; PI
A:Experimental source: cv. Kanzler
C:Genetics:
A:Superfamily: papain

Query Match          66.7%; Score 6; DB 2; Length 374;

```

Best Local Similarity 100.0%; Pred. No. 4.9; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0

QY 1 GLYDGM 6
|||||
DB 293 GLYDGM 298

RESULT 8
B82492
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: B82492
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: B82492
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-472 <HEI>
A:Cross-references: UNIPROT:Q9KN05; UNIPARC:UPI00001370A0; GB:AE004357; GB:AE003853; NID
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCA0161
A:Map position: 2
C:Superfamily: tryptophanase

Query Match 66.7%; Score 6; DB 2; Length 472;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGM 6
|||||
DB 321 GLYDGM 326

RESULT 9
WZEC
C:Species: Escherichia coli
C:Date: 14-Nov-1983 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: E65173; A91789; I41097; I69358; A01136
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: E65173
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-476 <BLAT>
A:Cross-references: UNIPROT:P00913; UNIPARC:UPI00000480C7; GB:AE000448; GB:U00096; NID:9
A:Experimental source: strain K-12, substrain MG1655
R:Deeley, M.C.; Yanofsky, C.
J. Bacteriol. 147, 787-796, 1981
A:Title: Nucleotide sequence of the structural gene for tryptophanase of *Escherichia coli* K-12.
A:Reference number: A91789; MUID:82007678; PMID:6268608
A:Accession: A91789
A:Molecule type: DNA
A:Residues: 6-141, 'T', 143, 'QG', 146-383, 'TG', 386-476 <DEE>
A:Cross-references: UNIPARC:UPI0000172P7C
A:Experimental source: strain K-12
R:Kagamiyama, H.; Matsubara, H.; Snell, E.E.
J. Biol. Chem. 247, 1576-1586, 1972
A:Title: The chemical structure of tryptophanase from *Escherichia coli*. III. Isolation and characterization of the active site.
A:Reference number: A92100; MUID:7213434; PMID:4551944
A:Contents: annotation; sequences of tryptic peptides; strain K-12
A:Note: Lys-275 binds pyridoxal 5'-phosphate

R;Tokushige, M.; Tsujimoto, N.; Oda, T.; Honda, T.; Yumoto, N.; Ito, S.; Yamamoto, M.; K. Blochm 71, 711-720, 1989
A:Title: Role of cysteine residues in tryptophanase for monovalent cation-induced activation.
A:Reference number: I41097; MUID:89323226; PMID:2502187
A:Accession: I41097
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 6-383, 'TG', 386-476 <RES>
A:Cross-references: UNIPARC:UPI000016F2BA; EMBL:X15974; NID:G41935; PIDN:CAA34096.1; RID:R
Stewart, V.J.; Yanofsky, C.
J. Bacteriol. 164, 731-740, 1985
A:Title: Evidence for transcription antitermination control of tryptophanase operon expression.
A:Reference number: I54862; MUID:86033334; PMID:3902796
A:Accession: I69358
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 6-27 <RE2>
A:Cross-references: UNIPARC:UPI000016F52C; GB:M11990; NID:G147999; PIDN:AAA24679.1; PID
C:Genetics:
A:Gene: tnaA
A:Map position: 83 min
A:Complex: homotetramer
C:Function:
A:Description: catalyzes the degradation of tryptophan to indole, pyruvate, and ammonia.
C:Superfamily: tryptophanase
C:Keywords: carbon-carbon lyase; homotetramer

Query Match 66.7%; Score 6; DB 1; Length 476;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGM 6
|||||
DB 326 GLYDGM 331

RESULT 10
E91209
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: E91209
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic
A:Reference number: A99629; MUID:21156231; PMID:11256796
A:Accession: E91209
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-476 <HAY>
A:Cross-references: UNIPARC:UPI000016552E; GB:BA000007; PIDN:BAB38068.1; PID:G13364120;
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: EC84645
C:Superfamily: tryptophanase

Query Match 66.7%; Score 6; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGM 6
|||||
DB 326 GLYDGM 331

RESULT 11
H86055
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
A:Accession: H86055
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: H86055
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-476 <STO>
A:Cross-references: UNIPARC:UPI000016552E; GB:AE005174; NID:g12518553; PIDN:AAGS8908.1;
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: tnaA
C:Superfamily: tryptophanase

Query Match 66.7%; Score 6; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDGM 6
Db 326 GLYDGM 331

RESULT 12
PW0044
estrogen receptor beta 1 protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 31-Dec-2004
C:Accession: PW0044

R:Moore, J.T.; McKee, D.D.; Slentz-Kesler, K.; Moore, L.B.; Jones, S.A.; Horne, E.L.; Su Biochem. Biophys. Res. Commun. 247, 75-78, 1998
A:Title: Cloning and characterization of human estrogen receptor beta isoforms.
A:Reference number: PW0044; MUID:98300286; PMID:9636857
A:Accession: PW0044
A:Molecule type: mRNA
A:Residues: 1-80 <MOO>
A:Cross-references: UNIPARC:UPI0000177C04
C:Superfamily: estrogen receptor; erba transforming protein homology

Query Match 55.6%; Score 5; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GMEHL 9
Db 22 GMEHL 26

RESULT 13
T02717
ribosomal protein S21 - maize
C:Species: Zea mays (maize)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T02717
R:Dresselhaus, T.; Loerz, H.; Kranz, E.
submitted to the EMBL Data Library, November 1996
A:Description: Isolation of the Gl-induced ribosomal protein S21 that is differentially
A:Reference number: Z14704
A:Accession: T02717
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-81 <DRE>
A:Cross-references: UNIPROT:P93626; UNIPARC:UPI00000AB6CA; EMBL:Y09636; PIDN:CAA70852.1
C:Superfamily: rat ribosomal protein S21
C:Keywords: protein biosynthesis; ribosome

Query Match 55.6%; Score 5; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDG 5
Db 43 GLYDG 47

RESULT 14
T03945
ribosomal protein S21 - maize
C:Species: Zea mays (maize)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T03945
R:Dresselhaus, T.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z15152
A:Accession: T03945
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-81 <DRE>
A:Cross-references: UNIPROT:Q41852; UNIPARC:UPI0000134E7B; EMBL:X98656; PIDN:CAA67225.1
C:Genetics:
A:Gene: rps21
C:Superfamily: rat ribosomal protein S21
C:Keywords: protein biosynthesis; ribosome

Query Match 55.6%; Score 5; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDG 5
Db 43 GLYDG 47

RESULT 15
S38357
ribosomal protein S21, cytosolic - rice
C:Species: Oryza sativa (rice)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jul-2004
C:Accession: S38357
R:Nishi, R.; Hashimoto, H.; Uchimiya, H.; Kato, A.
Biochim. Biophys. Acta 1216, 113-114, 1993
A:Title: The primary structure of two proteins from the small ribosomal subunit of rice.
A:Reference number: S38356; MUID:94032468; PMID:8218399
A:Accession: S38357
A:Molecule type: mRNA
A:Residues: 1-82 <NIS>
A:Cross-references: UNIPROT:P35687; UNIPARC:UPI0000134E81; GB:D12633; NID:g303838; PIDN:
C:Superfamily: rat ribosomal protein S21
C:Keywords: protein biosynthesis; ribosome

Query Match 55.6%; Score 5; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLYDG 5
Db 43 GLYDG 47

Search completed: March 18, 2006, 00:20:44
Job time : 42 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 18, 2006, 00:13:00 ; Search time 229 Seconds
(without alignments)
27.728 Million cell updates/sec

Title: US-09-856-812B-1_COPY_254_262
Perfect score: 9
Sequence: 1 GLYDGMHL 9

Scoring table: OLIGO3
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Uniprot 05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	100.0	369	1 MAGAA_HUMAN	P43363 homo sapien
2	7	77.8	687	2 Q5ZKJ8 CHICK	Q5ZKJ8 gallus gall
3	6	66.7	171	2 Q9U5B3 CAREEL	Q9U5B3 caenorhabd
4	6	66.7	172	2 Q84QH8 WHEAT	Q84QH8 triticum ae
5	6	66.7	233	1 HDA_PHOLL	Q7N3G5 photorhabdu
6	6	66.7	241	1 HDA_SALTY	Q8xeq0 salmonella
7	6	66.7	241	1 HDA_SALTY	Q7cd21 salmonella
8	6	66.7	241	2 Q57LL3 SALCH	Q57LL3 salmonella
9	6	66.7	241	2 Q5PL41 SALPA	Q03474 vibrio para
10	6	66.7	242	1 LAFS_VTBPA	Q03474 vibrio para
11	6	66.7	248	1 HDA_ECO57	P69333 escherichia
12	6	66.7	248	1 HDA_ECOL6	P69332 escherichia
13	6	66.7	248	1 HDA_ECOL1	P69331 escherichia
14	6	66.7	248	1 HDA_SHIFL	P69331 escherichia
15	6	66.7	284	2 Q5UES4 ECOLI	Q5UES4 shigella fl
16	6	66.7	374	2 Q41522 WHEAT	Q41522 escherichia
17	6	66.7	394	2 Q84EGL1 ORYSA	Q41522 triticum ae
18	6	66.7	444	2 Q8R659 FUSNN	Q94eq1 oryza sativ
19	6	66.7	471	1 TNAA_ECO57	Q8R659 fusobacteri
20	6	66.7	471	1 TNAA_ECOL6	Q8xb34 escherichia
21	6	66.7	471	1 TNAA_ECOL1	Q8fb23 escherichia
22	6	66.7	471	1 TNAA_SHIFL	P0a854 shigella fl
23	6	66.7	472	1 TNAA_VTBCH	Q9kn05 vibrio chol
24	6	66.7	473	1 TNAA_VIBVU	Q8d5q4 vibrio vuln
25	6	66.7	473	1 TNAA_VIBVY	Q5ue88 escherichia
26	6	66.7	476	2 Q5UES8 ECOLI	Q5ue88 escherichia
27	6	66.7	476	2 Q5UEV2 ECOLI	Q5uev2 escherichia
28	6	66.7	476	2 Q5UEV4 ECOLI	Q5uev4 escherichia
29	6	66.7	488	2 Q6LP64 PHOPR	Q6lp64 photobacter
30	6	66.7	497	2 Q5EP68 AZOSE	Q5ep68 azarcus sp
31	6	66.7	535	2 Q88PT0_PSEPK	Q88pt0 pseudomonas

32	6	66.7	1026	2	Q62NU6_BACLD	Q62nu6 bacillus li
33	6	66.7	1036	2	Q65DC5_BACLD	Q65dc5 bacillus li
34	5	55.6	16	1	ARC_D_PSEPU	P41147 pseudomonas
35	5	55.6	36	2	Q5BX80 SCHJA	Q5bx80 schistosoma
36	5	55.6	43	2	Q7WK06 BORBR	Q7wk06 bordetella
37	5	55.6	62	2	Q6LDD8_PSEAE	Q6ldd8 pseudomonas
38	5	55.6	66	2	Q6LMD8_ORYSA	Q6ldm8 oryza sativ
39	5	55.6	72	2	Q8CVC8_STRMU	Q8cvc8 streptococc
40	5	55.6	76	2	Q4GZ87_9TRYP	Q4gz87 trypanosoma
41	5	55.6	81	1	RS21_MAIZE	Q41852 zea mays (m
42	5	55.6	81	2	P93626_MAIZE	P93626 zea mays (m
43	5	55.6	82	1	RS21_ORYSA	P35687 oryza sativ
44	5	55.6	82	2	Q7Y139_ORYSA	Q7y139 oryza sativ
45	5	55.6	87	2	Q92FK1_LISTIN	Q92fk1 listeria in

ALIGNMENTS

RESULT 1
MAGAA_HUMAN STANDARD; PRT; 369 AA.
ID MAGAA_HUMAN
AC P43363;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Melanoma-associated antigen 10 (MAGE-10 antigen).
GN Name=MAGEA10; Synonyms=MAGE10;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95012457; PubMed=7927540;
RA de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,
RA de Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C.,
RA Brasseur R., Chomez P., de Backer O., Cavenee W., Boon T.;
RT "Structure, chromosomal localization, and expression of 12 genes of
RT the MAGE family.";
RL Immunogenetics 40:360-369(1994).
[2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
TX TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Not known, though may play a role in embryonal
CC development and tumor transformation or aspects of tumor
CC progression.
CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
CC such as melanoma, head and neck squamous cell carcinoma, lung
CC carcinoma and breast carcinoma, but not in normal tissues except
CC for testes and placenta.

```

CC -!- SIMILARITY: Contains 1 MAGE domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U10685; AA68869.1; -; Genomic_DNA.
CC EMBL; BC004105; AAH04105.1; -; mRNA.
CC PIR; I38659; I38659.
CC ENSEMBL; ENSG00000124260; Homo sapiens.
CC HGNC; HGNC:6797; MAGEA10.
CC H-InvDB; HIX0017116; -.
CC MIM; 300343; -.
CC InterPro; IPR002190; MAGE.
CC PANTHER; PTHR11736; MAGE; 2.
CC Pfam; PF01454; MAGE; 1.
CC PROSITE; PS50838; MAGE; 1.
KW Antigen; Multigene family; Tumor antigen.
FT DOMAIN 134 333 MAGE.
FT COMPBIAS 54 62 Poly-Ser.
SQ SEQUENCE 369 AA; 40767 MW; 16FA3301CAB716A6 CRC64;
Query Match 100.0%; Score 9; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.0084; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 GLYDGM 9
DB 254 GLYDGM 262
|||||

RESULT 2
Q5ZKJ8 CHICK
ID Q5ZKJ8 CHICK PRELIMINARY; PRT; 687 AA.
AC Q5ZKJ8-
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein.
GN ORFNames=RCJMB04.10e24;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezubov Y., Zaim J.,
RA Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT gene function analysis".
RL Genome Biol. 6:R6-K6(2005).
DR EMBL; AJ720086; CAG31745.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00023; Ank; 8.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR01415; ANKYRIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00248; ANK; 8.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS50297; ANK REP REGION; 1.
DR PROSITE; PS50088; ANK REPEAT; 3.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein.

```

```

SQ SEQUENCE 687 AA; 78261 MW; E8507345476E9DB5 CRC64;
Query Match 77.8%; Score 7; DB 2; Length 687;
Best Local Similarity 100.0%; Pred. No. 3.6; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 GLYDGM 7
DB 366 GLYDGM 372
|||||

RESULT 3
Q9USB3 CAEL
ID Q9USB3 CAEL PRELIMINARY; PRT; 171 AA.
AC Q9USB3-
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein F43C11.1.
GN ORFNames=F43C11.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2; PubMed=9851916;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AC017117; AAF16613.1; -; Genomic_DNA.
DR Ensembl; F43C11.1; Caenorhabditis elegans.
DR WormBase; WBGene0018378; F43C11.1.
DR WormPep; F43C11.1; CE20785.
DR InterPro; IPR003326; DUF130.
DR Pfam; PF02343; DUF130; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 171 AA; 19470 MW; 4649F8EC22CD135C CRC64;
Query Match 66.7%; Score 6; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGM 6
DB 157 GLYDGM 162
|||||

RESULT 4
Q84QH8 WHEAT
ID Q84QH8 WHEAT PRELIMINARY; PRT; 172 AA.
AC Q84QH8-
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative thiol protease (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf;
RA Ray S., Anderson J.M., Urmeev F.I., Goodwin S.B.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DDAJ databases.
CC -!- SIMILARITY: Belongs to the peptidase C1 family.
DR EMBL; AY253445; AAP12731.1; -; mRNA.
DR HSSP; P07711; 1CJL.
DR Gramene; Q84QH8; -.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.

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DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000688; Peptidase_C1.
 DR InterPro; IPR000169; Pept_cys_AS.
 DR Pfam; PF00112; Peptidase_C1; 1.
 DR SMART; SM00645; Pept C1; 1.
 DR PROSITE; PS00640; TH1OL_PROTEASE_ASN; 1.
 KW PROTEASE.
 FT NON_TER 1
 SQ SEQUENCE 172 AA; 19371 MW; 17396PFB60906BD34 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 172;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGM 6
 |||||
 Db 91 GLYDGM 96

RESULT 5
 HDA_PHOLL
 ID HDA PHOLL STANDARD; PRT; 233 AA.
 AC Q7N3G5;
 DT 01-FEB-2005 (Rel. 46, Created)
 DT 01-FEB-2005 (Rel. 46, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE DnaA-homolog protein hda.
 GN Name=hda; OrderedLocNames=plu2752;
 OS Photorhabdus luminescens (subsp. laumondii).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Photorhabdus.
 OX NCBI_TaxID=141679;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=TT01;
 RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
 RA Duchaud E., Ruenrok C., Frangeul L., Buchrieser C., Givaudan A.,
 RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
 RA Dassa E., Derose R., Freysinet S., Freysinet G., Gaudriault S.,
 RA Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V.,
 RA Zouline M., Glaser P., Boemmel N., Danchin A., Kunst F.,
 RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
 RT luminescens.";
 RL Nat. Biotechnol. 21:1307-1313(2003).
 CC -!- FUNCTION: Mediates the interactions of dnaA with the beta subunit
 CC sliding clamp, promoting hydrolysis of dnaA-bound ATP. It is
 CC essential for the control of initiation of DNA replication by
 CC inhibiting re-initiation of replication (By similarity).
 CC -!- SIMILARITY: Belongs to the dnaA family. Hda subfamily.

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 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; BX571868; CAE15126.1; -; Genomic_DNA.
 DR PhotoList; plu2752; -.
 DR HAMAP; MF_01158; -; 1.
 DR InterPro; IPR001957; Bac_DnaA.
 DR PRINTS; PR00051; DNAA.
 KW Complete proteome; DNA replication.
 SQ SEQUENCE 233 AA; 26533 MW; 0A51601393CBD9A0 CRC64;

Query Match 66.7%; Score 6; DB 1; Length 233;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGMHEHL 9
 |||||
 Db 91 DGMHEHL 96

RESULT 7
 HDA_SALTY
 ID HDA_SALTY STANDARD; PRT; 241 AA.
 AC Q7CQ21;
 DT 01-FEB-2005 (Rel. 46, Created)
 DT 01-FEB-2005 (Rel. 46, Last sequence update)

RESULT 6
 HDA_SALTY
 ID HDA_SALTY STANDARD; PRT; 241 AA.
 AC Q8XEQ0; Q7AM18;
 DT 01-FEB-2005 (Rel. 46, Created)
 DT 01-FEB-2005 (Rel. 46, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE DnaA-homolog protein hda.
 GN Name=hda; OrderedLocNames=STV2737, t0361;
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=601;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Ty2 / ATCC 700931;
 RX MEDLINE=22531367; PubMed=12644504;
 DOI=10.1128/JB.185.7.2330-2337.2003;
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
 RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
 RT and CT18.";
 RL J. Bacteriol. 185:2330-2337(2003).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., K.,
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrall B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 CC -!- FUNCTION: Mediates the interactions of dnaA with the beta subunit
 CC sliding clamp, promoting hydrolysis of dnaA-bound ATP. It is
 CC essential for the control of initiation of DNA replication by
 CC inhibiting re-initiation of replication (By similarity).
 CC -!- SIMILARITY: Belongs to the dnaA family. Hda subfamily.

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 CC EMBL; AE016835; AAO68080.1; -; Genomic_DNA.
 DR EMBL; AL627275; CAD02698.1; -; Genomic_DNA.
 DR HAMAP; MF_01158; -; 1.
 DR InterPro; IPR001957; Bac_DnaA.
 DR PRINTS; PR00051; DNAA.
 KW Complete proteome; DNA replication.
 SQ SEQUENCE 241 AA; 27472 MW; F27B42EF7FAAA63E CRC64;

Query Match 66.7%; Score 6; DB 1; Length 241;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGMHEHL 9
 |||||
 Db 99 DGMHEHL 104

RESULT 7
 HDA_SALTY
 ID HDA_SALTY STANDARD; PRT; 241 AA.
 AC Q7CQ21;
 DT 01-FEB-2005 (Rel. 46, Created)
 DT 01-FEB-2005 (Rel. 46, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE DnaA-homolog protein hda.
 GN Name=hda; OrderedLocusNames=STW2496;
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 LT2.";
 RL Nature 413:852-856(2001).
 CC -!- FUNCTION: Mediates the interactions of dnaA with the beta subunit
 CC sliding clamp, promoting hydrolysis of dnaA-bound ATP. It is
 CC essential for the control of initiation of DNA replication by
 CC inhibiting re-initiation of replication (By similarity).
 CC -!- SIMILARITY: Belongs to the dnaA family. Hda subfamily.
 CC -----
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AE008812; AAL21390.1; -; Genomic_DNA.
 DR StyGene; SGR????; hda.
 DR HAMAP; MF_01158; -; 1.
 DR InterPro; IPR001957; Bac_DnaA.
 DR PRINTS; PR00051; DNA.
 KW Complete proteome; DnaA replication.
 SQ SEQUENCE 241 AA; 27472 MW; F27B42EF7FAAA63E CRC64;

 Query Match 66.7%; Score 6; DB 1; Length 241;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 4 DGMHLL 9
 DB 99 DGMHLL 104

 RESULT 8
 Q57LL3 SALCH PRELIMINARY; PRT; 241 AA.
 AC Q57LL3;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Putative ATPase involved in DNA replication initiation.
 GN Name=yfgg; OrderedLocusNames=SC2493;
 OS Salmonella cholerae-suis (Salmonella enterica).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=591;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=SC-B67;
 RX PubMed=15781495;
 RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
 RA Wang H.-S., Lee Y.-S.;
 RT "The genome sequence of Salmonella enterica serovar Choleraesuis, a
 RT highly invasive and resistant zoonotic pathogen.";
 RL Nucleic Acids Res. 33:1690-1698(2005).
 DR EMBL; AE017220; AAX66399.1; -; Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 241 AA; 27471 MW; F27B42EF7FAAA63E CRC64;

Query Match 66.7%; Score 6; DB 2; Length 241;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 4 DGMHLL 9
 DB 99 DGMHLL 104

 RESULT 9
 Q5PL41 SALPA PRELIMINARY; PRT; 241 AA.
 AC Q5PL41;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Hypothetical protein yfge.
 GN Name=yfge; OrderedLocusNames=SPA0371;
 OS Salmonella paratyphi-a.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=54388;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 9150;
 RX PubMed=15531882; DOI=10.1038/ngl470;
 RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
 RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., Mclellan M.,
 RA Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
 RA Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,
 RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,
 RA Delehaanty K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
 RA Spieth J., Wilson R.K.;
 RT "Comparison of genome degradation in Paratyphi A and Typhi, human-
 RT restricted serovars of Salmonella enterica that cause typhoid.";
 RL Nat. Genet. 36:1268-1274(2004).
 DR EMBL; CP000026; AAV76384.1; -; Genomic_DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003688; F:DNA replication origin binding; IEA.
 DR GO; GO:0006260; F:DNA replication; IEA.
 DR GO; GO:0006270; F:DNA replication initiation; IEA.
 DR GO; GO:0006275; P:regulation of DNA replication; IEA.
 DR InterPro; IPR001957; Bac_DnaA.
 DR PRINTS; PR00051; DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 241 AA; 27531 MW; E8D1E7EF7FAAA22P CRC64;

 Query Match 66.7%; Score 6; DB 2; Length 241;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 4 DGMHLL 9
 DB 99 DGMHLL 104

 RESULT 10
 LAFS_VIBPA STANDARD; PRT; 242 AA.
 AC Q03474;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE RNA polymerase sigma factor for flagellar operon (Sigma-P factor)
 DE (Sigma-27).
 GN Name=lafs; OrderedLocusNames=VPA1555;
 OS Vibrio parahaemolyticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 CC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=670;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.


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RC STRAIN=BB22;
RX MEDLINE=93273702; PubMed=8501040;
RA McCarter L.L., Wright M.B.;
RT "Identification of genes encoding components of the swarmer cell
RT flagellar motor and propeller and a sigma factor controlling
RT differentiation of Vibrio parahaemolyticus.";
RL J. Bacteriol. 175:3361-3371 (1993).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=H7; DOI=10.1016/S0140-6736(03)12659-1;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749 (2003).
CC -!- FUNCTION: Sigma factors are initiation factors that promote the
CC attachment of RNA polymerase to specific initiation sites and are
CC then released. This alternative sigma factor is specific for the
CC flagellin gene (fliC) expression.
CC -!- INDUCTION: Under conditions in which the polar flagellum is not
CC functional.
CC -!- SIMILARITY: Belongs to the sigma-70 factor family.
CC
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CC
CC EMBL; U20541; AAA62353.1; -; Genomic DNA.
CC EMBL; U52957; AAB07356.1; -; Genomic DNA.
CC EMBL; BA000032; BAC62898.1; -; Genomic DNA.
CC PIR; D40590; D40590.
CC InterPro; IPR012845; Flia_WhiG.
CC InterPro; IPR007627; Sigma70_r2.
CC InterPro; IPR007630; Sigma70_r4.
CC InterPro; IPR000943; Sigma70.
CC Pfam; PF04542; Sigma70_r2; 1.
CC Pfam; PF04545; Sigma70_r4; 1.
CC PRINTS; PR00046; SIGMA70FCT.
CC TIGRfam; TIGR02479; Flia_WhiG; 1.
CC PROSITE; PS00715; SIGMA70_1; FALSE_NEG.
CC PROSITE; PS00716; SIGMA70_2; 1.
CC Complete proteome; DNA-binding; DNA-directed RNA polymerase;
CC Nucleotidyltransferase; Sigma factor; Transcription;
CC Transcription regulation; Transferase.
CC FT DNA_BIND 211 230 H-R-H motif (By similarity).
CC FT MOTIF 55 68 Polymerase core binding (potential).
CC SEQUENCE 242 AA; 27835 MW; 39A3C7152DE2FC95 CRC64;

Query Match 66.7%; Score 6; DB 1; Length 242;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YDGMH 8
DB 174 YDGMH 179
|||||
HDA_ECO57
PRT; 248 AA.
ID HDA_ECO57 STANDARD; PRT; 248 AA.
AC P69333; P76570; P76979;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE DnaA-homolog protein hda.
GN Name=hda; OrderedLocNames=z3759, ECe33358;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.

RESULT 11
HDA_ECO57
PRT; 248 AA.
ID HDA_ECO57 STANDARD; PRT; 248 AA.
AC P69333; P76570; P76979;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE DnaA-homolog protein hda.
GN Name=hda; OrderedLocNames=c3013;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.

Query Match 66.7%; Score 6; DB 1; Length 248;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGMH 9
DB 106 DGMH 111
|||||
HDA_ECOL6
PRT; 248 AA.
ID HDA_ECOL6 STANDARD; PRT; 248 AA.
AC P69332; P76570; P76979;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE DnaA-homolog protein hda.
GN Name=hda; OrderedLocNames=c3013;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O6.H1 / CFT073 / ATCC 700928 / UPEC;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

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RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
CC -!- FUNCTION: Mediates the interactions of dnaA with the beta subunit
CC sliding clamp, promoting hydrolysis of dnaA-bound ATP. It is
CC essential for the control of initiation of DNA replication by
CC inhibiting re-initiation of replication (By similarity).
CC -!- SIMILARITY: Belongs to the dnaA family. Hda subfamily.
CC -----
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CC removed.
CC -----
DR EMBL; AE016764; AAN81463.1; -; Genomic_DNA.
DR HAMAP; MF_01158; -; 1.
DR InterPro; IPR001957; Bac_DnaA.
DR PRINTS; PR00051; DNAA.
KW Complete proteome; DNA replication.
SQ SEQUENCE 248 AA; 28370 MW; A8FDFB3C5813681E CRC64;

Query Match 66.7%; Score 6; DB 1; Length 248;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGMHLL 9
DB 106 DGMHLL 111

RESULT 13
HDA_ECOLI STANDARD; PRT; 248 AA.
AC P69331; P76570; P76979;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE DnaA-homolog protein hda.
GN Name=hda; OrderedLocusNames=b2496;
OS Escherichia coli
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K12; MG1655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K12;
RX MEDLINE=97349980; PubMed=9205837;
RA Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Nakano K., Miki T., Mitsuhashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,
RA Oshima T., Oyama S., Saio N., Sampei G., Satoh Y., Sivasubaram S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horiuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli-
RT K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
RN [3]
RP FUNCTION.

```

```

RX PubMed=11483528; DOI=10.1093/emboj/20.15.4253;
RA Kato J., Katayama T.;
RT "Hda, a novel DnaA-related protein, regulates the replication cycle in
RT Escherichia coli.";
RL EMBO J. 20:4253-4262(2001).
RN [4]
RP FUNCTION.
RX PubMed=12730188; DOI=10.1128/JB.185.10.3244-3248.2003;
RA Camara J.E., Skarstad K., Crooke E.;
RT "Controlled initiation of chromosomal replication in Escherichia coli
RT requires functional Hda protein.";
RL J. Bacteriol. 185:3244-3248(2003).
CC -!- FUNCTION: Mediates the interactions of dnaA with the beta subunit
CC sliding clamp, promoting hydrolysis of dnaA-bound ATP. It is
CC essential for the control of initiation of DNA replication by
CC inhibiting re-initiation of replication.
CC -!- INTERACTION:
CC P00583:dnaN; NbExp=1; IntAct=EBI-545453; EBI-542385;
CC P31600:nfrA; NbExp=1; IntAct=EBI-545453; EBI-545461;
CC P30302:rho; NbExp=1; IntAct=EBI-545453; EBI-545468;
CC P0A7K2:rpL; NbExp=1; IntAct=EBI-545453; EBI-543702;
CC P0A7N9:rpMg; NbExp=1; IntAct=EBI-545453; EBI-542475;
CC P0A7V0:rpB; NbExp=1; IntAct=EBI-545453; EBI-543439;
CC P0A7R5:rpBj; NbExp=1; IntAct=EBI-545453; EBI-544602;
CC Q47536:yajp; NbExp=1; IntAct=EBI-545453; EBI-545560;
CC P33915:yejE; NbExp=1; IntAct=EBI-545453; EBI-545567;
CC -!- SIMILARITY: Belongs to the dnaA family. Hda subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U00096; AAC75549.1; -; Genomic_DNA.
DR EMBL; D90878; BAA16384.1; ALT_INIT; Genomic_DNA.
DR PIR; G65025; G65025.
DR InterAct; P69931; -.
DR EchoBASE; EB3953; -.
DR EcoGene; EG14201; hda.
DR HAMAP; MF_01158; -; 1.
DR InterPro; IPR001957; Bac_DnaA.
DR PRINTS; PR00051; DNAA.
KW Complete proteome; DNA replication.
SQ SEQUENCE 248 AA; 28370 MW; A8FDFB3C5813681E CRC64;

Query Match 66.7%; Score 6; DB 1; Length 248;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGMHLL 9
DB 106 DGMHLL 111

RESULT 14
HDA_SHIFL STANDARD; PRT; 248 AA.
ID HDA_SHIFL
AC P69334; P76570; P76979;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE DnaA-homolog protein hda.
GN Name=hda; OrderedLocusNames=SP2540, S2689;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=2227406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,

```

RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RX DOI=10.1128/JAI.71.5.2775-2786.2003;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786 (2003).
CC -!- FUNCTION: Mediates the interactions of dnaA with the beta subunit
CC sliding clamp, promoting hydrolysis of dnaA-bound ATP. It is
CC essential for the control of initiation of DNA replication by
CC inhibiting re-initiation of replication (By similarity).
CC -!- SIMILARITY: Belongs to the dnaA family. Hda subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE005674; AAN44041.1; -; Genomic DNA.
CC EMBL; AE016986; AAP17851.1; -; Genomic DNA.
CC HAMAP; MF 01158; -; 1.
CC InterPro: IPR001957; Bac_DnaA.
CC PRINTS; PR00051; DNAA.
KW Complete proteome; DNA replication.
SQ SEQUENCE 248 AA; 28370 MW; A8FDFB3C5813691E CRC64;

Query Match 66.7%; Score 6; DB 1; Length 248;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DGMHLL 9
DB 106 DGMHLL 111

RESULT 15
QSUES4 ECOLI
ID QSUES4 ECOLI PRELIMINARY; PRT; 284 AA.
AC QSUES4;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Tryptophanase (Fragment).
GN Name=tnaA;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=M1367 D10;
RX PubMed=15489459; DOI=10.1128/JB.186.21.7460-7465.2004;
RA Rezwan F., Ian R., Reeves P.R.;
RT "Molecular basis of the indole-negative reaction in Shigella strains:
RT extensive damages to the tna operon by insertion sequences.";
RL J. Bacteriol. 186:7460-7465 (2004).
RL EMBL; AY746494; AAV34671.1; -; Genomic DNA.
DR GO; GO:0016829; F1yase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro: IPR001597; Beta_elim_lyase.

DR InterPro: IPR011166; TNase.
DR Pfam; PF01212; Beta_elim_lyase; 1.
DR PRODom; PD005927; Beta_elim_lyase; 1.
DR PROSITE; PS00953; BETA_ELIM_LYASE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 284 AA; 31502 MW; 2E48D2C23C7FDC2B CRC64;

Query Match 66.7%; Score 6; DB 2; Length 284;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLYDGM 6
DB 134 GLYDGM 139

Search completed: March 18, 2006, 00:20:04
Job time : 236 secs

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GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 17, 2006, 23:53:49 ; Search time 27.9 Seconds
(without alignments)
1842.556 Million cell updates/sec

Title: US-09-856-812B-7_COPY_334_918
Perfect score: 195
Sequence: 1 atgcctcgagctccaaagc.....ttgatgtaaggagtgatggaat 585

Scoring table: OLIgo
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4589790

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
-MODE=frame+n2p.model -DEV=xlp
-Q=abss/ABSSWEB spool/US09856812/runat_17032006_150554_5439/app_query.fasta_1
-DB=A_Geneseq -QFM=fastan -SUFFIX=n2p_olig.rag -MINWATCH=0.1 -LOOPCPU=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abes02p
-USER=US09856812 @CGN 1 1 348 @runat_17032006_150554_5439 -NCPU=3
-NO_WMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : A_Geneseq.21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	195	100.0	369	3 AAY71485	Aay71485 Human MAG
2	195	100.0	369	4 AAB80297	Aab80297 Human pro
3	195	100.0	369	6 ABR48215	AbR48215 Human bla
4	195	100.0	369	6 ABU56516	Abu56516 Lung canc
5	195	100.0	383	8 ABO58424	AbO58424 Human gen
6	12	6.2	211	8 ADU02782	Adu02782 Novel hum
7	12	6.2	260	8 ABO59740	AbO59740 Human gen
8	12	6.2	525	8 ADO26850	AdO26850 Human rec
9	12	6.2	759	3 AAY99487	Aay99487 Yeast acy

10	12	6.2	856	3 AAB27656	Aab27656 Human pro
11	12	6.2	856	5 ABB84833	Abb84833 Human PRO
12	12	6.2	856	5 ABB95439	Abb95439 Human ang
13	12	6.2	856	7 ADD10323	Add10323 Human sec
14	12	6.2	856	7 ADD11283	Add11283 Human sec
15	12	6.2	856	7 ADD37076	Add37076 Human sec
16	12	6.2	856	8 ADA11284	Ada11284 Human sec
17	12	6.2	856	8 ADH43467	Adh43467 Human PRO
18	12	6.2	856	8 ADK82812	Adk82812 Human PRO
19	12	6.2	898	8 ABM83008	Abm83008 Human dia
20	12	6.2	939	8 ABM83006	Abm83006 Human dia
21	12	6.2	1006	2 AAW70525	Aaw70525 Human thy
22	12	6.2	1006	2 AAW72256	Aaw72256 Human rec
23	12	6.2	1006	7 ADN40057	Adn40057 Cancer/an
24	12	6.2	1006	8 ADP12416	Adp12416 Protein e
25	12	6.2	1021	2 AAW70526	Aaw70526 Human thy
26	12	6.2	1061	8 ABM83005	Abm83005 Human dia
27	12	6.2	2166	4 ABB64769	Abb64769 Drosophil
28	11	5.6	20	3 ABA45163	AbA45163 Human sec
29	11	5.6	52	4 ABG27886	Abg27886 Novel hum
30	11	5.6	69	4 AAM18311	Aam18311 Peptide #
31	11	5.6	69	4 ABB37344	Abb37344 Peptide #
32	11	5.6	69	4 AAM30795	Aam30795 Peptide #
33	11	5.6	69	4 ABB32089	Abb32089 Peptide #
34	11	5.6	69	4 ABB22632	Abb22632 Protein #
35	11	5.6	69	4 AAM70474	Aam70474 Human bon
36	11	5.6	69	4 AAM58033	Aam58033 Human bra
37	11	5.6	69	4 ABG52159	Abg52159 Human liv
38	11	5.6	69	4 AAM05917	Aam05917 Peptide #
39	11	5.6	69	5 ABG40113	Abg40113 Human pep
40	11	5.6	76	8 ABO56430	AbO56430 Human gen
41	11	5.6	99	5 ABP58958	Abp58958 Human zin
42	11	5.6	111	4 ABG11273	Abg11273 Novel hum
43	11	5.6	113	5 ABP41890	Abp41890 Human ova
44	11	5.6	148	5 ADK34937	Adk34937 Novel hum
45	11	5.6	166	6 ABU61024	Abu61024 Human ova

ALIGNMENTS

RESULT 1
AAY71485
ID AAY71485 standard; protein; 369 AA.
XX
AC AAY71485;
DT 12-OCT-2000 (first entry)
DE Human MAGE-A10 protein.
XX
KW MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen; HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL; immune response stimulator; prophylaxis; therapy; diagnosis; tumour; cancer; TNF; tumour necrosis factor; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200032769-A2.
XX
PD 08-JUN-2000.
XX
PF 26-NOV-1999; 99WO-IB002018.
XX
PR 27-NOV-1998; 98GB-00026143.
XX
(LUDW-) LUDWIG INST CANCER RES.
XX
HU Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
WPI: 2000-412317/35.
DR N-PSDB; AAD01311, AAD01312, AAD01313.
PT Novel polypeptides expressed in tumor cells useful for treating cancers


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DB: 4 Gaps: 0
US-09-856-812B-7_COPY_334_918 (1-585) x AAB80297 (1-369)
QY 1 ATGCTTCGAGCTCCAAAGCGTCAGCGCTGCATGCTCCGTAAGAGATCTTCAATCCCAAGT 60
DB 1 MetProArgAlaProLysArgGlnArgCysMetProGluGluAspLeuGlnSerGlnSer 20
QY 61 GAGACACAGGGCTCGAGGGTGCACAGGCTCCCTCGCTGTGTGGAGGAGGATGCTTCATCA 120
DB 21 GluThrGlnGlyLeuGluGlyAlaGlnAlaProLeuAlaValGluGluAspAlaSerSer 40
QY 121 TCCACTTCACAGCTCCTTTTCCATCTCTTTTCCCTCTCTCTCTCTCTCTCTCTCTCTCC 180
DB 41 SerThrSerThrSerPheProSerSerPheProSerSerPheProSerSerSerSerSer 60
QY 181 TCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 61 SerSerCysTyrProLeuLeuProSerThrProGluGluValSerAlaAspGluThr 80
QY 241 CCAAAATCTCCCGAGAGTCTCAGATAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
DB 81 ProAsnProGlnSerAlaGlnIleAlaCysSerSerProSerValValAlaSerLeu 100
QY 301 CCAATTAGATCAATCTGCTTTCAGTATCAATGAGAGGCCGATCAAAAGGCAGAAATA 360
DB 101 ProLeuAspGlnSerAspGluGlySerSerGlnLysGluGluSerProSerThrLeu 120
QY 361 CAGGTCCTGCCACAGACAGTGAGTCTTTTACCCAGAAGTGAGATGAAAAGGTGACTGAT 420
DB 121 GlnValLeuProAspSerGluSerLeuProArgSerGluIleAspGluLysValThrAsp 140
QY 421 TTGGTGCGAGTTTCTGCTCTTCAAGTATCAATGAGAGGCCGATCAAAAGGCAGAAATA 480
DB 141 LeuValGlnPheLeuLeuPheLysTyrGlnMetLysGluProIleThrLysAlaGluIle 160
QY 481 CTGGAGAGTGTCTATAAAAAATATGAAGACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
DB 161 LeuGluSerValIleLysAsnTyrGluAspHisPheProLeuLeuPheSerGluAlaSer 180
QY 541 GAGTGCATCTCTGCTCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCT 585
DB 181 GluCysMetLeuLeuValPheGlyIleAspValLysGluValAsp 195
RESULT 3
ID ABR48215
XX ABR48215 standard; protein; 369 AA.
AC ABR48215;
XX
XX 12-JUN-2003 (first entry)
DE Human bladder cancer associated protein sequence SEQ ID NO:149.
XX
XX Human; bladder cancer; cytostatic; gene therapy; vaccine.
XX
XX Homo sapiens.
XX
XX WO200303906-A2.
XX
XX 16-JAN-2003.
XX
XX 03-JUL-2002; 2002WO-US021338.
XX
XX 03-JUL-2001; 2001US-0302814P.
XX
XX 03-AUG-2001; 2001US-0310099P.
XX
XX 08-NOV-2001; 2001US-0343705P.
XX
XX 13-NOV-2001; 2001US-0350666P.
XX
XX 12-APR-2002; 2002US-0372246P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Mack DH, Aziz N;
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```
XX WPI; 2003-201532/19.
DR N-PSDB; ACC51029.
XX
PT Detecting a bladder cancer-associated transcript in a cell from a
PT patient, comprises contacting a biological sample from the patient with a
PT bladder cancer-associated polynucleotide or antibody.
XX
XX Claim 10; Page 282; 307pp; English.
XX
XX The present invention describes a method for detecting a bladder cancer-
XX associated transcript in a cell from a patient. The method comprises
XX contacting a biological sample from the patient with a polynucleotide
XX that selectively hybridizes to a sequence that is 80 % identical to a
XX table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
XX encodes the human bladder cancer-associated proteins given in ABR48146 to
XX ABR48242). Bladder cancer-associated sequences from the present invention
XX have cytostatic activities, and can be used in antisense gene therapy and
XX in vaccine production. The method can be used for detecting a bladder
XX cancer-associated transcript in a cell from a patient. The method is
XX useful in diagnosing or treating bladder cancer and in screening for
XX compounds that modulate bladder cancer, such as hormones or antibodies.
XX The nucleic acid molecules from the present invention may be used in
XX various screening and diagnostic methods, and for gene therapy, vaccine
XX and/or antisense/inhibition applications
XX
XX Sequence 369 AA;
SQ
Alignment Scores:
Pred. No.: 7 5e-165 Length: 369
Score: 195.00 Matches: 195
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0
US-09-856-812B-7_COPY_334_918 (1-585) x ABR48215 (1-369)
QY 1 ATGCTTCGAGCTCCAAAGCGTCAGCGCTGCATGCTCCGTAAGAGATCTTCAATCCCAAGT 60
DB 1 MetProArgAlaProLysArgGlnArgCysMetProGluGluAspLeuGlnSerGlnSer 20
QY 61 GAGACACAGGGCTCGAGGGTGCACAGGCTCCCTCGCTGTGTGGAGGAGGATGCTTCATCA 120
DB 21 GluThrGlnGlyLeuGluGlyAlaGlnAlaProLeuAlaValGluGluAspAlaSerSer 40
QY 121 TCCACTTCACAGCTCCTTTTCCATCTCTTTTCCCTCTCTCTCTCTCTCTCTCTCTCTCC 180
DB 41 SerThrSerThrSerSerPheProSerSerPheProSerSerPheProSerSerSerSer 60
QY 181 TCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 61 SerSerCysTyrProLeuLeuProSerThrProGluGluValSerAlaAspGluThr 80
QY 241 CCAAAATCTCCCGAGAGTCTCAGATAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
DB 81 ProAsnProGlnSerAlaGlnIleAlaCysSerSerProSerValValAlaSerLeu 100
QY 301 CCAATTAGATCAATCTGAGGGCTCCAGAGCCCAAAAGGCAGAGAGTCCAGACCCCTA 360
DB 101 ProLeuAspGlnSerAspGluGlySerSerGlnLysGluGluSerProSerThrLeu 120
QY 361 CAGGTCCTGCCACAGACAGTGAGTCTTTTACCCAGAAGTGAGATGAAAAGGTGACTGAT 420
DB 121 GlnValLeuProAspSerGluSerLeuProArgSerGluIleAspGluLysValThrAsp 140
QY 421 TTGGTGCGAGTTTCTGCTCTTCAAGTATCAATGAGAGGCCGATCAAAAGGCAGAAATA 480
DB 141 LeuValGlnPheLeuLeuPheLysTyrGlnMetLysGluProIleThrLysAlaGluIle 160
QY 481 CTGGAGAGTGTCTATAAAAAATATGAAGACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
DB 161 LeuGluSerValIleLysAsnTyrGluAspHisPheProLeuLeuPheSerGluAlaSer 180
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QY 541 GAGTGCATGCTGCTGCTTTCGTCATTGATGTAAGAGAGTGGAT 585
Db 181 GluCysMetLeuValPheGlyIleAspValLysGluValAsp 195

RESULT 4

ABU56516
ID ABU56516 standard; protein; 369 AA.

AC ABU56516;

XX 02-APR-2003 (first entry)

XX Lung cancer-associated polypeptide #109.

XX Lung cancer-associated polypeptide; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX Unidentified.

XX WO200286443-A2.

XX 31-OCT-2002.

XX 18-APR-2002; 2002WO-US012476.

XX 18-APR-2001; 2001US-0284770P.

XX 10-MAY-2001; 2001US-0290492P.

XX 09-NOV-2001; 2001US-0339245P.

XX 13-NOV-2001; 2001US-0350866P.

XX 29-NOV-2001; 2001US-0334370P.

XX 12-APR-2002; 2002US-0372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Aziz N, Murray R;

XX WPI; 2003-093161/08.

XX N-PSDB; ABX76240.

XX Detecting a lung cancer-associated transcript in a cell from a patient
XX for treating lung cancer, by contacting a biological sample from the
XX patient with a polynucleotide that exhibits increased or decreased
XX expression in lung cancer.

XX Claim 27; Page 276-277; 453pp; English.

XX The invention relates to a method for detecting a lung cancer-associated
XX transcript in a cell from a patient, comprising contacting a biological
XX sample from the patient with a polynucleotide that selectively hybridizes
XX to a sequence that is at least 80 % identical to a gene that exhibits
XX increased or decreased expression in lung cancer samples. Lung cancer-
XX associated polynucleotides and polypeptides are used for identifying a
XX compound that modulates a lung cancer-associated polypeptide, for
XX inhibiting proliferation of a lung cancer-associated cell to treat lung
XX cancer in a patient and for treating a mammal having lung cancer by
XX administering a modulatory compound identified. The methods are useful
XX for treating lung cancer, such as small cell lung cancer, non-small cell
XX lung cancer or other benign or precancerous lesions, e.g. atelectasis,
XX emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
XX hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
XX bronchiectasis. The genes, polynucleotides and polypeptides are useful
XX for diagnostic purposes and as targets for screening for therapeutic
XX compounds that modulate lung cancer, such as antibodies. Sequences
XX ABU56408-ABU56745 represent lung cancer-associated polypeptides of the
XX invention

XX Sequence 369 AA;

XX Alignment Scores:

Pred. No.: 7.5e-165 Length: 369
Score: 195.00 Matches: 195
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

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QY 301 CCATTAGATCAATCTGATGAGGGCTCCAGCAGCCAAAGAGAGAGTCCAGCACCCCTA 360

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QY 421 TTGGTGCAGTTTCTGCTCTTCAAGTATCAATGAGAGGCCGATCAAAAGGCAGAAATA 480

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QY 481 CTGAGAGTGTCTATAAAAAATTATGAGACCACTTCCCTTTTGTGTTTGTAGTAGAGCTCC 540

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QY 541 GAGTGCATGCTGCTGCTCTTTGTCATTGATGTAAGAGAGTGGAT 585

Db 181 GluCysMetLeuValPheGlyIleAspValLysGluValAsp 195

RESULT 5

ABO58424

ID ABO58424 standard; protein; 383 AA.

XX ABO58424;

XX 29-JUL-2004 (first entry)

XX Human genome derived single exon protein #4658.

XX Human; gene expression; single exon probe; microarray;

XX alternative splicing event; genomic alteration.

XX Homo sapiens.

XX US2003194704-A1.

XX 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX (PENN/) PENN S G.

Alignment Scores:

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RESULT 13

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DT 01-JAN-2004 (first entry)

AC ADD11283;
XX
XX
DT 01-JAN-2004 (first entry)
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XX Human secreted/transmembrane PRO polypeptide #17.

xx Human secreted/transmembrane PRO polypeptide #17.
 DE
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 xx human; secreted protein; transmembrane protein; cardiovascular disorder;
 KW endothelial disorder; angiogenic disorder; myocardial infarction;
 KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
 KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
 KW endothelial cell tube formation.

AA
PN
IIS2003105011-A1

PN IIS2003105011-A1

OS Homo sapiens.

PN US2003105013-A1.

05-JUN-2003.

PF 16-AUG-2002: 2002US-00223090.

PR 20-JUN-2001; 2001WO-US019692.

PR 09-JUL-2001; 2001WO-US021735.

PR 20-FEB-2002; 2002US-00081056.

XX
B3
CENTEX / CENTRECH INC

PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, et al. 2003

PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JP;
PI Watanabe CK, Williams PM, Wood WI, Ye W;

PI Godowski PJ, Gurney AL, Hillan KJ, Marst

PI Watanabe CK, Williams PM, Wood WI, Ye W;

XX

DR WPI; 2003-801242/15.

DR N-PSDB; ADD11202.
VV

XX
BT
New isolated nucleic

PT polypeptide, useful

PT anqioqenic disorder

PT degeneration.

XX

PS Claim 11; SEQ ID NO

XX

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GenCore version 5.1.1.7
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Run on: March 18, 2006, 00:06:45 ; Search time 26.4 Seconds
(without alignments)
1851.744 Million cell updates/sec

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Perfect score: 195

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	195	100.0	369	4 US-10-036-542-84	Sequence 84, Appl
2	195	100.0	369	4 US-10-188-832-149	Sequence 149, Appl
3	195	100.0	369	5 US-10-658-884-4	Sequence 4, Appli
4	195	100.0	369	5 US-10-756-149-4721	Sequence 4721, Ap
5	195	100.0	383	4 US-10-029-386-32058	Sequence 32058, A
6	12	6.2	260	4 US-10-029-386-33374	Sequence 33374, A
7	12	6.2	750	4 US-10-332-995-8	Sequence 8, Appli
8	12	6.2	856	4 US-10-223-085-34	Sequence 34, Appl
9	12	6.2	856	4 US-10-223-084-34	Sequence 34, Appl
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Alignment Scores:
Pred. No.: 1.15e-158 Length: 369
Score: 195.00 Matches: 195
Percent Similarity: 100.0% Conservative: 0
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ALIGNMENTS

RESULT 1

US-10-036-542-84
; Sequence 84, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: PA002P1
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-036-542-84

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16	12	6.2	856	4	US-10-223-082-34	Sequence 34, Appl
17	12	6.2	856	4	US-10-305-654-34	Sequence 34, Appl
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28	11	5.6	113	4	US-10-264-049-3022	Sequence 3022, Ap
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32	11	5.6	213	4	US-10-424-599-212445	Sequence 212445, A
33	11	5.6	224	4	US-10-424-599-268213	Sequence 268213, A
34	11	5.6	229	4	US-10-437-963-138424	Sequence 138424, A
35	11	5.6	310	4	US-10-094-749-3057	Sequence 3057, Ap
36	11	5.6	319	5	US-10-450-763-36690	Sequence 36690, A
37	11	5.6	347	4	US-10-094-749-3202	Sequence 3202, Ap
38	11	5.6	356	5	US-10-450-763-34719	Sequence 34719, A
39	11	5.6	369	4	US-10-437-963-196554	Sequence 196554, A
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42	11	5.6	442	4	US-10-425-114-44185	Sequence 44185, A
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44	11	5.6	612	4	US-10-193-452-30	Sequence 30, Appl
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RESULT 2
US-10-188-832-149
; Sequence 149, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; TITLE OF INVENTION: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 149
; LENGTH: 369
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-149

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Score: 195.00 Matches: 195
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QY 361 CAGGTCTGCGACAGTGTGAGTCTTTACCCAGAGTGTGAGATGATGAAAGGTGACTGAT 420
DB 121 GlnValLeuProAspSerGluSerLeuProArgSerGluIleAspGluLysValThrAsp 140
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RESULT 3
US-10-658-884-4
; Sequence 4, Application US/10658884
; Publication No. US20050019304A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MAGE-LIKE PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
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; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/658,884
; FILING DATE: 09-Sep-2003
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/773,870
; FILING DATE: 27-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0179 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <UNKNOWN>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 533511
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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RESULT 4
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; Sequence 4721, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOS
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANC
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4721
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-4721

Alignment Scores:
Pred. No.: 1,15e-158 Length: 369

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Db	21	GluThrGlnGlyLeuGluGlyAlaGlnAlaProLeuAlaValGluGluAspAlaSerSer	40
Qy	121	TCCACTTCCACAGCTCCTCTTTTCCATCCTCTTTTCTCCTCTCTCTCTCTCTCTCT	180
Db	41	SerThrSerThrSerSerSerPheProSerSerPheProSerSerSerSerSerSerSer	60
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Qy	241	CCAAATCTCCCGCAGAGTGTCTAGATAGCTGTCTCTCCCTCCGTGGTTCCTTCCCTT	300
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Qy	361	CAGTCTCTCCAGACAGTGAGTCTTTATCCCAAGAGTGAGATAGATGAAAGGTGACTGAT	420
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Db	141	LeuValGlnPheLeuLeuPheLysTyrGlnMetLysGluProIleThrLysAlaGluIle	160
Qy	481	CTGCGAGAGTGTCAATAAAAAATTATGAAGCACCTTCCCTTTGTTGTATGTCAGAGCTCC	540
Db	161	LeuGluSerValIleLysAsnTyrGlnAspHisPheProLeuLeuPheSerGluAlaSer	180
Qy	541	GAGTGCATGTCTGCTGGTCTTTGGCATTTGATGTTAAAGGAAGTGGAT	585


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; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 09/854,208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/854,280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/866,034
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/17092
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/870,574
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17443
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 34
; LENGTH: 856
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-087-34

Alignment Scores:
Pred. No.:          0.181      Length:      856
Score:              12.00     Matches:    12
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US-09-856-812B-7_COPY_334_918 (1-585) x US-10-223-087-34 (1-856)

Qy      151 TCTTTTCCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 186
Db      163 SerPheProSerSerSerSerSerSerSerSerSerSerSerSerSerSer 174

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; Sequence 34, Application US/10223083
; Publication No. US20030119112A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235PlC8
; CURRENT APPLICATION NUMBER: US/10/223,083
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23

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; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 34
; LENGTH: 856
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-223-089-34

Alignment Scores:
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US-09-856-812B-7_COPY_334_918 (1-585) x US-10-223-089-34 (1-856)

Qy  151 TCGTTTCCTCCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 186
Db  163 SerPheProSerSerSerSerSerSerSerSerSerSerSerSerSer 174

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; Sequence 34, Application US/10223081
; Publication No. US2003018686A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Phillippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITL OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235PLC7
; CURRENT APPLICATION NUMBER: US/10/223,081
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
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; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383

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Alignment Scores:		
Pred. No.:	0.181	Length:
Score:	12.00	Matches:
Percent Similarity:	100.0%	Conservative:
Best Local Similarity:	100.0%	Mismatches:
Query Match:	6.2%	Indels:
DB:	4	Gaps:
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		12

US-09-856-812B-7 COPY 334 918 (1-585) x US-10-223-081-34 (1-856)

Qy 151 TCTTTTCCCTCCTCCTCCTCTCTCCTCCTCCTCTCC 186
|||
Db 163 SerPheProSerSerSerSerSerSerSerSerSerSer 174

Search completed: March 18, 2006, 00:12:15
Job time : 138 secs

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GenCore version 5.1.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 18, 2006, 00:07:55 ; Search time 3.1 Seconds
(without alignments)
1080.283 Million cell updates/sec

Title: US-09-856-812B-7_COPY_334_918

Perfect score: 195

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Ygapop 60.0 , Ygapext 60.0	
Fgapop 6.0 , Fgapext 7.0	
Delopt 6.0 , Delext 7.0	

Searched: 169630 seqs, 28622889 residues

Word size: 1

Total number of hits satisfying chosen parameters: 303540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=6 -FGAPOP=6 -FGAPEXT=7
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- 2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pap.*
- 3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pap.*
- 4: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pap.*
- 5: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pap.*
- 6: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pap.*
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- 8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	12	6.2	1006	7	US-11-203-251A-90
2	10	5.1	10	7	US-11-044-051-83
3	10	5.1	57	7	US-11-096-568A-3481
C 4	10	5.1	94	7	US-11-096-568A-9318
C 5	10	5.1	101	7	US-11-096-568A-9320
C 6	10	5.1	102	7	US-11-096-568A-10322
C 7	10	5.1	105	7	US-11-087-099-1414
C 8	10	5.1	112	7	US-11-096-568A-9317
9	10	5.1	132	7	US-11-096-568A-8663

C	10	5.1	142	7	US-11-087-099-4752	Sequence 4752, Ap
	11	10	153	7	US-11-096-568A-8662	Sequence 8662, Ap
	12	10	154	7	US-11-096-568A-8661	Sequence 8661, Ap
C	13	10	156	7	US-11-087-099-3277	Sequence 3277, Ap
C	14	10	157	6	US-10-957-569-64	Sequence 64, Appl
C	15	10	157	7	US-11-097-589-63	Sequence 63, Appl
C	16	10	159	7	US-11-096-568A-32244	Sequence 32244, A
C	17	10	166	7	US-11-087-099-10919	Sequence 10919, A
C	18	10	169	7	US-11-087-099-7673	Sequence 7673, Ap
C	19	10	175	7	US-11-096-568A-3912	Sequence 3912, Ap
	20	10	179	7	US-11-096-568A-19169	Sequence 19169, A
C	21	10	191	6	US-10-501-035-247	Sequence 247, App
	22	10	209	7	US-11-096-568A-22097	Sequence 22097, A
	23	10	228	7	US-11-096-568A-7793	Sequence 7793, Ap
	24	10	235	7	US-11-096-568A-22096	Sequence 22096, A
C	25	10	241	7	US-11-096-568A-3835	Sequence 3835, Ap
C	26	10	242	7	US-11-096-568A-3834	Sequence 3834, Ap
	27	10	247	7	US-11-096-568A-7792	Sequence 7792, Ap
	28	10	258	7	US-11-072-512-3034	Sequence 3034, Ap
C	29	10	259	7	US-11-096-568A-22095	Sequence 22095, A
	30	10	272	7	US-11-096-568A-3833	Sequence 3833, Ap
	31	10	281	6	US-10-861-934-8	Sequence 8, Appl
	32	10	281	6	US-10-861-934-30	Sequence 10, Appl
	33	10	281	7	US-11-213-368-11	Sequence 11, Appl
	34	10	281	7	US-11-213-368-12	Sequence 12, Appl
	35	10	286	6	US-10-714-887-196	Sequence 196, App
	36	10	302	7	US-11-096-568A-28036	Sequence 28036, A
	37	10	331	7	US-11-096-568A-3911	Sequence 3911, Ap
	38	10	352	7	US-11-096-568A-28035	Sequence 28035, A
	39	10	371	7	US-11-096-568A-31720	Sequence 31720, A
	40	10	374	6	US-10-537-094-6	Sequence 6, Appl
	41	10	374	6	US-10-537-094-8	Sequence 8, Appl
	42	10	377	7	US-11-096-568A-28034	Sequence 28034, A
	43	10	387	7	US-11-096-568A-6334	Sequence 6334, Ap
	44	10	406	7	US-11-096-568A-1547	Sequence 1547, Ap
	45	10	428	7	US-11-096-568A-9065	Sequence 9065, Ap

ALIGNMENTS

RESULT 1

US-11-203-251A-90

; Sequence 90, Application US/11203251A

; Publication No. US20060039904A1

; GENERAL INFORMATION:

; APPLICANT: MedImmune Inc.

; TITLE OF INVENTION: EPH RECEPTOR FC VARIANTS WITH ENHANCED ANTIBODY DEPENDENT

; TITLE OF INVENTION: CELL-MEDIATED CYTOTOXICITY ACTIVITY

; FILE REFERENCE: AE702US

; CURRENT APPLICATION NUMBER: US/11/203,251A

; CURRENT FILING DATE: 2005-08-15

; PRIOR APPLICATION NUMBER: 60/601,634

; PRIOR FILING DATE: 2004-08-16

; PRIOR APPLICATION NUMBER: 60/608,852

; PRIOR FILING DATE: 2004-09-13

; NUMBER OF SEQ ID NOS: 101

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 90

; LENGTH: 1006

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-203-251A-90

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Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	6.2%	Indels:	0
DB:	7	Gaps:	0

US-09-856-812B-7_COPY_334_918 (1-585) x US-11-203-251A-90 (1-1006)

QY 186 GGAGGAGGAGGAGGAGGAGGAGG 157
Db 62 GlyGlyGlyGlyGlyArgGlyGlyGly 71

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US-11-096-568A-10322
; Sequence 10322, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 10322
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(102)
; OTHER INFORMATION: Ceres Seq. ID no. 13590887
US-11-096-568A-10322

Alignment Scores:
Pred. No.: 0.963 Length: 102
Score: 10.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 5.1% Indels: 0
Gaps: 0

US-09-856-812B-7_COPY_334_918 (1-585) x US-11-096-568A-10322 (1-102)

QY 186 GGAGGAGGAGGAGGAGGAGGAGG 157
Db 74 GlyGlyGlyGlyGlyArgGlyGlyGly 83

RESULT 7
US-11-087-099-1414
; Sequence 1414, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1414
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Medicago sativa
US-11-087-099-1414

Alignment Scores:
Pred. No.: 0.956 Length: 105
Score: 10.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 5.1% Indels: 0
Gaps: 0

US-09-856-812B-7_COPY_334_918 (1-585) x US-11-087-099-1414 (1-105)

QY 186 GGAGGAGGAGGAGGAGGAGGAGG 157
Db 89 GlyGlyGlyGlyGlyArgGlyGlyGly 98

RESULT 8
US-11-096-568A-9317

; Sequence 9317, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 9317
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(112)
; OTHER INFORMATION: Ceres Seq. ID no. 15226316
US-11-096-568A-9317

Alignment Scores:
Pred. No.: 0.942 Length: 112
Score: 10.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 5.1% Indels: 0
Gaps: 0

US-09-856-812B-7_COPY_334_918 (1-585) x US-11-096-568A-9317 (1-112)

QY 186 GGAGGAGGAGGAGGAGGAGGAGG 157
Db 80 GlyGlyGlyGlyGlyArgGlyGlyGly 89

RESULT 9
US-11-096-568A-8663
; Sequence 8663, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 8663
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(132)
; OTHER INFORMATION: Ceres Seq. ID no. 13584649
US-11-096-568A-8663

Alignment Scores:
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Score: 10.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 5.1% Indels: 0
Gaps: 0

US-09-856-812B-7_COPY_334_918 (1-585) x US-11-096-568A-8663 (1-132)

QY 158 CTTCTCTCTCTCTCTCTCTCTCTCT 187
Db 25 ProProProLeuProProProPro 34

RESULT 10
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; Sequence 4752, Application US/11087099

; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 4752
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Glycine max
US-11-087-099-4752

Alignment Scores:
Pred. No.: 0.889 Length: 142
Score: 10.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 5.1% Indels: 0
DB: 7 Gaps: 0

US-09-856-812B-7_COPY_334_918 (1-585) x US-11-087-099-4752 (1-142)

QY 186 GGAGGAGGAGGAGGAGGAGGAGGAGG 157
DB 91 GlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100

RESULT 11
US-11-096-568A-8662
; Sequence 8662, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: Therby
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 8662
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(153)
; OTHER INFORMATION: Ceres Seq. ID no. 13584648
US-11-096-568A-8662

Alignment Scores:
Pred. No.: 0.873 Length: 153
Score: 10.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 5.1% Indels: 0
DB: 7 Gaps: 0

US-09-856-812B-7_COPY_334_918 (1-585) x US-11-096-568A-8662 (1-153)

QY 158 CCTCCTCCTCTCTCTCTCTCTCTCTCTCT 187
DB 46 ProProProProLeuProProProPro 55

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; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: Therby
; CURRENT APPLICATION NUMBER: US/11/096,569
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/950,321
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.3

; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
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; LENGTH: 154
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(154)
; OTHER INFORMATION: Ceres Seq. ID no. 13584647
US-11-096-568A-8661

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Query Match: 5.1% Indels: 0
DB: 7 Gaps: 0

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QY 158 CCTCCTCCTCTCTCTCTCTCTCTCTCTCT 187
DB 47 ProProProProLeuProProProPro 56

RESULT 13
US-11-087-099-3277
; Sequence 3277, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3277
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Fagus sylvatica
US-11-087-099-3277

Alignment Scores:
Pred. No.: 0.869 Length: 156
Score: 10.00 Matches: 10
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 5.1% Indels: 0
DB: 7 Gaps: 0

US-09-856-812B-7_COPY_334_918 (1-585) x US-11-087-099-3277 (1-156)

QY 186 GGAGGAGGAGGAGGAGGAGGAGGAGG 157
DB 77 GlyGlyGlyGlyGlyGlyGlyGlyGlyGly 86

RESULT 14
US-10-957-569-64
; Sequence 64, Application US/10957569
; Publication No. US20050246785A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Zhihong et al.
; TITLE OF INVENTION: PROMOTER, PROMOTER CONTROL ELEMENTS, AND COMBINATIONS, AND USES
; FILE REFERENCE: THEREOF
; CURRENT APPLICATION NUMBER: US/10/957,569
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/950,321
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.3

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; SEQ ID NO 64
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-957-569-64

Alignment Scores:
Pred. No.:      0.868      Length:      157
Score:          10.00      Matches:     10
Percent Similarity: 100.0%  Conservatives: 0
Best Local Similarity: 100.0%  Mismatches:  0
Query Match:    5.1%      Indels:     0
DB:             6        Gaps:       0

US-09-856-812B-7_COPY_334_918 (1-585) x US-10-957-569-64 (1-157)

QY      186 GGAGGAGGAGGAGGAGGAGGAGGAGG 157
Db      70 GlyGlyGlyGlyGlyArgGlyGlyGly 79

RESULT 15
US-11-097-589-63
; Sequence 63, Application US/11097589
; Publication No. US20060021083A1
; GENERAL INFORMATION:
; APPLICANT: COOK, Zhihong
; APPLICANT: FANG, Yiwen
; APPLICANT: FELDMANN, Kenneth A.
; APPLICANT: KIEGLE, Edward A.
; APPLICANT: KWOK, Shing
; TITLE OF INVENTION: PROMOTER, PROMOTER CONTROL ELEMENTS, AND COMBINATIONS, AND USES
; FILE REFERENCE: 2750-1593PUS2
; CURRENT APPLICATION NUMBER: US/11/097,589
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 63
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-097-589-63

Alignment Scores:
Pred. No.:      0.868      Length:      157
Score:          10.00      Matches:     10
Percent Similarity: 100.0%  Conservatives: 0
Best Local Similarity: 100.0%  Mismatches:  0
Query Match:    5.1%      Indels:     0
DB:             7        Gaps:       0

US-09-856-812B-7_COPY_334_918 (1-585) x US-11-097-589-63 (1-157)

QY      186 GGAGGAGGAGGAGGAGGAGGAGGAGG 157
Db      70 GlyGlyGlyGlyGlyArgGlyGlyGly 79

Search completed: March 18, 2006, 00:12:48
Job time : 16.5 secs
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GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 17, 2006, 23:54:19 ; Search time 37.5 Seconds

(without alignments)
2201.248 Million cell updates/sec

Title: US-09-856-812B-7_COPY_334_918

Perfect score: 195

Sequence: 1 atgcctcgagctccaaagcg.....ttgatgtaaaggaagtggat 585

Scoring table:

OLIGO:
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4332514

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-DB=UniProt -QFWT=fastan -SUFFIX=n2p_olig.rup -MINMATCH=0.1 -LOOFCU=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abes02p
-USER=US09856812 @CGN 1.1 466 @runat.17032006.150556.5451 -NCPU=6 -ICPU=3
-NO WMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	195	100.0	369	1 MAGAA HUMAN	P43363 homo sapien
2	12	6.2	759	1 GPT1 YEAST	P32784 s glycerol-
3	12	6.2	844	2 Q5SR17 CRYNE	Q55r17 cryptococcu
4	12	6.2	1006	1 EPHB6 HUMAN	O15197 homo sapien
5	12	6.2	1581	2 Q5CUA3 CRYPV	Q5cu43 cryptospori
6	12	6.2	2171	2 Q9VG42 DROME	Q9vk42 drosophila
7	11	5.6	78	2 Q6LJH4 DROME	Q6ljh4 drosophila
8	11	5.6	150	2 Q556J7 DICDI	Q556j7 dictyosteli
9	11	5.6	170	2 Q9B278 HUMAN	Q9b278 homo sapien
10	11	5.6	229	2 Q7X867 ORYSA	Q7x867 oryza sativ
11	11	5.6	230	2 Q9FGI2 ARATH	Q9fgi2 arabidopsis
12	11	5.6	245	2 Q59LC8 CANAL	Q59lc8 candida alb
13	11	5.6	247	2 Q7PI3 RAT	Q7pi3 rattus norv
14	11	5.6	251	2 Q4S8F1 TETNG	Q4s8f1 tetraodon n
15	11	5.6	287	2 Q95JH0 SHEEP	Q95jh0 ovis aries
16	11	5.6	287	2 Q95JH2_BOVIN	Q95jh2 bos taurus

ALIGNMENTS

RESULT 1

MAGAA HUMAN

ID MAGAA HUMAN STANDARD; PRT; 369 AA.

AC P43363;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Melanoma-associated antigen 10 (MAGE-10 antigen).

GN Name=MAGE10; Synonyms=MAGE10;

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

[1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=95012457; PubMed=7927540;

RA de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,

RA de Smet C., Brasseur P., van der Bruggen P., Lethe B., Lurquin C.,

RA Brasseur R., Chomez P., de Backer O., Cavenes W., Boon T.;

RT "structure, chromosomal localization, and expression of 12 genes of

RT the MAGE family.";

RL Immunogenetics 40:360-369(1994).

[2]

RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RP TISSUE=Skin;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Heiton E., Kettelman M., Madan A., Rodríguez S., Sanchez A.,

RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinaki M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Not known, though may play a role in embryonal
CC development and tumor transformation or aspects of tumor
CC progression.
CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
CC such as melanoma, head and neck squamous cell carcinoma, lung
CC carcinoma and breast carcinoma, but not in normal tissues except
CC for testes and placenta.
CC -!- SIMILARITY: Contains 1 MAGE domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC DR EMBL; U10685; AAA68869.1; -; Genomic DNA.
CC DR EMBL; BC004105; AA04105.1; -; mRNA.
CC DR PIR; I38659; I38659.
CC DR Ensembl; ENSG00000124260; Homo sapiens.
CC DR HGNC; HGNC:6797; MAGEA10.
CC DR H-InvDB; HIX0017116; -.
CC DR MIM; 300343; -.
CC DR InterPro; IPR002190; MAGE.
CC DR PANTHER; PTHR11736; MAGE; 2.
CC DR Pfam; PF01454; MAGE; 1.
CC DR PROSITE; PS00838; MAGE; 1.
KW Antigen; Multigene family; Tumor antigen.
FT DOMAIN 134 333
FT COMPBIAS 54 62 Poly-Ser.
SQ SEQUENCE 369 AA; 40767 MW; 16FA3301CAB716A6 CRC64;

Alignment Scores:
Pred. No.: 1.34e-169 Length: 369
Score: 195.00 Matches: 195
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-09-856-812b-7_COPY_334_918 (1-585) x MAGAA_HUMAN (1-369)

QY 1 ATGCGCTCGAGCTCCAAAGCGTCAGCGCTGCATGCTGAAGAAGATCTTCAATCCCAAGT 60
DB 1 MetProArgAlaProLysArgGlnA-gcyMetProGluGluAspLeuGlnSerGlnSer 20

QY 61 GAGACACAGGCGCTCCAGGGGTGCACAGCTCCCGCTGGCTGGAGGAGGATGCTTCATCA 120
DB 21 GluThrGlnGlyLeuGluGlyAlaGlnAlaProLeuAlaValGluGluAspAlaSerSer 40

QY 121 TCACCTTCCACAGCTCCTCTTTTCATCTCTTTTCCCTCCCTCCTCTCTCTCTCTCTCC 180
DB 41 SerThrSerThrSerSerPheProSerSerPheProSerSerSerSerSerSerSer 60

QY 181 TCCTCTCTGCTATCTCTTAATACCAAGCACCCAGAGGAGGTTCGTGCTGATGATGAGACA 240
DB 61 SerSerCysTyrProLeuIleProSerThrProGluGluValSerAlaAspAspGluThr 80

QY 241 CCAATCTCTCCAGAGTGTCTGATAGCTGCTCTCTCCCTCGGTGCTGCTCTCTCTCTCT 300
DB 81 ProAsnProGlnSerAlaGlnIleAlaCysSerSerProSerValValAlaSerLeu 100

QY 301 CCATTAGATCAATCTGATGAGGGCTCCAGAGCCCAAGAGGAGGAGTCCAGCACCTTA 360
DB 101 ProLeuAspGlnSerAspGluGlySerSerSerGlnGlySerGluGluSerProSerThrLeu 120

QY 361 CAGGTCTCTGCCAGACAGTGAGTCTTTTACCAGAGAGTGATAGATAGAAAGGTGACTGAT 420

DB 121 GlnValLeuProAspSerGluSerLeuProArgSerGluIleAspGluLysValThrAsp 140
QY 421 TTGGTGCAGTTTCTGCTCTTCAAGTATCAAAATGAGGAGCCGATCACAAGGCAGAAATA 480
DB 141 LeuValGlnPheLeuLeuPheLysTyrGlnMetLysGluProIleThrLysAlaGluIle 160
QY 481 CTGGAGAGTGTCATAAAAAATATGAGACCACTTCCCTTTTGTGTTTGTAGTGAAGCTCC 540
DB 161 LeuGluSerValIleLysAsnTyrGluAspHisPheProLeuLeuPheSerGluAlaSer 180
QY 541 GAGTGCATCTGCTGCTCTTTCGCATTGATGTAAAGAAAGTGGAT 585
DB 181 GluCysMetLeuLeuValPheGlyIleAspValLysGluValAsp 195

RESULT 2
GPT1_YEAST STANDARD; PRT; 759 AA.
ID AC P32784; Q07062; Q96TV1;
DT 01-OCT-1993 (Rel. 27, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Glycero1-3-phosphate O-acyltransferase 1 (EC 2.3.1.15) (G-3-P
DE acyltransferase 1) (Dihydroxyacetone phosphate acyltransferase 1)
DE (EC 2.3.1.42) (DHAP-AT 1) (Glycerol-3-phosphate / dihydroxyacetone
DE phosphate acyltransferase 1).
DE Names-GPT1; Synonyms=GAT2; SCT1; OrderedLocusNames=YBL011W;
GN ORFNames=YBL0315, YBL0309;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95332274; PubMed=7608137;
RA Matsushita M., Nakawa J.;
RT "Isolation and characterization of a SCT1 gene which can suppress a
RT choline-transport mutant of Saccharomyces cerevisiae.";
RL J. Biochem. 117:447-451(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE, AND FUNCTION.
RX STRAIN=DSY746;
RX MEDLINE=21551208; PubMed=11544256; DOI=10.1074/jbc.M104749200;
RA Zheng Z., Zou J.;
RT "The initial step of the glycerolipid pathway: identification of
RT glycerol-3-phosphate / dihydroxyacetone phosphate dual substrate
RT acyltransferases in Saccharomyces cerevisiae.";
RL J. Biol. Chem. 276:41710-41716(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=S288C;
RX MEDLINE=93070615; PubMed=1332308;
RA Skala J., van Dyck L., Purnelle B., Goffeau A.;
RT "The sequence of an 8 kb segment on the left arm of chromosome II from
RT Saccharomyces cerevisiae identifies five new open reading frames of
RT unknown functions, two tRNA genes and two transposable elements.";
RL Yeast 8:777-785(1992).
RN [4]
RP NUCLEOTIDE SEQUENCE OF 609-759.
RX STRAIN=S288C;
RX MEDLINE=93070613; PubMed=1441753;
RA Delaveau T., Jacq C., Perea J.;
RT "Sequence of a 12.7 kb segment of yeast chromosome II identifies a
RT PDR-like gene and several new open reading frames.";
RL Yeast 8:761-768(1992).
CC -!- FUNCTION: G-3-P/dihydroxyacetone phosphate dual substrate-specific
CC sn-1 acyltransferase.
CC -!- CATALYTIC ACTIVITY: Acyl-CoA + sn-glycerol 3-phosphate = CoA + 1-
CC acyl-sn-glycerol 3-phosphate.
CC -!- CATALYTIC ACTIVITY: Acyl-CoA + glycerone phosphate = CoA +
CC acylglycerone phosphate.
CC -!- PATHWAY: De novo phospholipid biosynthesis; first step.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).

FT	SIGNAL	1	16
FT	CHAIN	17	1006
FT	TOPO_DOM	17	579
FT	TRANSMEM	580	1006
FT	TOPO_DOM	601	1006
FT	DOMA1N	354	463
FT	DOMA1N	473	584
FT	DOMA1N	655	904
FT	DOMA1N	933	997
FT	NP_BIND	661	669
FT	MOTIF	1004	1006
FT	CMBPIAS	151	161
FT	CMBPIAS	204	331
FT	CMBPIAS	866	869
FT	CARBOHYD	465	465
FT	VARIANT	107	107
FT	VARIANT	267	267
FT	VARIANT	309	309
FT	VARIANT	484	484
FT	SEQUENCE	1006 AA;	109273 MW; 614EC4AGD2EEDSA9 CRC64;
 Alignment Scores:			
Pred.	No.:	0.0979	Length: 1006
Score:		12.00	Matches: 12
Percent Similarity:		100.0%	Conservative: 0
Best Local Similarity:		100.0%	Mismatches: 0
Query Match:		6.2%	Indels: 0
DB:		1	Gaps: 0
 US-09-856-812B-7_COPY_334_918 (1-585) x EPHB6_HUMAN (1-1006)			
Qy	151	TCTTTTCCTCCCTCCCTTCTCCTCTCCCTCCCTCC	186
Db	148	SerPheProSerSerSerSerSerSerSerSerSer	159
 RESULT 5			
Q5CUA3	CRYPV		
ID	Q5CUA3_CRYPV PRELIMINARY;	PRT;	1501 AA.
AC	Q5CUA3;		
DT	10-MAY-2005 (TrEMBLrel. 30, Created)		
DT	10-MAY-2005 (TrEMBLrel. 30, Last sequence update)		
DT	10-MAY-2005 (TrEMBLrel. 30, Last annotation update)		
DE	Hypothetical protein (Fragment).		
GN	ORFNames=cgd3_3620;		
OS	Cryptosporidium parvum.		
OC	Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;		
OC	Cryptosporidiidae; Cryptosporidium.		
OX	NCBI_TaxID=5807;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=Iowa type II;		
RX	PubMed=15044751; DOI=10.1126/science.1094786;		
RA	Abrahamson M.S., Templeton T.J., Enomoto S., Abrahante J.E., Zhu,		
RA	Lancio C.A., Deng M., Liu C., Widmer G., Tzipori S., Buck G.A.,		
RA	Bankier A.T., Dear P.H., Konfortov B.A., Spriggs H.F., Iyer L.,		
RA	Anantharaman V., Aravind L., Kapur V.;		
RT	"Complete genome sequence of the apicomplexan, Cryptosporidium		
RL	parvum."		
SC	Science 304:441-445 (2004).		
CC	-!- CAUTION: The sequence shown here is derived from an		
CC	EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is		
CC	preliminary data.		
DR	EMBL; ABEE01000004; EAK89252.1; -; Genomic_DNA.		
DR	InterPro; IPRO11989; ARM-like.		
DR	InterPro; IPRO11029; DEATH like.		
DR	InterPro; IPRO11992; EF-Hand_type.		
DR	InterPro; IPRO09065; FERM.		
DR	InterPro; IPRO12292; Globin-related.		
DR	InterPro; IPRO12287; Homodomain-rel.		

RA	Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F., Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P., Pilcher K., Chen G., Saunders D., Sodergren E., Davis P., Karhornou A., Nie X., Hall N., Anjard C., Hemphill L., Basom N., Ferhrouher P., Desany B., Just E., Morio T., Rost R., Churcher C., Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I., Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsey R., Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C., Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A., Loulsges H., Mungall K., Oliver K., Price C., Quail M.A., Urushihara H., Hernandez J., Rabinowitch E., Steffen D., Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A., Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y., Shauskys G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C., Chisholm R.L., Gibbs R., Loomis W.F., Platzner M., Kay R.R., Williams J., Dear P.H., Noegel A.A., Barrell B., Kuypa A.; The genome of the social amoeba Dictyostelium discoideum." ; RL Nature 0-0-0(2005).
CC	-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
CC	EMBL; AFJ01000026; EAL70436.1; -; Genomic DNA.
CC	EMBL; AFJ01000022; EAL71081.1; -; Genomic DNA.
KW	Hypothetical protein.
DQ	SEQUENCE 150 AA; 18233 MW; E20AD8BD179A48C0 CRC64;
SQ	
DB:	
Alignment Scores:	
Pred. No.:	0.936 Length: 150
Score:	11.00 Matches: 11
Percent Similarity:	100.0% Conservatives: 0
Best Local Similarity:	100.0% Mismatches: 0
Query Match:	5.6% Indels: 0
Gaps:	2
US-09-856-812B-7_COPY_334_918 (1-585) x Q556J7_DICDI (1-150)	
QY	159 CTCCTCTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTGTA 191
Db	41 LeuLeuLeuPheLeuLeuLeuLeuLeuLeu 51
RESULT 9	
Q9BZ78 HUMAN	
ID	PRELIMINARY; PRT; 170 AA.
AC	Q9BZ78;
DT	01-JUN-2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE	MAGE family testis and tumor-specific protein (Fragment).
GN	Name=MAGEB10;
OS	homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OX	NCBI_TaxID=9606;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Whole blood;
RA	Lucas S., Boon T.;
RL	Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF333708; AAA00360.1; -; Genomic DNA.
DR	InterPro; IPR002190; MAGE.
DR	pfam; PF01454; MAGE; 1.
DR	PROSITE; PS50838; MAGE; 1.
FT	NON_TER 1 1
FT	NON_TER 170 170
SQ	SEQUENCE 170 AA; 18807 MW; DS5DD86951BD957A CRC64;
Alignment Scores:	
Pred. No.:	0.927 Length: 170
Score:	11.00 Matches: 11
Percent Similarity:	100.0% Conservatives: 0
Best Local Similarity:	100.0% Mismatches: 0
Query Match:	5.6% Indels: 0

DR ENBL; BT010710; AAR20767.1; -; mRNA.
DR ENBL; BT010982; AAR24760.1; -; mRNA.
DR ENBL; AB018107; BAB10672.1; JOINED; Genomic DNA.
SQ SEQUENCE 230 AA; 26246 MW; 78239AA11B2249B7 CRC64;

Alignment Scores:
Pred. No.: 0.906 Length: 230
Score: 11.00 Matches: 11
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 5.6% Indels: 0
DB: 2 Gaps: 0

US-09-856-812B-7_COPY_334_918 (1-585) x O9FG12_ARATH (1-230)

Qy 189 GCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 157
Db 38 AlaGlyGlyGlyGlyGlyArgGlyGlyGlyGly 48

RESULT 12

ID Q59LC8 CANAL PRELIMINARY; PRT; 245 AA.
AC Q59LC8_7
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Cao19.5502;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=1513810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S., T. P. Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P. T., Davis R.W., Scherer S.;
RA "The diploid genome sequence of Candida albicans."; Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O., Roberts J., Persson K., Donnelly S., Favoreto S., Tsung K.-W., Jones T., Scherer S., Agabian N.;
RA "Annotation of the Genome of Candida albicans."; R. L. Stannard (APR-2004) to the EMBL/GenBank/DBJ databases.
CC CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
CC ENBL; AACQ0100260; EAK91276.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 245 AA; 26687 MW; AFF2717493F14B0C CRC64;

Alignment Scores:
Pred. No.: 0.901 Length: 245
Score: 11.00 Matches: 11
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 5.6% Indels: 0
DB: 2 Gaps: 0

US-09-856-812B-7_COPY_334_918 (1-585) x Q59LC8_CANAL (1-245)

Qy 160 TCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTAT 192
Db 92 SerSerSerSerSerSerSerSerSerSerSerSerSerSer 102

RESULT 13

ID Q7TF13 RAT PRELIMINARY; PRT; 247 AA.
ID Q7TF13 RAT

Q7PTI3;
01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ac2-628
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Xu C.S., Li W.Q., Li Y.C., Wang S.F., Han H.P., Wang G.P., Chai L.Q.,
RA Yuan J.Y., Yang K.J., Yan H.M., Zhang C.F., Zhao L.F., Ma H., Wang L.,
RA Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; AY321352; AAP86284.1; -; mRNA.
SQ SEQUENCE 247 AA; 27879 MW; 7719DB6063913FDA CRC64;

Alignment Scores:
Pred. No.: 0.901 Length: 247
Score: 11.00 Matches: 11
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 5.6% Indels: 0
DB: 2 Gaps: 0

US-09-856-812B-7_COPY_334_918 (1-585) x Q7PTI3_RAT (1-247)

Qy 182 GAGGAGGAGAGAGAGAGAGAGAGAGAGAG 150
|||
Db 181 GluGlugluGluGluGluGluGluGluGlu 191

RESULT 14
Q4S8F1_TETNG
ID ID Q4S8F1_TETNG PRELIMINARY; PRT; 251 AA.
AC AC Q4S8F1;
DT DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCF14706, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00022362001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OC NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet E., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anhouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappie P., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schacher V., Quetier F., Saurin V., Scarpelli C.,
RA Winkler P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

[illegible]

Search completed: March 18, 2006, 00:05:17
Job time : 195.5 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:21:17 ; Search time 118 Seconds
(without alignments)
33.512 Million cell updates/sec

Title: US-09-856-812b-48
Perfect score: 47
Sequence: 1 FLLFKYQMK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	9	2 AAR79845	Aar79845 Tumour re
2	47	100.0	9	3 AAY71491	Aay71491 Human MAG
3	47	100.0	9	8 ADI47250	Adi47250 Anti-canc
4	47	100.0	369	3 AAY71485	Aay71485 Human MAG
5	47	100.0	369	4 AAB80297	Aab80297 Human pro
6	47	100.0	369	6 ABR48215	Abr48215 Human bla
7	47	100.0	369	6 ABUS5616	Abu56516 Lung canc
8	47	100.0	383	8 ABO58424	Abos8424 Human gen
9	41	87.2	260	5 ABB98179	Abb98179 Human 520
10	41	87.2	260	7 ADD22980	Add22980 Melanoma
11	41	87.2	347	6 ADA55634	Ada55634 Human pro
12	37	78.7	276	4 ABB37733	Abb37733 Peptide #
13	37	78.7	276	4 ABB23008	Abb23008 Protein #
14	37	78.7	473	4 ABB23023	Abb23023 Protein #
15	37	78.7	1142	2 AAW81546	Aaw81546 Tumour re
16	37	78.7	1142	3 AAY43876	Aay43876 Amino aci
17	37	78.7	1142	6 ABU08929	Abu08929 Human tum
18	37	78.7	1142	7 ADD25518	Add25518 Binding d
19	37	78.7	1142	7 ADG18025	Adg18025 MAGS-C1 p
20	37	78.7	1142	7 ADM33107	Adm33107 Human tum
21	37	78.7	1142	8 ADI79399	Adi79399 Human MAG
22	37	78.7	1142	8 ADJ54140	Adj54140 Human CT7
23	37	78.7	1142	8 ADM68724	Adm68724 Human MAG
24	37	78.7	1142	9 ADV85853	Adv85853 Human CT7

ALIGNMENTS

RESULT 1

AAR79845

ID AAR79845 standard; peptide; 9 AA.

XX AC AAR79845;

XX DT 08-MAY-1996 (first entry)

XX DE Tumour rejection antigen peptide #9.

XX KW Tumour rejection antigen; MAGE tumour rejection precursor; complex;

XX KW HLA-2; immunogen; antibody; cytolytic T cell clone.

XX OS Synthetic.

XX PN WO9525740-A1.

XX PD 28-SEP-1995.

XX PF 22-MAR-1995; 95WO-US003657.

XX PR 24-MAR-1994; 94US-00217186.

XX PR 17-JUN-1994; 94US-00261160.

XX PR 15-AUG-1994; 94US-00290381.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (UYOX-) UNIV OXFORD.

XX (UYLE-) RIJKSUNIV LEIDEN.

XX Townsend A, Bastin J, Boon-Falleur T, Van Der Bruggen P, Coulie P;

XX Gajewski T, Melief CJ, Visseren MW, Kast WM;

XX WPI; 1995-344584/44.

XX Isolated peptide(s) which complex with HLA-A2 - used as immunogens for

XX the prodn. of antibodies, or as targets for the generation of cytolytic T

XX cell clones.

XX Claim 15; Page 23; 44pp; English.

XX The peptides given in AAR79845-47 represent tumour rejection antigens

XX derived from MAGE tumour rejection precursor. These peptides form a

XX strong complex with HLA-2 which may be used diagnostically and as an

XX immunogen in the production of antibodies. They may also be used as

XX targets for the generation of cytolytic T cell clones. This cytolytic T

XX cell clone is used to treat a cancerous condition characterised by the

XX fact that the cancer cells present the HLA-2/ peptide complex on their

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CC surface
XX Sequence 9 AA;
SQ Query Match 100.0%; Score 47; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLLFKYQMK 9
Db 1 FLLFKYQMK 9

RESULT 2
AA71491
ID AAY71491 standard; peptide; 9 AA.
XX
AC AAY71491;
XX
DT 12-OCT-2000 (first entry)
XX
DE Human MAGE-A10 nonapeptide-2.
XX
KW MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
KW immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
KW cancer; TNF; tumour necrosis factor; vaccine; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200032769-A2.
XX
PD 08-JUN-2000.
XX
PF 26-NOV-1999; 99WO-IB002018.
XX
PR 27-NOV-1998; 98GB-00026143.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
XX WPI; 2000-412317/35.
XX
DR Novel polypeptides expressed in tumor cells useful for treating cancers
PT have an ability to complex with a major histocompatibility complex
PT molecule and comprises a specific unbroken amino acid sequence.
XX
PS Claim 5; Page 36; 80pp; English.
XX
CC The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
CC decapeptide sequences, that function as tumour rejection antigens (TRAs).
CC These peptides are capable of forming a complex with major
CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
CC Antigen), that are recognised by T-lymphocytes and elicit an immune
CC response from cytolytic T-lymphocytes (CTL). They function as an immune
CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
CC therapy and diagnosis of tumours and are effective in controlling or
CC preventing tumour growth. The present peptide sequence is the human MAGE-
CC A10 nonapeptide-2, that corresponds to residues 144-152 of the MAGE-A10
CC protein. This peptide can serve as a tumour rejection antigen (TRA) and
CC in combination with adjuvants, can produce vaccines useful for treating a
CC variety of tumours that express MAGE-A10
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 47; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLLFKYQMK 9
Db 1 FLLFKYQMK 9

us-09-856-812b-48.rag
```

```
CC surface
XX Sequence 9 AA;
SQ Query Match 100.0%; Score 47; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLLFKYQMK 9
Db 1 FLLFKYQMK 9

RESULT 3
ADI47250
ID ADI47250 standard; peptide; 9 AA.
XX
AC ADI47250;
XX
DT 22-APR-2004 (first entry)
XX
DE Anti-cancer HLA-A2 complex associated peptide seq id 17.
XX
KW cytostatic; gene therapy; cancer; cytolytic T cell; HLA-A2.
XX
OS Synthetic.
XX
PN US6682731-B1.
XX
PD 27-JAN-2004.
XX
PF 23-MAR-2000; 2000US-00533499.
XX
PR 24-MAR-1994; 94US-00217186.
XX
PR 24-MAR-1994; 94US-00217188.
XX
PR 17-JUN-1994; 94US-00261160.
XX
PR 15-AUG-1994; 94US-00290381.
XX
PR 06-FEB-1997; 97US-00722115.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PA (UYOX-) UNIV OXFORD.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Townsend A, Bastin J, Boon-Falleur T, Van Der Bruggen P, Coulie P;
PI Gajewski T, Melief CJM, Visseren MJW, Kast MW;
XX WPI; 2004-118569/12.
XX
DR Treating a subject with a cancerous condition by administering cytolytic
PT T cells specific for the complexes to lyse the cancer cells.
XX
XX Example 13; SEQ ID NO 18; 27pp; English.
XX
CC The invention describes a method of treating a subject with a cancerous
CC condition comprising administering cytolytic T cells specific for the
CC complexes to lyse the cancer cells of the subject. The cancer cells
CC present complexes of HLA-A2 molecules and a peptide with a fully defined
CC sequence comprising 9 amino acids. The method is useful for treating a
CC subject with a cancerous condition. This is the amino acid sequence of a
CC HLA-A2 complex associated peptide.
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 47; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLLFKYQMK 9
Db 1 FLLFKYQMK 9

RESULT 4
AAY71485
ID AAY71485 standard; protein; 369 AA.
XX
AC AAY71485;
XX
DT 12-OCT-2000 (first entry)
XX
DE Human MAGE-A10 protein.
XX
KW MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
```

KW immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
KW cancer; TNF; tumour necrosis factor; cytostatic.
XX Homo sapiens.
XX WO200032769-A2.
XX
XX 08-JUN-2000.
XX
XX 26-NOV-1999; 99WO-TB02018.
XX
XX 27-NOV-1998; 98GB-00026143.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
XX WPI; 2000-412317/35.
XX N-PSDB; AAD01311, AAD01312, AAD01313.
XX
XX Novel polypeptides expressed in tumor cells useful for treating cancers
XX have an ability to complex with a major histocompatibility complex
XX molecule and comprises a specific unbroken amino acid sequence.
XX
XX Claim 1; Fig 7; 80pp; English.
XX
XX The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
XX decapeptide sequences, that function as tumour rejection antigens (TRAAs).
XX These peptides are capable of forming a complex with major
XX histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
XX Antigen), that are recognised by T-lymphocytes and elicit an immune
XX response from cytolytic T-lymphocytes (CTL). They function as an immune
XX response stimulator. Tumour rejection antigens are useful in prophylaxis,
XX therapy and diagnosis of tumours and are effective in controlling or
XX preventing tumour growth. The present sequence is the human MAGE-A10
XX protein, comprising nonapeptides and decapeptides, that serve as tumour
XX rejection antigens (TRAAs). The novel TRAAs encoded by MAGE-A10 is
XX identified using melanoma cell line (LBI751-MEL), stimulated by
XX autologous CTL clone (447A/5) to produce TNF (tumour necrosis factor).
XX Expression of MAGE-A10 has been detected in a variety of tumours like
XX melanomas, carcinomas of the head and neck, bladder and prostate,
XX myelomas and lung cancer. The only normal tissue expressing MAGE-A10 is
XX the testis
XX
SQ Sequence 369 AA;
Query Match 100.0%; Score 47; DB 3; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLLPKYQMK 9
Db 144 FLLPKYQMK 152
RESULT 5
AAB80297
ID AAB80297 standard; protein; 369 AA.
XX
XX AAB80297;
XX
XX 24-APR-2001 (first entry)
XX
XX Human prostate cancer antigen #25.
XX
XX Immunosuppressive; nootropic; neuroprotective; antiviral; vulnery;
KW anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant;
KW immune disorder; cardiovascular disorder; neurological disease;
KW infection; cancer; cytostatic; antiarthritic; antirheumatic;
KW antiasthmatic; anticonvulsant; vasotropic; vulnery; human;
KW secreted protein; prostate cancer antigen.
XX
XX Homo sapiens.

XX WO200107476-A1.
XX
XX 01-FEB-2001.
XX
XX 20-JUL-2000; 2000WO-US019666.
XX
XX 21-JUL-1999; 99US-0144972P.
XX 13-AUG-1999; 99US-0148681P.
XX 17-AUG-1999; 99US-0149173P.
XX 06-OCT-1999; 99US-0158004P.
XX 05-APR-2000; 2000US-0194689P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (ROSE/) ROSEN C A.
XX Rosen CA, Birse C;
XX
XX WPI; 2001-138554/14.
XX N-PSDB; AAF72765.
XX
XX New nucleic acid molecule encoding human secreted prostate cancer
XX antigens, useful for the diagnosis and treatment of disorders such as
XX cancer, leukemia and autoimmune disease.
XX
XX Claim 11; Page 399-400; 433pp; English.
XX
XX The present invention relates to human secreted prostate cancer antigen
XX coding sequences (AAF72741-AAF72789) and proteins (AAB80273-AAB80321).
XX The coding sequences and proteins of the present invention are useful for
XX preventing, treating or ameliorating a medical condition; and for the
XX diagnosis and treatment of diseases and disorders. Diseases and disorders
XX that can be diagnosed and treated include (auto)immune diseases (e.g.
XX graft versus host disease and rheumatoid arthritis), inflammatory and
XX allergic disorders (e.g. asthma), hyperproliferative disorders (e.g.
XX cancers and leukemias), cardiovascular disorders (e.g. heart attacks and
XX arrhythmias), cerebrovascular disorders (e.g. stroke), arterial occlusive
XX disorders (e.g. arteriosclerosis), angiogenesis related disorders (e.g.
XX retinopathy and kelooid scars), ocular disorders (e.g. glaucoma),
XX neurological disorders (e.g. Alzheimer's, Parkinson's disease, epilepsy
XX and Creutzfeld-Jakob disease) and infections caused by bacteria, fungi,
XX viruses or parasites. They may also be useful for wound healing,
XX epithelial cell proliferation, supporting cell culture, tissue
XX regeneration, birth control and as a food additive or preservative
XX
SQ Sequence 369 AA;
Query Match 100.0%; Score 47; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLLPKYQMK 9
Db 144 FLLPKYQMK 152
RESULT 6
ABR48215
ID ABR48215 standard; protein; 369 AA.
XX
XX ABR48215;
XX
XX 12-JUN-2003 (first entry)
XX
XX Human bladder cancer associated protein sequence SEQ ID NO:149.
XX
XX Human; bladder cancer; cytostatic; gene therapy; vaccine.
XX
XX Homo sapiens.
XX
XX WO2003003906-A2.
XX
XX 16-JAN-2003.

```

XX 03-JUL-2002; 2002WO-US021338.
PF
XX
XX 03-JUL-2001; 2001US-0302814P.
PR
XX 03-AUG-2001; 2001US-0310099P.
PR
XX 08-NOV-2001; 2001US-0343705P.
PR
XX 13-NOV-2001; 2001US-0350666P.
PR
XX 12-APR-2002; 2002US-0372246P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
PA
XX Mack DH, Aziz N;
XX
XX WPI; 2003-201532/19.
DR
XX N-PSDB; ACC51029.
XX
XX Detecting a bladder cancer-associated transcript in a cell from a
PT patient, comprises contacting a biological sample from the patient with a
PT bladder cancer-associated polynucleotide or antibody.
XX
XX Claim 10; Page 282; 307pp; English.
XX
XX The present invention describes a method for detecting a bladder cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with a polynucleotide
CC that selectively hybridizes to a sequence that is 80 % identical to a
CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
CC encode the human bladder cancer-associated proteins given in ABR48146 to
CC ABR48242). Bladder cancer-associated sequences from the present invention
CC have cytostatic activities, and can be used in antisense gene therapy and
CC in vaccine production. The method can be used for detecting a bladder
CC cancer-associated transcript in a cell from a patient. The method is
CC useful in diagnosing or treating bladder cancer and in screening for
CC compounds that modulate bladder cancer, such as hormones or antibodies.
CC The nucleic acid molecules from the present invention may be used in
CC various screening and diagnostic methods, and for gene therapy, vaccine
CC and/or antisense/inhibition applications
XX
XX Sequence 369 AA;
SQ
Query Match 100.0%; Score 47; DB 6; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLLFKYQMK 9
Db 144 FLLFKYQMK 152
RESULT 7
ABUS6516
ID ABUS6516 standard; protein; 369 AA.
XX
XX ABUS6516;
AC
XX
XX 02-APR-2003 (first entry)
DT
XX
XX Lung cancer-associated polypeptide #109.
XX
XX Lung cancer-associated polypeptide; cytostatic; emphysema;
KW antiinflammatory; antiaesthetic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
XX Unidentified.
OS
XX
XX WO200286443-A2.
PN
XX
XX 31-OCT-2002.
PD
XX
XX 18-APR-2002; 2002WO-US012476.
PF
XX

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PR 18-APR-2001; 2001US-0284770P.
PR
XX 10-MAY-2001; 2001US-0290492P.
PR
XX 09-NOV-2001; 2001US-0339245P.
PR
XX 13-NOV-2001; 2001US-0350666P.
PR
XX 29-NOV-2001; 2001US-0334370P.
PR
XX 12-APR-2002; 2002US-0372246P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
PA
XX Aziz N, Murray R;
XX
XX WPI; 2003-093161/08.
DR
XX N-PSDB; ABX76240.
XX
XX Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
XX Claim 27; Page 276-277; 453pp; English.
XX
XX The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridizes
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
CC invention
XX
XX Sequence 369 AA;
SQ
Query Match 100.0%; Score 47; DB 6; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLLFKYQMK 9
Db 144 FLLFKYQMK 152
RESULT 8
ABOS8424
ID ABOS8424 standard; protein; 383 AA.
XX
XX ABOS8424;
AC
XX
XX 29-JUL-2004 (first entry)
DT
XX
XX Human genome derived single exon protein #4658.
XX
XX Human; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
XX
XX Homo sapiens.
OS
XX
XX US2003194704-A1.
PN
XX
XX 16-OCT-2003.
PD
XX
XX 03-APR-2002; 2002US-00029386.
PF
XX

```

PR 03-APR-2002; 2002US-00029386.
XX (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
XX
PI Penn SG, Rank DR, Hanzel DK;
XX
XX WPI; 2004-119264/12.
DR
XX
XX New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX
XX Claim 45; SEQ ID NO 32058; 80pp; English.
XX
XX The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 688 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridizes under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subsequence, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterizing
CC alternative splicing events, in detecting and characterizing gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe protein of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
XX Seq Sequence 383 AA;
SQ
Query Match 100.0%; Score 47; DB 8; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FLLFKYQMK 9
Db 165 FLLFKYQMK 173
RESULT 9
ABB98179
ID ABB98179 standard; protein; 260 AA.
XX
XX ABB98179;
XX
XX
DT 05-NOV-2002 (first entry)
XX Human 52020 MAGE-like protein consensus sequence.

XX Human; 52020 MAGE-like protein; nootropic; neuroprotective;
KW antiparkinsonian; dermatological; immunosuppressive; antiinflammatory;
KW vulnery; cytostatic; neuroleptic; anticonvulsant; gene therapy;
KW vaccine; melanoma associated antigen-like protein; cancer;
KW neurodegenerative disorder; epilepsy; Alzheimer's disease;
KW Parkinson's disease; schizophrenia; autoimmune disorder; systemic lupus;
KW erythematous; inflammatory disorder.
XX
OS Synthetic.
XX
PN WO200259314-A2.
XX
PD 01-AUG-2002.
XX
XX 28-DEC-2001; 2001WO-US049597.
XX
XX 28-DEC-2000; 2000US-0258517P.
XX 27-DEC-2001; 2001US-00034864.
XX (MILL-) MILLENNIUM PHARM INC.
XX
PI Meyers RA;
XX
XX WPI; 2002-599790/64.
DR
XX Nucleic acid molecule and 52020 protein, useful in treating 52020-
XX mediated or -related disorders, e.g. cancers, neurodegenerative or
XX autoimmune diseases, in predictive medicine, e.g. diagnostic assays, and
XX as vaccines.
XX
XX Disclosure; Fig 3; 105pp; English.
XX
XX The invention relates to a newly identified protein designated 52020, a
XX human melanoma associated antigen-like (MAGE-like) protein. The activity
XX of the protein of the invention may be described as, nootropic,
XX neuroprotective, antiparkinsonian, dermatological, immunosuppressive,
XX antiinflammatory, vulnery, cytostatic, neuroleptic and anticonvulsant.
XX The isolated nucleic acid molecule is useful in expressing a 52020
XX protein (e.g. via a recombinant expression vector in a host cell in gene
XX therapy applications), in detecting a 52020 mRNA or a genetic alteration
XX in a 52020 gene, and in modulating the activity of the 52020 protein. The
XX 52020 proteins are useful in treating disorders characterised by
XX insufficient or excessive production of a 52020 binding partner or
XX production of 52020 inhibitors, such as cancers, neurodegenerative
XX disorders (e.g. epilepsy, Alzheimer's and Parkinson's disease,
XX schizophrenia), autoimmune disorders such as systemic lupus
XX erythematous, and inflammatory disorders, and may also be used for
XX tissue repair. The nucleic acid molecules, proteins, protein homologues,
XX and antibodies may also be used in predictive medicine (e.g. diagnostic
XX assays, prognostic assays, monitoring clinical trials) and as vaccines.
XX The current sequence represents the human 52020 MAGE-like protein
XX consensus sequence
XX
SQ Sequence 260 AA;
Query Match 87.2%; Score 41; DB 5; Length 260;
Best Local Similarity 88.9%; Pred. No. 8.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 FLLFKYQMK 9
Db 148 FLLFKYQMK 156
RESULT 10
ADD22980
ID ADD22980 standard; peptide; 260 AA.
XX
XX ADD22980;
XX
XX 15-JAN-2004 (first entry)
XX
XX

DE Melanoma associated antigen consensus sequence.

XX Pyridoxal-phosphate dependent enzyme; 22406; acyltransferase; 32447;

KW ATPase; 7716; aminotransferase; 25233; ring finger protein; 8035; 84242;

KW aminopeptidase; 55304; metalloproteinase; 52999; ADP-ribosyltransferase;

KW 21999; melanoma associated antigen; 52020; heart failure;

KW ischaemic heart disease; myocardial infarction; hypertension;

KW pericarditis; atherosclerosis; hepatic failure; viral hepatitis; cancer;

KW intracerebral haemorrhage; brain abscess; Alzheimer's disease;

KW Pick disease; Parkinson's disease; Huntington's disease;

KW amyotrophic lateral sclerosis; inflammatory bowel disease;

KW Crohn's disease; benign prostatic hypertrophy;

KW systemic lupus erythematosus; cardiac; hepatotropic; virucide;

KW cytostatic; cerebroprotective; nontropic; neuroprotective;

KW anticonvulsant; antiinflammatory; immunosuppressive.

XX

OS Synthetic.

XX

XX US2003064439-A1.

PN 03-APR-2003.

XX

XX 07-JUN-2002; 2002US-00164965.

PF

XX 17-FEB-2000; 2000US-0183208P.

PR 26-JUN-2000; 2000US-0214138P.

XX 20-JUL-2000; 2000US-0219740P.

PR 20-JUL-2000; 2000US-0220465P.

XX 29-NOV-2000; 2000US-0253878P.

PR 30-NOV-2000; 2000US-0250073P.

XX 30-NOV-2000; 2000US-0250338P.

PR 30-NOV-2000; 2000US-0250348P.

XX 28-DEC-2000; 2000US-0258517P.

PR 20-FEB-2001; 2001US-00789300.

XX 22-JUN-2001; 2001US-00887389.

PR 18-JUL-2001; 2001US-00908180.

XX 19-JUL-2001; 2001US-00908928.

PR 28-NOV-2001; 2001US-00996194.

XX 27-DEC-2001; 2001US-00034864.

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX

XX Bandaru R, Gluckmann MA, Meyers RE, Rudolph-Owen LA;

PI WPI; 2003-625445/59.

XX

XX New isolated 22406 nucleic acids and polypeptides, useful for diagnosing

PT and treating 22406-mediated disorders, such as myocardial infarction,

PT hypertension, atherosclerosis, viral hepatitis, cancer and/or Alzheimer's

PT disease.

XX

PS Disclosure; SEQ ID NO 43; 349pp; English.

XX

XX The present invention relates to the isolation of a novel human pyridoxal

CC -phosphate dependent enzyme family member (22406), a human

CC acyltransferase (32447), a human ATPase (7716), a human aminotransferase

CC (25233), human ring finger proteins (8035 and 84242), a human

CC aminopeptidase (55304), a human metalloproteinase (52999), a human ADP-

CC ribosyltransferase (21999), and a human melanoma associated antigen

CC (52020). Also disclosed are the polynucleotide sequences encoding these

CC novel human proteins. The polynucleotides and polypeptides of the present

CC invention are useful for diagnosing and treating disorders, such as heart

CC failure, ischaemic heart disease, myocardial infarction, hypertension,

CC pericarditis, atherosclerosis, hepatic failure, viral hepatitis, cancer,

CC intracerebral haemorrhage, brain abscess, Alzheimer's disease, Pick

CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral

CC sclerosis, inflammatory bowel disease, Crohn's disease, benign prostatic

CC hypertrophy and systemic lupus erythematosus. The present sequence

CC represents a consensus sequence.

XX

SQ Sequence 260 AA;

XX Query Match 87.2%; Score 41; DB 7; Length 260;

Best Local Similarity 87.2%; Score 41; DB 6; Length 347;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLLPKYQMK 9

DB 148 FLLLYQMK 156

RESULT 11

ADA55634

ID ADA55634 standard; protein; 347 AA.

XX

AC ADA55634;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human protein, SEQ ID 3202.

XX

KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;

KW Gene Therapy; human; secretory protein; membrane proteins; cancer;

KW inflammatory disease; osteoporosis; neurological disease.

XX

OS Homo sapiens.

XX

PN EP1293569-A2.

XX

PD 19-MAR-2003.

XX

PF 21-MAR-2002; 2002EP-00006586.

XX

PR 14-SEP-2001; 2001JP-00328381.

PR 24-JAN-2002; 2002US-0350435P.

XX

XX (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;

PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX

DR WPI; 2003-395539/38.

DR N-PSDB; ADA53995.

XX

XX New polynucleotides encoding full-length polypeptides, e.g. secretory

PT and/or membrane proteins, useful for developing medicines for diseases in

PT which the gene is involved, or as target molecules for gene therapy.

XX

PS Claim 14; SEQ ID NO 3202; 205pp; English.

XX

CC The present invention relates to novel human secretory or membrane

CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-

CC ADA54071). The coding sequences are useful in the gene therapy of

CC diseases caused by abnormalities of the proteins, e.g. cancer,

CC inflammatory diseases, osteoporosis or neurological disease.

XX

SQ Sequence 347 AA;

XX Query Match 87.2%; Score 41; DB 6; Length 347;

Best Local Similarity 77.8%; Pred. No. 11;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLPKYQMK 9

DB 121 YLLLYQMK 129

RESULT 12

ABB37733

ID ABB37733 standard; peptide; 276 AA.

XX

AC ABB37733;

XX

DT 04-FEB-2002 (first entry)

XX Peptide #5239 encoded by human foetal liver single exon probe.
DE Human; foetal liver; gene expression; single exon nucleic acid probe.
KW Homo sapiens.
OS WO200157277-A2.
PN 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000669.
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human foetal liver.
XX Claim 27; SEQ ID NO 30369; 639pp + Sequence Listing; English.
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human foetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 276 AA;
SQ
Query Match 78.7%; Score 37; DB 4; Length 276;
Best Local Similarity 77.8%; Pred. No. 54;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FLLFKYQMK 9
DB 241 FLLKYQVK 249
RESULT 13
ABB23008
ID ABB23008 standard; protein; 276 AA.
XX ABB23008;
XX 23-JAN-2002 (first entry)
DT
DE Protein #5007 encoded by probe for measuring heart cell gene expression.
XX Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX Homo sapiens.
OS WO200157274-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000666.
XX

XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488899/53.
XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
XX Claim 15; SEQ ID NO 24778; 530pp; English.
XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 276 AA;
SQ
Query Match 78.7%; Score 37; DB 4; Length 276;
Best Local Similarity 77.8%; Pred. No. 54;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FLLFKYQMK 9
DB 241 FLLKYQVK 249
RESULT 14
ABB23023
ID ABB23023 standard; protein; 473 AA.
XX ABB23023;
XX 23-JAN-2002 (first entry)
DT
DE Protein #5022 encoded by probe for measuring heart cell gene expression.
XX Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX Homo sapiens.
OS WO200157274-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000666.
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR

XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488899/53.
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts.
 XX Claim 15; SEQ ID NO 24793; 530pp; English.
 XX The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC ABA1535-ABA41305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting,
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the
 CC human heart and vascular system e.g. cardiovascular disease,
 CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 473 AA;
 Query Match 78.7%; Score 37; DB 4; Length 473;
 Best Local Similarity 77.8%; Pred. No. 92;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FLLFKYQMK 9
 DB 302 FLLKYQVK 310
 RESULT 15
 AAW81546
 ID AAW81546 standard; protein; 1142 AA.
 XX AC AAW81546;
 XX 01-MAR-1999 (first entry)
 XX Tumour rejection antigen precursor MAGE-C1.
 XX MAGE-C1; human; tumour rejection antigen precursor; TRAP; therapy;
 XX diagnosis.
 XX Homo sapiens.
 XX WO9849184-A1.
 XX 05-NOV-1998.
 XX 24-APR-1998; 98WO-US008493.
 XX 25-APR-1997; 97US-00845528.
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX Lucas S, De Smet C, Boon-Falleur T;
 XX WPI; 1999-024041/02.
 XX N-PSDB; AAV69720.
 XX Tumour rejection antigen precursors - used for determining presence of
 PT cytolytic T cells specific for complexes of a human leukocyte antigen.
 XX Disclosure; Page 43-46; 84pp; English.
 XX This is the amino acid sequence of novel human tumour rejection antigen
 CC precursor (TRAP) MAGE-C1, a novel member of the MAGE family that may be

CC recognised by cytotoxic T cells, leading to lysis of the tumour cells
 CC which express it. MACE-C1 and MACE-C2 (see AAW81547) are expressed in a
 CC variety of tumours and in normal testis cells, but not by other normal
 CC cells. MAGE-C1 cDNA (see AAV69720) was isolated from a melanoma LB373-MEL
 CC cDNA. MACE-C1 and MACE-C2 cDNAs (see AAV69726) are claimed, as are:
 CC expression vectors; transformed or transfected cell lines (e.g. COS and
 CC CHO); an isolated TRAP encoded by the cDNAs; a kit useful in a PCR based
 CC assay; a method for determining expression of a MACE-C1 gene using the
 CC kit; a polypeptide comprising a number of tumour rejection antigens derived
 CC from MAGE-C1 or MAGE-C2; and a polypeptide comprising at least one tumour
 CC rejection antigen derived from MAGE-C1 or MACE-C2 and at least one other
 CC tumour rejection antigen. MACE-C1 and MACE-C2 can be used in a method for
 CC determining the presence of cytolytic T cells specific for complexes of a
 CC human leukocyte antigen (HLA)
 XX
 SQ Sequence 1142 AA;
 Query Match 78.7%; Score 37; DB 2; Length 1142;
 Best Local Similarity 77.8%; Pred. No. 2.2e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FLLFKYQMK 9
 DB 918 FLLKYQVK 926

Search completed: March 17, 2006, 23:27:33
 Job time : 125 secs

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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:35:13 ; Search time 98.3333 Seconds
(without alignments)
38.242 Million cell updates/sec

Title: US-09-856-812b-48
Perfect score: 47
Sequence: 1 FLLFKYQMK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	369	4 US-10-036-542-84	Sequence 84, Appl
2	47	100.0	369	4 US-10-188-832-149	Sequence 149, Appl
3	47	100.0	369	5 US-10-658-884-4	Sequence 4, Appl
4	47	100.0	369	5 US-10-756-149-4721	Sequence 4721, Ap
5	47	100.0	383	4 US-10-029-386-32058	Sequence 32058, A
6	41	87.2	260	4 US-10-164-966-43	Sequence 43, Appl
7	41	87.2	260	4 US-10-034-864-4	Sequence 4, Appl
8	41	87.2	347	4 US-10-094-749-3202	Sequence 3202, Ap
9	37	78.7	276	3 US-09-864-761-38306	Sequence 38306, A
10	37	78.7	473	3 US-09-864-761-38321	Sequence 38321, A
11	37	78.7	1142	3 US-09-899-651-2	Sequence 2, Appl
12	37	78.7	1142	4 US-10-085-108-7	Sequence 7, Appl
13	37	78.7	1142	4 US-10-207-655-79	Sequence 79, Appl
14	37	78.7	1142	4 US-10-160-237-7	Sequence 7, Appl
15	37	78.7	1142	4 US-10-670-472A-73	Sequence 73, Appl
16	37	78.7	1155	5 US-10-450-763-54525	Sequence 54525, A
17	37	78.7	1208	5 US-10-450-763-54526	Sequence 54526, A
18	37	78.7	9222	5 US-10-450-763-51423	Sequence 51423, A
19	36	76.6	275	4 US-10-085-108-24	Sequence 24, Appl
20	35	74.5	34	3 US-09-764-887-160	Sequence 160, Appl
21	35	74.5	34	4 US-10-073-961-160	Sequence 160, Appl
22	35	74.5	141	3 US-09-864-761-37903	Sequence 37903, A
23	35	74.5	346	4 US-10-085-108-22	Sequence 22, Appl
24	35	74.5	346	4 US-10-321-802-24	Sequence 24, Appl
25	35	74.5	676	4 US-10-321-802-36	Sequence 36, Appl
26	35	74.5	676	4 US-10-424-599-268555	Sequence 268555,
27	34	72.3	51	4 US-10-424-599-275481	Sequence 275481,

28	34	72.3	92	4 US-10-424-599-130096	Sequence 130096,
29	34	72.3	100	4 US-10-425-115-338632	Sequence 338632,
30	34	72.3	606	4 US-10-282-122A-54392	Sequence 54392, A
31	33	70.2	84	4 US-10-425-115-361950	Sequence 361950,
32	33	70.2	244	5 US-10-732-923-9199	Sequence 9199, Ap
33	32	68.1	47	4 US-10-425-115-367202	Sequence 367202,
34	32	68.1	51	4 US-10-767-701-47922	Sequence 47922, A
35	32	68.1	63	4 US-10-424-599-225153	Sequence 225153,
36	32	68.1	67	4 US-10-425-115-262410	Sequence 262410,
37	32	68.1	104	4 US-10-425-115-199534	Sequence 199534,
38	32	68.1	126	4 US-10-424-599-153145	Sequence 153145,
39	32	68.1	132	4 US-10-437-963-19361	Sequence 19361,
40	32	68.1	152	4 US-10-437-963-168816	Sequence 168816,
41	32	68.1	315	4 US-10-093-766-40	Sequence 40, Appl
42	32	68.1	315	4 US-10-157-031-54	Sequence 54, Appl
43	32	68.1	315	4 US-10-295-027-366	Sequence 366, App
44	32	68.1	315	5 US-10-473-127-1079	Sequence 1079, Ap
45	32	68.1	315	5 US-10-473-127-1082	Sequence 1082, Ap

ALIGNMENTS

RESULT 1

US-10-036-542-84
; Sequence 84, Application US/10036542
; Publication NO. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: PA002P1
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-036-542-84

Query Match 100.0%; Score 47; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
DB 144 FLLFKYQMK 152

RESULT 2

US-10-188-832-149
; Sequence 149, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Nataasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer

```
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 149
; TYPE: PRT
; LENGTH: 369
; ORGANISM: Homo sapiens
US-10-188-832-149

Query Match      100.0%; Score 47; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLLFKYQMK 9
DB      144 FLLFKYQMK 152

RESULT 3
US-10-658-884-4
; Sequence 4, Application US/10658884
; Publication No. US20050019304A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: NOVEL HUMAN MAGE-LIKE PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/658,884
; FILING DATE: 09-Sep-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/773,870
; FILING DATE: 27-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0179 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
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; LIBRARY: GenBank
; CLONE: 533511
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-658-884-4

Query Match      100.0%; Score 47; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLLFKYQMK 9
DB      144 FLLFKYQMK 152

RESULT 4
US-10-756-149-4721
; Sequence 4721, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4721
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-756-149-4721

Query Match      100.0%; Score 47; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLLFKYQMK 9
DB      144 FLLFKYQMK 152

RESULT 5
US-10-029-386-32058
; Sequence 32058, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32058
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AF134576.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
; OTHER INFORMATION: SWISSPROT HIT: P43363, EVALUAE 0.00e+00
US-10-029-386-32058
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Query Match 100.0%; Score 47; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
|||||
DB 165 FLLFKYQMK 173

RESULT 6
US-10-164-966-43
; Sequence 43, Application US/10164966
; Publication No. US20030064439A1
; GENERAL INFORMATION:
; APPLICANT: Bandaru, Rajasekhara
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Encoding Melanoma
; TITLE OF INVENTION: Associated Antigen Molecules, Aminotransferase
; TITLE OF INVENTION: Molecules, ATPase Molecules, Acyltransferase Molecules,
; TITLE OF INVENTION: Pyridoxal-Phosphate Dependant Enzyme Molecules and Uses
; FILE REFERENCE: 35800/247400
; CURRENT APPLICATION NUMBER: US/10/164,966
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 10/034,864
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/258,517
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 09/996,194
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/250,348
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/250,073
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/253,878
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,338
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/908,928
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/220,465
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 09/908,180
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/219,740
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 09/887,389
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/214,138
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/789,300
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/183,208
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MAGE family PFAM consensus domain
US-10-164-966-43

Query Match 87.2%; Score 41; DB 4; Length 260;
Best Local Similarity 88.9%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 FLLFKYQMK 9
|||||

DB 148 FLLFKYQMK 156

RESULT 7
US-10-034-864-4
; Sequence 4, Application US/10034864
; Publication No. US20030166058A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 52020, A No. US20030166058A1el Human Melanoma Associated
; FILE REFERENCE: 35800/242058
; CURRENT APPLICATION NUMBER: US/10/034,864
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/258,517
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MAGE family PFAM consensus domain
US-10-034-864-4

Query Match 87.2%; Score 41; DB 4; Length 260;
Best Local Similarity 88.9%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 FLLFKYQMK 9
|||||
DB 148 FLLFKYQMK 156

RESULT 8
US-10-094-749-3202
; Sequence 3202, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3202
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-3202

Query Match 87.2%; Score 41; DB 4; Length 347;
Best Local Similarity 77.8%; Pred. No. 7.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLPKYQMK 9
:|:|:|:|
DB 121 YLLYKQMK 129

RESULT 9
US-09-864-761-38306
; Sequence 38306, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US 09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38306
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL022152.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
; OTHER INFORMATION: SWISSPROT HIT: P43361, EVALUATE 2.00e-11
; OTHER INFORMATION: EST_HUMAN HIT: BE727610.1, EVALUATE 6.00e-30

US-09-864-761-38306

Query Match 78.7%; Score 37; DB 3; Length 276;
Best Local Similarity 77.8%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLPKYQMK 9
:|:|:|:|
DB 241 FLLKYQVK 249

RESULT 10
US-09-864-761-38321
; Sequence 38321, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US 09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38321
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL023279.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.96
; OTHER INFORMATION: SWISSPROT HIT: P43363, EVALUATE 2.00e-48
; OTHER INFORMATION: EST_HUMAN HIT: BE895761.1, EVALUATE 4.00e-71

US-09-864-761-38321

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Query Match      78.7%; Score 37; DB 3; Length 473;
Best Local Similarity 77.8%; Pred. No. 67;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLLPKYQMK 9
Db 302 FLLPKYQVK 310

RESULT 11
US-09-899-651-2
; Sequence 2, Application US/09899651
; Patent No. US20020111470A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseeng
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer
; TITLE OF INVENTION: Associated
; TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
; FILE REFERENCE: LUD 5338
; CURRENT APPLICATION NUMBER: US/09/899,651
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/061,709
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-899-651-2

Query Match      78.7%; Score 37; DB 3; Length 1142;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLLPKYQMK 9
Db 918 FLLPKYQVK 926

RESULT 12
US-10-085-108-7
; Sequence 7, Application US/10085108
; Publication No. US20020176865A1
; GENERAL INFORMATION:
; APPLICANT: LUCAS, Sophie; BOON-FALLEUR, Thierry
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING
; FOR
; TUMOR REJECTION ANTIGEN PRECURSORS OF MEMBERS OF THE MAGE-C
; MAGE-B FAMILIES AND USES THEREOF
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/085,108
; FILING DATE: 01-Mar-2002
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/501,104
; FILING DATE: 09-Feb-2000
; APPLICATION NUMBER: 09/468,433
; FILING DATE: December 17, 1999
; APPLICATION NUMBER: 09/066,281
; FILING DATE: April 24, 1998
; APPLICATION NUMBER: 08/845,528
; FILING DATE: April 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary Anne Schofield
; REGISTRATION NUMBER: 36,669
; REFERENCE/DOCKET NUMBER: LUD 5611.1 JEL/MAS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3100
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1142
; TYPE: amino acids
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-085-108-7

Query Match      78.7%; Score 37; DB 4; Length 1142;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLLPKYQMK 9
Db 918 FLLPKYQVK 926

RESULT 13
US-10-207-655-79
; Sequence 79, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-79

Query Match      78.7%; Score 37; DB 4; Length 1142;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLLPKYQMK 9
Db 918 FLLPKYQVK 926

RESULT 14
US-10-160-237-7
; Sequence 7, Application US/10160237
; Publication No. US20030170256A1
; GENERAL INFORMATION:
; APPLICANT: LUCAS, Sophie; DE SMET, Charles; BOON-FALLEUR, Thierry
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING
; FOR TUMOR REJECTION ANTIGEN PRECURSOR MAGE-C1 AND MAGE-C2
; AND USES THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/160,237
FILING DATE: 04-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/066,281B
FILING DATE: April 24, 1998
APPLICATION NUMBER: 08/845,528
FILING DATE: April 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5455.2 US - JEL/MAS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3100
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1142
TYPE: amino acids
STRANDEDNESS: single-stranded
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-160-237-7

Query Match 78.7%; Score 37; DB 4; Length 1142;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
||| |||:
Db 918 FLLKYQVK 926

RESULT 15
US-10-670-472A-73
; Sequence 73, Application US/10670472A
; Publication No. US20040214779A1
; GENERAL INFORMATION:
; APPLICANT: MA, Wenbin
; APPLICANT: GERMEAU, Catherine
; APPLICANT: VAN DEN EYNDE, Benoit
; APPLICANT: COULIE, Pierre
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5780.2 US
; CURRENT APPLICATION NUMBER: US/10/670,472A
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/413,844
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/433,983
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 60/459,263
; PRIOR FILING DATE: 2003-04-02
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-670-472A-73

Query Match 78.7%; Score 37; DB 4; Length 1142;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FLLFKYQMK 9
||| |||:
Db 918 FLLKYQVK 926
Search completed: March 17, 2006, 23:41:20
Job time : 100.333 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:36:38 ; Search time 11.6667 Seconds
(without alignments)
22.081 Million cell updates/sec

Title: US-09-856-812B-48

Perfect score: 47

Sequence: 1 FLLFKYQMK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_New*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/PT_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	87.2	260	7	US-11-245-400-43
2	37	78.7	1142	7	US-11-044-051-73
3	32	68.1	447	7	US-11-087-099-3680
4	32	68.1	447	7	US-11-087-099-8381
5	32	68.1	448	7	US-11-087-099-10069
6	31	66.0	23	7	US-11-129-741-4113
7	31	66.0	251	7	US-11-080-991-38
8	30	63.8	20	6	US-10-895-064-1115
9	30	63.8	20	7	US-11-129-741-1115
10	30	63.8	89	7	US-11-096-568A-8788
11	30	63.8	96	7	US-11-096-568A-15129
12	30	63.8	102	7	US-11-096-568A-15128
13	30	63.8	156	7	US-11-096-568A-15127
14	30	63.8	282	7	US-11-096-568A-10623
15	30	63.8	288	7	US-11-096-568A-10622
16	30	63.8	342	7	US-11-096-568A-10621
17	29	61.7	116	7	US-11-096-568A-4025
18	29	61.7	165	7	US-11-098-686-11109
19	29	61.7	184	6	US-10-467-657-6490
20	29	61.7	221	7	US-11-096-568A-4900
21	29	61.7	269	7	US-11-098-686-11363
22	29	61.7	299	7	US-11-096-568A-1136
23	29	61.7	320	7	US-11-096-568A-12372
24	29	61.7	388	7	US-11-096-568A-1135
25	29	61.7	398	7	US-11-096-568A-1134

Sequence 36, Appl
Sequence 6, Appl
Sequence 79, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 7, Appl
Sequence 113, Appl
Sequence 12371, A
Sequence 3687, Ap
Sequence 12370, A
Sequence 1574, Ap
Sequence 1340, Ap
Sequence 69, Appl
Sequence 1587, Ap
Sequence 31, Appl
Sequence 33, Appl
Sequence 3262, Ap
Sequence 6856, Ap
Sequence 246, App
Sequence 321, App

26 29 61.7 419 7 US-11-112-882-36
27 29 61.7 419 7 US-11-166-993-6
28 29 61.7 419 7 US-11-146-428-79
29 29 61.7 421 7 US-11-166-993-2
30 29 61.7 421 7 US-11-166-993-4
31 29 61.7 422 7 US-11-166-993-7
32 29 61.7 422 7 US-11-166-993-113
33 29 61.7 425 7 US-11-098-568A-12371
34 29 61.7 466 7 US-11-072-512-3687
35 29 61.7 490 7 US-11-096-568A-12370
36 29 61.7 527 6 US-10-821-234-1574
37 29 61.7 564 6 US-10-821-234-1340
38 29 61.7 765 7 US-11-144-630-69
39 29 61.7 972 6 US-10-821-234-1587
40 28 59.6 14 7 US-11-032-498-31
41 28 59.6 14 7 US-11-032-498-33
42 28 59.6 58 6 US-10-467-657-3262
43 28 59.6 58 6 US-10-467-657-6856
44 28 59.6 123 6 US-10-793-626-246
45 28 59.6 124 6 US-10-485-517-321

ALIGNMENTS

RESULT 1

US-11-245-400-43
; Sequence 43, Application US/11245400
; Publication No. US20060040357A1
; GENERAL INFORMATION:
; APPLICANT: Bandaru, Rajasekhkar
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Encoding Melanoma
; TITLE OF INVENTION: Associated Antigen Molecules, Aminotransferase
; TITLE OF INVENTION: Molecules, ATPase Molecules, Acyltransferase Molecules,
; TITLE OF INVENTION: Pyridoxal-Phosphate Dependant Enzyme Molecules and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 35800/247400
; CURRENT APPLICATION NUMBER: US/11/245,400
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US/10/164,966
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 10/034,864
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/258,517
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 09/996,194
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/250,348
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/250,073
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/253,878
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,338
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/908,928
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/220,465
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MAGE family PFAM consensus domain
US-11-245-400-43

Query Match 87.2%; Score 41; DB 7; Length 260;
Best Local Similarity 88.9%; Pred. No. 0.67; Mismatches 0; Gaps 0;
Matches 8; Conservative 0; Indels 1; Indels 0;

QY 1 FLLFKYQMK 9
||| |||||
DB 148 FLLFKYQMK 156

RESULT 2

US-11-044-051-73
; Sequence 73, Application US/11044051
; Publication No. US2005025553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: GODELAINE, Danisle
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGS C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459,263
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-044-051-73

Query Match 78.7%; Score 37; DB 7; Length 1142;
Best Local Similarity 77.8%; Pred. No. 16; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 1; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
||| |||||
DB 918 FLLFKYQMK 926

RESULT 3

US-11-087-099-3680
; Sequence 3680, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3680
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Salmonella typhimurium LT2
US-11-087-099-3680

Query Match 68.1%; Score 32; DB 7; Length 447;
Best Local Similarity 55.6%; Pred. No. 62; Mismatches 3; Indels 1; Indels 0; Gaps 0;
Matches 5; Conservative 3; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
||| |||||
DB 373 FILFNRMK 381

RESULT 4

US-11-087-099-8381
; Sequence 8381, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 8381
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Salmonella enterica subsp. enterica serovar Typhi
US-11-087-099-8381

Query Match 68.1%; Score 32; DB 7; Length 447;
Best Local Similarity 55.6%; Pred. No. 62; Mismatches 3; Indels 1; Indels 0; Gaps 0;
Matches 5; Conservative 3; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
||| |||||
DB 373 FILFNRMK 381

RESULT 5

US-11-087-099-10069
; Sequence 10069, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 10069
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-11-087-099-10069

Query Match 68.1%; Score 32; DB 7; Length 448;
Best Local Similarity 55.6%; Pred. No. 62; Mismatches 3; Indels 1; Indels 0; Gaps 0;
Matches 5; Conservative 3; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
||| |||||
DB 374 FILFNRMK 382

RESULT 6

US-11-129-741-4113
; Sequence 4113, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4113
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-11-129-741-4113

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Query Match      66.0%; Score 31; DB 7; Length 23;
Best Local Similarity 62.5%; Pred. No. 6.1;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLLFKYQM 8
DB 5 FLLFRYSL 12

RESULT 7
US-11-080-991-38
; Sequence 38, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Vgiby, Petteer Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-38

Query Match      66.0%; Score 31; DB 7; Length 251;
Best Local Similarity 62.5%; Pred. No. 56;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLLFKYQM 8
DB 185 FLMFRPYM 192

RESULT 8
US-10-895-064-1115
; Sequence 1115, Application US/10895064
; Publication No. US20060018923A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; APPLICANT: LEUNG, FREDERICK C.
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: V0690.0031
; CURRENT APPLICATION NUMBER: US/10/895,064
; CURRENT FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 2918
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1115
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-10-895-064-1115

Query Match      63.8%; Score 30; DB 6; Length 20;
Best Local Similarity 62.5%; Pred. No. 8.4;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLLFKYQM 8
DB 5 FLLFRYAL 12
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RESULT 9
US-11-129-741-1115
; Sequence 1115, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; TITLE OF INVENTION: INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1115
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-11-129-741-1115

Query Match      63.8%; Score 30; DB 7; Length 20;
Best Local Similarity 62.5%; Pred. No. 8.4;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLLFKYQM 8
DB 5 FLLFRYAL 12

RESULT 10
US-11-096-568A-8788
; Sequence 8788, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 8788
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(89)
; OTHER INFORMATION: Ceres Seq. ID no. 11421034
US-11-096-568A-8788

Query Match      63.8%; Score 30; DB 7; Length 89;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLLFKYQM 9
DB 75 FLLFKFLSK 83

RESULT 11
US-11-096-568A-15129
; Sequence 15129, Application US/11096568A
; Publication No. US20060048240A1
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; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 15129
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(96)
; OTHER INFORMATION: Ceres Seq. ID no. 12342445
US-11-096-568A-15129

Query Match      63.8%; Score 30; DB 7; Length 96;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY 1 FLLFKYQMK 9
   |||||:
Db 15 FLLFKFLSK 23

RESULT 12
US-11-096-568A-15128
; Sequence 15128, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 15128
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(102)
; OTHER INFORMATION: Ceres Seq. ID no. 12342444
US-11-096-568A-15128

Query Match      63.8%; Score 30; DB 7; Length 102;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY 1 FLLFKYQMK 9
   |||||:
Db 21 FLLFKFLSK 29

RESULT 13
US-11-096-568A-15127
; Sequence 15127, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 15127
; LENGTH: 156
; TYPE: PRT
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; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(156)
; OTHER INFORMATION: Ceres Seq. ID no. 12342443
US-11-096-568A-15127

Query Match      63.8%; Score 30; DB 7; Length 156;
Best Local Similarity 66.7%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY 1 FLLFKYQMK 9
   |||||:
Db 75 FLLFKFLSK 83

RESULT 14
US-11-096-568A-10623
; Sequence 10623, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 10623
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(282)
; OTHER INFORMATION: Ceres Seq. ID no. 13596628
US-11-096-568A-10623

Query Match      63.8%; Score 30; DB 7; Length 282;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY 1 FLLFKYQMK 9
   |||||:
Db 15 FLLFKFLSK 23

RESULT 15
US-11-096-568A-10622
; Sequence 10622, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 10622
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(288)
; OTHER INFORMATION: Ceres Seq. ID no. 13596627
US-11-096-568A-10622

Query Match      63.8%; Score 30; DB 7; Length 288;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 0;
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Qy 1 FLLFYQMK 9
Db 21 FLLFKELSK 29

Search completed: March 17, 2006, 23:42:00
Job time : 12.6667 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:28:08 ; Search time 19.3333 Seconds
(without alignments)
44.791 Million cell updates/sec

Title: US-09-856-812b-48

Perfect score: 47

Sequence: 1 FLLPKYQMK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	369	I38659	melanoma antigen M
2	37	78.7	211	T32590	hypothetical prote
3	35	74.5	138	H6434	hypothetical prote
4	35	74.5	975	T30816	macrophage colony-
5	34	72.3	234	I38667	melanoma antigen M
6	34	72.3	606	B81338	KdPD truncated hom
7	34	72.3	674	D72329	hypothetical prote
8	34	72.3	1132	T44001	major DNA binding
9	33	70.2	244	F90126	hypothetical prote
10	33	70.2	493	T09919	hypothetical prote
11	33	70.2	686	A10020	probable membrane
12	32	68.1	126	G69990	conserved hypothet
13	32	68.1	170	S64488	regulatory protein
14	32	68.1	190	H85357	hypothetical prote
15	32	68.1	270	G69443	conserved hypothet
16	32	68.1	315	I38668	melanoma antigen M
17	32	68.1	332	D71274	probable prolipopr
18	32	68.1	382	AF2460	glycosyltransferase
19	32	68.1	408	T25644	hypothetical prote
20	32	68.1	447	A10701	probable amino aci
21	32	68.1	517	S73900	MG120 homolog A65
22	32	68.1	569	H87926	protein C17D12.7 [
23	32	68.1	639	A25486	kininogen, HMW I p
24	32	68.1	718	E71100	hypothetical prote
25	32	68.1	1131	T41943	major DNA binding
26	31	66.0	191	F89924	conserved hypothet
27	31	66.0	191	C89877	conserved hypothet
28	31	66.0	320	B97911	hypothetical prote
29	31	66.0	462	A41158	dipeptidyl-peptida

30	31	66.0	481	2	F95040	hypothetical prote
31	31	66.0	481	2	T50030	capsular polysacch
32	31	66.0	523	2	F86217	protein T27G7.12 [
33	31	66.0	555	2	T06491	beta-fructofuranos
34	31	66.0	558	2	S38614	hypothetical prote
35	31	66.0	582	2	T06380	beta-fructofuranos
36	31	66.0	744	2	C84527	probable receptor-
37	31	66.0	1160	2	A36256	DNA-binding protei
38	31	66.0	1262	2	T33074	hypothetical prote
39	31	66.0	1446	2	T30916	carboxypeptidase D
40	30	63.8	74	2	S72293	ribosomal protein
41	30	63.8	80	2	T11069	NADH2 dehydrogenas
42	30	63.8	92	2	AC2711	hypothetical prote
43	30	63.8	125	2	G91199	hypothetical prote
44	30	63.8	125	2	C86046	hypothetical prote
45	30	63.8	171	2	F90108	hypothetical prote

ALIGNMENTS

RESULT 1

I38659

melanoma antigen MAGE-10 - human

C:Species: Homo sapiens (man)

C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004

C:Accession: I38659

R:De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; B

oon, T.

Immunogenetics 40, 360-369, 1994

A:Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fa

A:Reference number: I38659; MUID:95012457; PMID:7927540

A:Accession: I38659

A:Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: DNA

A:Residues: 1-369 <RES>

A:Cross-references: UNIPROT:P43363; UNIPARC:UPI00000000C57; EMBL:U10685; MID:G533510; PI

C:Genetics:

A:Gene: GDB:MAGEA10; MAGE10

A:Cross-references: GDB:331126

A:Map position: Xq28-Xq28

A:Introns: #status absent

C:Superfamily: tumor associated protein MAGE

Query Match 100.0%; Score 47; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLPKYQMK 9

DB 144 FLLPKYQMK 152

RESULT 2

T32590

hypothetical protein C02B10.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T32590

R:Nelson, J.; White, S.; Hawkins, J.; Wohldmann, P.

submitted to the EMBL Data Library, December 1997

A:Description: The sequence of C. elegans cosmid C02B10.

A:Reference number: Z21196

A:Accession: T32590

A:Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: DNA

A:Residues: 1-211 <NLS>

A:Cross-references: UNIPROT:O44443; UNIPARC:UPI000017B714; EMBL:AF038605; PIDN:AAB92018

A:Experimental source: strain Bristol N2; clone C02B10

C:Genetics:

A:Gene: CESP:C02B10.3

A:Map position: 4

A:Introns: 63/2; 168/2

```
Query Match      78.7%; Score 37; DB 2; Length 211;
Best Local Similarity 75.0%; Pred. No. 2.7;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLLFKYQM 8
      ||:||||:
DB      19 FLIFKYQL 26

RESULT 3
H64434
hypothetical protein homolog MJ1081 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: H64434
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.;
raon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Raine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A>Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: H64434
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-138 <BUL>
A:Cross-references: UNIPROT:Q58481; UNIPARC:UPI0000139FB5; GB:U67551; GB:L77117; NID:G15
C:Genetics:
A:Map position: FOR1021224-1021640
A:Start codon: TTG
C:Superfamily: uncharacterized conserved protein

Query Match      74.5%; Score 35; DB 1; Length 138;
Best Local Similarity 75.0%; Pred. No. 4.7;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LLFKYQMK 9
      :||||:|
DB      6 MLFKYQIK 13

RESULT 4
T30816
macrophage colony-stimulating factor receptor - Japanese pufferfish
C:Species: Fugu rubripes (Japanese pufferfish)
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C:Accession: T30816
R:How, G.F.; Venkatesh, B.; Brenner, S.
Genome Res. 6, 1185-1191, 1996
A>Title: Conserved linkage between the pufferfish (Fugu rubripes) and human genes for pla
A:Reference number: Z20882; MUID:97129405; PMID:8973913
A:Accession: T30816
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-975 <HOW>
A:Cross-references: UNIPROT:P79750; UNIPARC:UPI00000FB6C2; EMBL:U63926; NID:G1752706; PI
C:Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homology

Query Match      74.5%; Score 35; DB 2; Length 975;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLLFKYQMK 9
      ||:||||:
DB      537 FLLYKYQK 545

RESULT 5
I38667
melanoma antigen Mage-8 - human
C:Species: Homo sapiens (man)
C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
```

```
C:Accession: I38667
R:De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Bar
con, T.
Immunogenetics 40, 360-369, 1994
A>Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fam
A:Reference number: I38659; MUID:95012457; PMID:7927540
A:Accession: I38667
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-234 <RES>
A:Cross-references: UNIPROT:P43361; UNIPARC:UPI00000335D6; EMBL:U10693; NID:G533525; PI
C:Genetics:
A:Gene: GDB:MAGEA8; MAGE8
A:Cross-references: GDB:331123
A:Map position: Xq28-Xq28
A:Introns: #status absent
C:Superfamily: tumor associated protein MAGE

Query Match      72.3%; Score 34; DB 2; Length 234;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLLFKYQMK 9
      |||||:|
DB      122 FLLRKYQIK 130

RESULT 6
B81338
KdpD truncated homolog Cj0679 [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: B81338
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilli
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barre
Nature 403, 665-668, 2000
A>Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals h
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: B81338
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-606 <PAR>
A:Cross-references: UNIPROT:Q9PPM8; UNIPARC:UPI00000C1CE7; GB:AL139076; GB:AL111168; NFI
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: kdpC; Cj0679
C:Keywords: phosphotransferase

Query Match      72.3%; Score 34; DB 2; Length 606;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FLLFKYQMK 9
      |||||:|
DB      370 FLLRKYEVK 378

RESULT 7
D72329
hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: D72329
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
Nature 399, 323-329, 1999
A>Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: D72329
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-674 <ARN>
```


A;Cross-references: UNIPROT:Q9WZS4; UNIPARC:UPI00000C137D; GB:AB001749; GB:AB000512; NID
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0817

Query Match 72.3%; Score 34; DB 2; Length 674;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLLPKYQMK 9
||| ||| |
Db 205 FLLFYQUR 213

RESULT 8
T44001
major DNA binding protein [imported] - human herpesvirus 6
C;Species: human herpesvirus 6
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T44001; T44188
C;Isegawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; Kawa
J.; Virol. 73, 8053-8063, 1999
A;Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and
A;Reference number: Z22732; MUID:99412319; PMID:10482554
A;Accession: T44001
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1132 <ISE>
A;Cross-references: UNIPROT:P52538; UNIPARC:UPI00000008EC; EMBL:AB021506; NID:g4995977;
A;Experimental source: strain HST; pop. variant B
R;Domínguez, G.; Dambagh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.
J. Virol. 73, 8040-8052, 1999
A;Title: Human herpesvirus 6B genome sequence: coding content and comparison with human
A;Reference number: Z22734; MUID:99412318; PMID:10482553
A;Accession: T44188
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1132 <DOM>
A;Cross-references: UNIPARC:UPI00000008EC; EMBL:AF157706; PIDN:AB06339.1
A;Experimental source: strain Z29; variant B
C;Genetics:
A;Gene: U41
C;Superfamily: herpesvirus DNA-binding protein

Query Match 72.3%; Score 34; DB 2; Length 1132;
Best Local Similarity 77.8%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLLPKYQMK 9
||| ||| |
Db 771 FLLPKYHDK 779

RESULT 9
F90126
hypothetical protein fkbp [imported] - Guillardia theta nucleomorph
C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: F90126
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reif
Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
A;Accession: F90126
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-244 <DOU>
A;Cross-references: UNIPROT:Q98S76; UNIPARC:UPI0000096E1E; GB:AF083031; NID:g13794329; F
C;Genetics:
A;Gene: fkbp
A;Map position: 3
A;Genome: nucleomorph

C;Keywords: nucleomorph

Query Match 70.2%; Score 33; DB 2; Length 244;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLLPKYQMK 9
||| ||| |
Db 9 FLLPKYTTK 17

RESULT 10
T09919
hypothetical protein T16L4.70 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09919
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.P.;
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16897
A;Accession: T09919
A;Molecule type: DNA
A;Residues: 1-493 <BEV>
A;Cross-references: UNIPROT:Q9SU89; UNIPARC:UPI00000AC268; EMBL:AL079344; GSPDB:GN00062
A;Experimental source: cultivar Columbia; BAC clone T16L4
C;Genetics:
A;Gene: ATSP:T16L4.70
A;Map position: 4
A;Introns: 65/2
C;Superfamily: Arabidopsis thaliana hypothetical protein T16L4.70

Query Match 70.2%; Score 33; DB 2; Length 493;
Best Local Similarity 85.7%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLPKYQ 7
||| ||| |
Db 83 FLLPEYQ 89

RESULT 11
A10020
probable membrane receptor protein YPO0164 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: A10020
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
geno-farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: A10020
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-686 <KUR>
A;Cross-references: UNIPROT:Q8ZJES; UNIPARC:UPI00000DCBFD; GB:AL590842; PIDN:CAC89027.1
C;Genetics:
A;Gene: YPO0164

Query Match 70.2%; Score 33; DB 2; Length 686;
Best Local Similarity 66.7%; Pred. No. 59;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FLLPKYQMK 9
||| ||| |
Db 513 FILPKYDPK 521

RESULT 12
G69990
conserved hypothetical protein ytep - Bacillus subtilis
C;Species: Bacillus subtilis

GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:21:42 ; Search time 123 Seconds
(without alignments)
51.624 Million cell updates/sec

Title: US-09-856-812B-48

Perfect score: 47

Sequence: 1 FLLFKYQMK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	369	1 MAGAA HUMAN	P43363 homo sapien
2	43	91.5	243	2 Q9J9R4 MOUSE	Q9j9r4 mus musculus
3	43	91.5	315	2 O89008 MOUSE	O89008 mus musculus
4	41	87.2	170	2 Q9BZ78 HUMAN	Q9bz78 homo sapien
5	41	87.2	347	2 Q9SLZ2 HUMAN	Q9slz2 homo sapien
6	41	87.2	378	2 Q9TYI4 CANPA	Q9tyi4 canis faml
7	40	85.1	270	2 Q4R5W1 MACFA	Q4r5w1 macaca fasc
8	40	85.1	346	1 MAGB4 HUMAN	O15481 homo sapien
9	40	85.1	346	2 Q6FHH4 HUMAN	Q6fhh4 homo sapien
10	40	85.1	346	2 Q81Z00 HUMAN	Q81z00 homo sapien
11	39	83.0	123	2 Q7MX06 PORGI	Q7mx06 porphyromon
12	38	80.9	320	2 O89009 MOUSE	O89009 mus musculus
13	37	78.7	175	1 IF3C CYAME	Q85977 cyanidiosch
14	37	78.7	376	2 Q9SKZ1 FELCA	Q9skz1 felis silve
15	37	78.7	1140	2 Q55EAO DICTDI	Q55eao dictyosteli
16	37	78.7	1142	1 MAGC1 HUMAN	O67032 homo sapien
17	36	76.6	319	1 MAGB2 HUMAN	O15479 homo sapien
18	36	76.6	590	2 Q81B68 PLAF7	O81b68 plasmodium
19	35	74.5	138	1 Y10B1 METJA	Q58481 methanococ
20	35	74.5	168	2 Q8C3B7 MOUSE	Q8c3b7 mus musculus
21	35	74.5	206	2 Q80V80 MOUSE	Q80v80 mus musculus
22	35	74.5	267	2 Q54UT5 DICTDI	Q54ut5 dictyosteli
23	35	74.5	360	2 Q6AY37 RAT	Q6ay37 rattus norv
24	35	74.5	363	2 Q9CWN4 MOUSE	Q9cwn4 mus musculus
25	35	74.5	394	2 Q519G9 ENTHI	Q519g9 entamoeba h
26	35	74.5	632	2 Q51BP6 ENTHI	Q51bp6 entamoeba h
27	35	74.5	643	1 MAGC3 HUMAN	O8td91 homo sapien
28	35	74.5	643	2 Q5JZ43 HUMAN	Q5jz43 homo sapien
29	35	74.5	843	2 Q8A408 BACTN	Q8a408 bacteroides
30	35	74.5	846	2 Q4RZ43 TETNG	Q4rz43 tetraodon n
31	35	74.5	891	2 Q5ND91 SPAAU	Q5nd91 sparus aura

32	35	74.5	945	2 Q5LB16 BACFN	Q5lb16 bacteroides
33	35	74.5	945	2 Q64S19 BACFR	Q64s19 bacteroides
34	35	74.5	975	2 P79750 FUGRU	P79750 fugu rubrip
35	35	74.5	979	2 Q4GWZ1 SPAAU	Q4gwz1 sparus aura
36	35	74.5	1523	2 Q4YSH2 PLABE	Q4ysh2 plasmodium
37	34	72.3	179	2 O5FI80 LACAC	O5fi80 lactobacill
38	34	72.3	193	2 O69295 CAMJE	O69295 campylobact
39	34	72.3	234	1 MAGAB HUMAN	P43361 homo sapien
40	34	72.3	251	2 Q5ZMF9 CHICK	Q5zmf9 gallus gall
41	34	72.3	251	2 Q6INM9 XENLA	Q6inm9 xenopus lae
42	34	72.3	253	2 Q6DJH4 XENLA	Q6djh4 xenopus lae
43	34	72.3	256	2 Q7ZVT9 BRARE	Q7zvt9 brachydanio
44	34	72.3	318	2 Q9BUN9 HUMAN	Q9bun9 homo sapien
45	34	72.3	364	2 O69293 CAMJE	O69293 campylobact

ALIGNMENTS

RESULT 1
MAGAA HUMAN STANDARD; PRT; 369 AA.
ID MAGAA HUMAN STANDARD; PRT; 369 AA.
AC P43363;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Melanoma-associated antigen 10 (MAGE-10 antigen)

GN Name=MAGE10; Synonyms=MAGE10;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=95012457; PubMed=7927540;

RA de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,

RA de Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C.,

RA Brasseur R., Chomez P., de Backer O., Cavenne W., Boon T.;

RT "Structure, chromosomal localization, and expression of 12 genes of

the MAGE family."

RL Immunogenetics 40:360-369(1994).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

TX TISSUE=Skin;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Hellon E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: Not known, though may play a role in embryonal

development and tumor transformation or aspects of tumor

progression.

CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,

CC such as melanoma, head and neck squamous cell carcinoma, lung

CC carcinoma and breast carcinoma, but not in normal tissues except

CC for testes and placenta.

```
CC -!- SIMILARITY: Contains 1 MAGE domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U10685; AA068869.1; -; Genomic_DNA.
CC EMBL; BC004105; AA04105.1; -; mRNA.
CC PIR; I38659; I38659.
CC Ensembl; ENSG00000124260; Homo sapiens.
CC HGNC; HGNC:6797; MAGEA10.
CC H-InvDB; HIX0017116; -.
CC MIM; 300343; -.
CC InterPro; IPR002190; MAGE.
CC PANTHER; PTHR11736; MAGE; 2.
CC Pfam; PF01454; MAGE; 1.
CC PROSITE; PS50838; MAGE; 1.
KW Antigen; Multigene family; Tumor antigen.
FT DOMAIN 134 333
FT COMPBIAS 54 62 Poly-Ser.
SQ SEQUENCE 369 AA; 40767 MW; 16FA3301CAB716A6 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
DB 144 FLLFKYQMK 152

RESULT 2
Q9JUR4 MOUSE PRELIMINARY; PRT; 243 AA.
AC Q9JUR4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MAGEa9 protein.
DE Name=MAGEa9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Mallon A.M., Platzer M., Bates R., Gloeckner G., Botcherby M.,
RA Nordiek G., Strivens M.A., Kioschis P., Dangel A., Cunningham D.,
RA Straw R., Weston C., Hunter C., Gilbert M., Fernando S., Goodall K.,
RA Kerry G., Greystrom P., Clark D., Goerdes M., Blechschmidt K.,
RA Rump A., Hinzmann B., Mundy C.R., Miller W., Poustka A., Herman G.E.,
RA Rhodes M., Denny P., Rosenthal A., Brown S.D.M.;
RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Botcherby M.R.M., Straw R.N.A., Clarke D., Hunter G., Kimberley C.,
RA Gilbert M., Greystrom J.S., Goodall K., Fernando S., Weston P.,
RA Mundy C.R., Rhodes M.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL021127; CAB8168.1; -; Genomic_DNA.
DR Ensembl; ENSMUSG00000046301; Mus musculus.
DR MGI; MGI:1350986; MAGEa9.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
SQ SEQUENCE 243 AA; 27198 MW; 198C58D74BE64863 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 243;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 FLLFKYQMK 9
DB 108 FLLFKYQMK 116

RESULT 3
O89008 MOUSE PRELIMINARY; PRT; 315 AA.
AC O89008;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MAGEa4 protein.
DE Name=MAGEa4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA TISSUE=Liver;
RX MEDLINE=99134295; PubMed=9933564; DOI=10.1006/geno.1998.5638;
RA De Plaen E., de Backer O., Arnaud D., Bonjean B., Chomez P.,
RA Martelange V., Avner P., Baldacci P., Babinet C., Hwang S.Y.,
RA Knowles B., Boon T.;
RT "A new family of mouse genes homologous to the human MAGE genes.";
RL Genomics 55:176-184(1999).
DR EMBL; AJ005528; CAA06582.1; -; Genomic DNA.
DR Ensembl; ENSMUSG00000033343; Mus musculus.
DR MGI; MGI:1333839; MAGEa4.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
SQ SEQUENCE 315 AA; 35677 MW; 05E1AB2CB636C325 CRC64;

Query Match 91.5%; Score 43; DB 2; Length 315;
Best Local Similarity 88.9%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
DB 106 FLLFKYQMK 114

RESULT 4
Q9BZ78 HUMAN PRELIMINARY; PRT; 170 AA.
AC Q9BZ78;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MAGE family testis and tumor-specific protein (Fragment).
DE Name=MAGEB10;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lucas S., Boon T.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF333708; AAK00360.1; -; Genomic_DNA.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
FT NON_TER 170 170
FT NON_TER 170 170
SQ SEQUENCE 170 AA; 18807 MW; DESDD86951BD957A CRC64;
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Query Match      87.2%; Score 41; DB 2; Length 170;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
   :||:|||||
DB 69 YLLYKYQMK 77

RESULT 5
Q96L22 HUMAN
ID Q96L22_HUMAN PRELIMINARY; PRT; 347 AA.
AC Q96L22;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE Hypothetical protein FLJ32965.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX PubMed=14702039; DOI=10.1038/ngl1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohayashi M., Nishi T., Shibahara T., Tanaka K., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano Y., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yohikawa Y., Matsunawa H., Ichihara T., Shiohara T., Sano S.,
RA Moriya S., Moniyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
   cDNAs.";
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK057527; BAB71522.1; -; mRNA.
DR Ensembl; ENSG00000177689; Homo sapiens.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
SQ SEQUENCE 347 AA; 38878 MW; 3B52411D840D873F CRC64;

Query Match      87.2%; Score 41; DB 2; Length 347;
Best Local Similarity 77.8%; Pred. No. 5.6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
   :||:|||||
DB 121 YLLYKYQMK 129

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RESULT 6
Q9TTY4 CANFA
ID Q9TTY4_CANFA PRELIMINARY; PRT; 378 AA.
AC Q9TTY4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Melanoma antigen.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=breed beagle; TISSUE=Testis;
RX MEDLINE=20470598; PubMed=11019919;
RA DOI=10.1034/j.1359-0039.2000.560210.x;
RA Ma Z., Khatlani T.S., Ohno K., Sasaki K., Inokuma H., Onishi T.;
RT "Cloning and sequencing of canine MAGE cDNA.";
RL Tissue Antigens 56:166-169(2000).
DR EMBL; AF187325; AAF01438.1; -; mRNA.
DR Ensembl; ENSCAF00000013604; Canis familiaris.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
SQ SEQUENCE 378 AA; 42214 MW; AD09C6DC8E3C8D57 CRC64;

Query Match      87.2%; Score 41; DB 2; Length 378;
Best Local Similarity 77.8%; Pred. No. 6.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
   :||:|||||
DB 118 YLLYKYQMK 126

RESULT 7
Q4RSW1 MACFA
ID Q4RSW1_MACFA PRELIMINARY; PRT; 270 AA.
AC Q4RSW1;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Testis cDNA, clone: QtsA-20339, similar to human melanoma antigen,
   family B, 4 (MAGEB4).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopithecinæ; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA International consortium for macaque cDNA sequencing, analysis;
RT "DNA sequences of macaque genes expressed in brain or testis and its
   evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
RT "Substitution rate and structural divergence of 5'UTR evolution:
   Comparative analysis between human and cynomolgus monkey cDNAs.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB169432; BAE01514.1; -; mRNA.
SQ SEQUENCE 270 AA; 29874 MW; D4839758D5FB3726 CRC64;

Query Match      85.1%; Score 40; DB 2; Length 270;
Best Local Similarity 77.8%; Pred. No. 7.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
   :||:|||||

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Db      119 FLLYKYQMK 127

RESULT 8
MAGB4 HUMAN      STANDARD;          PRT;    346 AA.
AC      O15481;
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      10-MAY-2005 (Rel. 47, Last annotation update)
DE      Melanoma-associated antigen B4 (MAGE-B4 antigen).
GN      Name=MAGEB4;
OS      Homo sapiens (Human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=98110575; PubMed=9441743; DOI=10.1006/geno.1997.5052;
RA      Lurquin C., de Smet C., Brasseur F., Muscatelli F., Martelange V.,
RA      de Plaen E., Brasseur R., Monaco A.P., Boon T.;
RT      "Two members of the human MAGE gene family located in Xp21.3 are
RT      expressed in tumors of various histological origins.";
RL      Genomics 46:397-408(1997).
RN      [2]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX      PubMed=15772651; DOI=10.1038/nature03440;
RA      Ross M.T., Grafham D.V., Coffey A.J., Scherer S., McLay K., Muzny D.,
RA      Platzer M., Howell G.R., Burrows C., Bird C.P., Frankish A.,
RA      Lovell F.L., Howe K.L., Ashurst J.L., Fulton R.S., Sudbrak R., Wen G.,
RA      Jones M.C., Hurler M.E., Andrews T.D., Scott C.E., Searle S.,
RA      Ramser J., Whittaker A., Deadman R., Carter N.P., Hunt S.E., Chen R.,
RA      Cree A., Gunaratne P., Havlik P., Hodgson A., Metzker M.L.,
RA      Richards S., Scott G., Steffen D., Sodergren E., Wheeler D.A.,
RA      Worley K.C., Ainscough R., Ambrose K.D., Ansari-Lari M.A., Aradhya S.,
RA      Ashwell R.I., Babbage A.K., Baguley C.L., Ballabio A., Banerjee R.,
RA      Barker G.E., Barlow K.F., Barrett I.P., Bates K.N., Beare D.M.,
RA      Beasley H., Beasley O., Beck A., Bethel G., Blechschmidt K., Brady N.,
RA      Bray-Allen S., Bridgeman A.M., Brown A.J., Brown M.J., Bonnin D.,
RA      Bruford E.A., Buhay C., Burch P., Burford D., Burgess J., Burrill W.,
RA      Burton J., Bye J.M., Carder C., Carrel L., Chako J., Chapman J.C.,
RA      Chavez D., Chen E., Chen G., Chen Y., Chen Z., Chinault C.,
RA      Ciccodicola A., Clark S.Y., Clarke G., Clee C.M., Clegg S.,
RA      Clerc-Blankenburg K., Clifford K., Cobley V., Cole C.G., Conquer J.S.,
RA      Corby N., Connor R.E., David R., Davies J., Davis C., Davis J.,
RA      Delgado O., Deshazo D., Dhani P., Ding Y., Dinh H., Dodsworth S.,
RA      Draper H., Dugan-Rocha S., Dunham A., Dunn M., Durbin K.J., Dutta I.,
RA      Fades T., Ellwood M., Emery-Cohen A., Errington H., Evans K.L.,
RA      Faulkner L., Francis P., Frankland J., Fraser A.E., Galoczzy P.,
RA      Gilbert J., Gill R., Gloeckner G., Gregory S.G., Gribble S.,
RA      Griffiths C., Grocock R., Gu Y., Gwilliam R., Hamilton C., Hart E.A.,
RA      Hawes A., Heath P.D., Heilmann K., Hennig S., Hernandez J.,
RA      Hinmann B., Ho S., Hoffs M., Howden P.J., Huckle E.J., Hume J.,
RA      Hunt P.J., Hunt A.R., Inderwood J., Jacob L., Johnson D., Jones S.,
RA      de Jong P.J., Joseph S.S., Keenan S., Kelly S., Kershaw J.K., Khan Z.,
RA      Kioschis P., Klages A., Knights A.J., Koslura A., Kovar-Smith C.,
RA      Laird G.K., Langford C., Lawlor S., Leversha M., Lewis L., Liu W.,
RA      Lloyd C., Lloyd D.M., Loulseghe H., Loveland J.E., Lovell J.D.,
RA      Lozadó R., Lu J., Lyne R., Ma J., Maheshwari M., Matthews L.H.,
RA      McDowall J., McLaren S., McMurray A., Meidl P., Mettinger T.,
RA      Milne S., Miner G., Mistry S.L., Morgan M., Morris S., Mueller I.,
RA      Mullikin J.C., Nguyen N., Nordliek G., Nyakatura G., O'dell C.N.,
RA      Okwuonu G., Palmer S., Pandian R., Parker D., Parrish J.,
RA      Pasternak S., Patel D., Pearce A.V., Pearson D.M., Pelan S.E.,
RA      Perez L., Porter K.M., Ramsey Y., Reichwald K., Rhodes S.,
RA      Ridler K.A., Schlessinger D., Schueler M.G., Sehra H.K.,
RA      Shaw-Smith C., Shen H., Sheridan E.M., Shownkeen R., Skuce C.D.,
RA      Smith M.L., Sotheran E.C., Steingruber H.B., Steward A.C., Storey R.,
RA      Swann R.M., Swarbreck D., Tabor P.E., Taudien S., Taylor T.,
RA      Teague B., Thomas K., Thorpe A., Timms K., Tracey A., Trevanion S.,
RA      Tromans A.C., d'Urso M., Verduzco D., Villasana D., Waldron L.,
RA      Wall M., Wang Q., Warren J., Warry G.L., Wei X., West A.,

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RA      Whitehead S.L., Whiteley M.N., Wilkinson J.E., Willey D.L.,
RA      Williams G., Williams L., Williamson A., Williamson H., Wilming L.,
RA      Woodmansey R.L., Wray P.W., Yen J., Zhang J., Zhou J., Zoghbi H.,
RA      Zorilla S., Buck D., Reinhardt R., Poustka A., Rosenthal A.,
RA      Lehrach H., Meindl A., Minx P.J., Hillier L.W., Willard H.F.,
RA      Wilson R.K., Waterston R.H., Rice C.M., Vaudin M., Coulson A.,
RA      Nelson D.L., Weinstein G., Sulston J.E., Durbin R., Hubbard T.,
RA      Gibbs R.A., Beck S., Rogers J., Bentley D.R.;
RT      "The DNA sequence of the human X chromosome.";
RL      Nature 434:325-337(2005).
CC      -!- TISSUE SPECIFICITY: Expressed in testis.
CC      -!- SIMILARITY: Contains 1 MAGE domain.
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      EMBL; U93163; AAC23619.1; -; Genomic DNA.
CC      EMBL; AC005185; AAD10637.1; -; Genomic DNA.
CC      Ensembl; ENSG00000120289; Homo sapiens.
CC      HGNC; HGNC:6811; MAGEB4.
CC      MIM; 300153; -.
CC      InterPro; IPR002190; MAGE.
CC      PANTHER; PTHR11736; MAGE; 1.
CC      Pfam; PF01454; MAGE; 1.
CC      PROSITE; PS50838; MAGE; 1.
CC      Antigen; Multigene family.
KW      DOMAIN 109 307
FT      DOMAIN 109 307
SQ      SEQUENCE 346 AA; 38923 MW; 804F260BD50F036A CRC64;

Query Match      85.1%; Score 40; DB 1; Length 346;
Best Local Similarity 77.8%; Pred. No. 9.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLLYKYQMK 9
      |||:|:|
Db      119 FLLYKYQMK 127

RESULT 9
Q6FHH4 HUMAN      PRELIMINARY;          PRT;    346 AA.
AC      Q6FHH4;
DT      10-MAY-2005 (TrEMBLrel. 30, Created)
DT      10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT      10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE      MAGEB4 protein (Fragment).
GN      Name=MAGEB4;
OS      Homo sapiens (Human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RA      Halbeck A., Ebert L., Mkundinya M., Schlick M., Eisenstein S.,
RA      Neubert P., Katrang K., Schatten R., Shen B., Henze S., Mar W.,
RA      Korn B., Zuo Y., Labaer J.;
RL      Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL; CR541779; CAG46578.1; -; mRNA.
DR      NON_TER 346 346
FT      SEQUENCE 346 AA; 38923 MW; 804F260BD50F036A CRC64;

Query Match      85.1%; Score 40; DB 2; Length 346;
Best Local Similarity 77.8%; Pred. No. 9.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 FLLYKYQMK 9
      |||:|:|
Db      119 FLLYKYQMK 127

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RESULT 10
Q81200 HUMAN
ID Q81200 HUMAN PRELIMINARY; PRT; 346 AA.
AC Q81200;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Melanoma antigen family B, 4.
GN Name=MAGEB4;
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feilgold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heltan E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RG NIH MGC Project;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032852; AAH32852.1; -; mRNA.
DR Ensembl; ENSG00000120289; Homo sapiens.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
SQ SEQUENCE 346 AA; 38981 MW; 724359116DBC8BE9 CRC64;

Query Match 85.1%; Score 40; DB 2; Length 346;
Best Local Similarity 77.8%; Pred. No. 9.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLPKYQMK 9
Db 119 FLLPKYQMK 127
|||:|||||

RESULT 11
Q7MX06 PORGI
ID Q7MX06 PORGI PRELIMINARY; PRT; 123 AA.
AC Q7MX06;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=PG0422;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (Class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;

Query Match 85.1%; Score 40; DB 2; Length 346;
Best Local Similarity 77.8%; Pred. No. 9.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLPKYQMK 9
Db 119 FLLPKYQMK 127
|||:|||||

RESULT 12
Q89009 MOUSE
ID Q89009 MOUSE PRELIMINARY; PRT; 320 AA.
AC Q89009;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-MAR-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-2004 (TrEMBLrel. 26, Last annotation update)
DE MAGE5 protein.
GN Name=MAGE5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=99134295; PubMed=9933564; DOI=10.1006/geno.1998.5638;
RA De Plaen E., de Backer O., Arnaud D., Bonjean B., Chomez P.,
RA Martelange V., Avner P., Baldacci P., Babinet C., Hwang S.Y.,
RA Knowles B., Boon T.;
RT "A new family of mouse genes homologous to the human MAGE genes.";
RL Genomics 55:176-184 (1999).
DR EMBL; AJ005529; CAA06583.1; -; Genomic DNA.
DR Ensembl; ENSMUSG0000055816; Mus musculus.
DR MGI; MGI:1333838; MAGE5.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
SQ SEQUENCE 320 AA; 36262 MW; FD187E4762CAFC30 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 320;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLLPKYQMK 9
Db 106 FLVLKYQMK 114
|||:|||||

RESULT 13
IF3C CYAME
ID IF3C CYAME STANDARD; PRT; 175 AA.
AC Q8SG77;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)

```

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RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=W83;
RX MEDLINE=22829867; PubMed=12949112;
DOI=10.1128/JB.185.18.5591-5601.2003;
RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
RA Dewhirst F.E., Fraser C.M.;
RT "Complete genome sequence of the oral pathogenic bacterium
RT Porphyromonas gingivalis strain W83.";
RL J. Bacteriol. 185:5591-5601 (2003).
DR EMBL; AE017173; AAQ65622.1; -; Genomic_DNA.
DR TIGR; PG0422; -.
SQ SEQUENCE 123 AA; 14411 MW; ECF62BEAFD7DOA9F CRC64;

Query Match 83.0%; Score 39; DB 2; Length 123;
Best Local Similarity 87.5%; Pred. No. 5.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLPKYQMK 8
Db 38 FLVLKYQMK 45
|||:|||||

RESULT 13
Q89009 MOUSE
ID Q89009 MOUSE PRELIMINARY; PRT; 320 AA.
AC Q89009;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-MAR-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-2004 (TrEMBLrel. 26, Last annotation update)
DE MAGE5 protein.
GN Name=MAGE5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=99134295; PubMed=9933564; DOI=10.1006/geno.1998.5638;
RA De Plaen E., de Backer O., Arnaud D., Bonjean B., Chomez P.,
RA Martelange V., Avner P., Baldacci P., Babinet C., Hwang S.Y.,
RA Knowles B., Boon T.;
RT "A new family of mouse genes homologous to the human MAGE genes.";
RL Genomics 55:176-184 (1999).
DR EMBL; AJ005529; CAA06583.1; -; Genomic DNA.
DR Ensembl; ENSMUSG0000055816; Mus musculus.
DR MGI; MGI:1333838; MAGE5.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
SQ SEQUENCE 320 AA; 36262 MW; FD187E4762CAFC30 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 320;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLLPKYQMK 9
Db 106 FLVLKYQMK 114
|||:|||||

RESULT 13
IF3C CYAME
ID IF3C CYAME STANDARD; PRT; 175 AA.
AC Q8SG77;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)

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```
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Translation initiation factor IF-3, chloroplast.
GN Name=InfC;
OS Cyanidioschyzon merolae (Red alga).
OG Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Cyanidiales; Cyanidiaceae;
OC Cyanidioschyzon.
OX NCBI_TaxID=45157;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=10D;
RX MEDLINE=22639682; PubMed=12751171;
RA Ohta N., Matsuzaki M., Misumi O., Miyagishima S.-Y., Nozaki H.,
RA Tanaka K., Shin-I T., Kohara Y., Kuroiwa T.;
RT "Complete sequence and analysis of the plastid genome of the
RT unicellular red alga Cyanidioschyzon merolae.";
RL DNA Res. 10:67-77(2003).
CC -|- FUNCTION: IF-3 binds to the 30S ribosomal subunit and shifts the
CC equilibrium between 70S ribosomes and their 50S and 30S subunits in
CC favor of the free subunits, thus enhancing the availability of 30S
CC subunits on which protein synthesis initiation begins.
CC -|- SUBUNIT: Monomer (By similarity).
CC -|- SUBCELLULAR LOCATION: Chloroplast.
CC -|- SIMILARITY: Belongs to the IF-3 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DE EMBL; AB002593; BAC76113.1; -; Genomic_DNA.
DR HSSP; P02999; 2IFE.
DR HAMAP; MF_00080; -; 1.
DR InterPro; IPR001288; IF3.
DR PANTHER; PTHR10938; IF3; 1.
DR Pfam; PF00707; IF3_C; 1.
DR Pfam; PF00707; IF3_N; 1.
DR ProDom; PD002880; IF3; 1.
DR TIGRFAMs; TIGR00168; infc; 1.
DR PROSITE; PS00938; IF3; 1.
KW Chloroplast; Initiation factor; Protein biosynthesis.
SQ SEQUENCE 175 AA; 19871 MW; BFA481CDB8480A69 CRC64;

Query Match      78.7%; Score 37; DB 1; Length 175;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
   |||:|
DB 5 FLLMKPQMK 13

RESULT 14
Q95KZ1_FELCA PRELIMINARY; PRT; 376 AA.
AC Q95KZ1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Melanoma antigen 2.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22025778; PubMed=12028540;
RX DOI=10.1034/j.1359-0039.2002.590209.x;
RA Ma Z., Khatlani T.S., Sasaki K., Okuda M., Inokuma H., Onishi T.;
RT "Molecular cloning and sequencing of feline melanoma antigen 2 (fMAGE-
RT 2) obtained from a lymphoma cell line.";
```

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RL Tissue Antigens 59:127-132(2002).
DR EMBL; AY052501; AAL14113.1; -; mRNA.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50839; MAGE; 1.
SQ SEQUENCE 376 AA; 41521 MW; 467B5C75F30F7338 CRC64;

Query Match      78.7%; Score 37; DB 2; Length 376;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLFKYQMK 9
   |||:|
DB 133 YLLYKYMK 141

RESULT 15
Q55EA0_DICDI PRELIMINARY; PRT; 1140 AA.
AC Q55EA0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=ODB0190180;
OS Dictyostelia discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivoero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Basan N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Lousaged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -|- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAFI0100011; EAL72014.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1140 AA; 129713 MW; 7C9B80994748EA80 CRC64;

Query Match      78.7%; Score 37; DB 2; Length 1140;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLLFKYQ 7
   |||
DB 1088 FLLFKYQ 1094

Search completed: March 17, 2006, 23:33:48
Job time : 129 secs
```


GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:21:17 ; Search time 118 Seconds
(without alignments)
33.512 Million cell updates/sec

Title: US-09-856-812b-49
Perfect score: 54
Sequence: 1 FIEGYCTPE 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*
9: Geneseqp2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	9	2 AAR79847	Aar79847 Tumour re
2	54	100.0	9	3 AAY71492	Aay71492 Human MAG
3	54	100.0	9	8 ADI47251	Adi47251 Anti-canc
4	54	100.0	369	3 AAY71485	Aay71485 Human MAG
5	54	100.0	369	4 AAB80297	Aab80297 Human pro
6	54	100.0	369	6 ABR48215	AbR48215 Human bia
7	54	100.0	369	6 ABUS6516	Abu56516 Lung canc
8	54	100.0	383	8 ABO58424	AbO58424 Human gen
9	41	75.9	91	2 AAY37790	Aay37790 Chlamydia
10	40	74.1	277	4 AAU86754	Aau86754 Novel hum
11	40	74.1	277	7 ADB60088	Adb60088 Connectiv
12	40	74.1	489	3 AAB19380	Aab19380 Amino aci
13	40	74.1	615	3 AAB19383	Aab19383 Amino aci
14	40	74.1	645	3 AAB19391	Aab19391 Amino aci
15	40	74.1	671	8 ABM84236	Abm84236 Human dia
16	40	74.1	711	3 AAB19379	Aab19379 Amino aci
17	40	74.1	711	5 AAB08203	AbB08203 Human lip
18	40	74.1	711	5 ABP69704	AbP69704 Human pol
19	40	74.1	711	5 ABB04578	AbB04578 Human lip
20	40	74.1	711	7 AAE39890	Aae39890 Human lip
21	40	74.1	711	8 ADQ48419	AdQ48419 Human lip
22	40	74.1	717	8 ADN23120	Adn23120 Bacterial
23	40	74.1	771	3 AAB19392	Aab19392 Amino aci
24	40	74.1	867	3 AAB19390	Aab19390 Amino aci

25	39	72.2	130	6	ABU41017	Abu41017 Protein e
26	39	72.2	133	7	ADP06604	AdP06604 Bacterial
27	39	72.2	226	4	AAE00716	Aae00716 Corn glyc
28	39	72.2	226	4	AAG67278	Aag67278 Amino aci
29	39	72.2	469	6	ADA48058	Ada48058 Rice prot
30	39	72.2	493	8	ADX96238	Adx96238 Plant ful
31	39	72.2	603	2	AAV35593	Aay35593 Protein i
32	39	72.2	727	7	ABO70066	AbO70066 Pseudomon
33	38	70.4	54	8	ABO59145	AbO59145 Human gen
34	38	70.4	141	7	ABO72040	AbO72040 Pseudomon
35	38	70.4	314	8	ADY12043	AdY12043 Plant ful
36	38	70.4	724	7	ABO82138	AbO82138 Pseudomon
37	37	68.5	156	4	ABG26656	Abg26656 Novel hum
38	37	68.5	208	9	ABM94502	Abm94502 M. xanthu
39	37	68.5	532	2	AAW80446	Aaw80446 Human int
40	37	68.5	532	2	AAW86193	Aaw86193 Human int
41	37	68.5	532	6	ABU04080	Abu04080 Human exp
42	37	68.5	532	6	ABU04081	Abu04081 Human exp
43	36	66.7	105	8	ABO57647	AbO57647 Human gen
44	36	66.7	117	4	AAU45332	Aau45332 Propionib
45	36	66.7	117	6	ABM41851	Abm41851 Propionib

ALIGNMENTS

RESULT 1
AAR79847
ID AAR79847 standard; peptide; 9 AA.
XX
AC AAR79847;
XX
DT 08-MAY-1996 (first entry)
XX
DE Tumour rejection antigen peptide #11.
XX
KW Tumour rejection antigen; MAGE tumour rejection precursor; complex;
KW HLA-2; immunogen; antibody; cytolytic T cell clone.
XX
OS Synthetic.
XX
PN WO9525740-A1.
XX
PD 28-SEP-1995.
XX
PF 22-MAR-1995; 95WO-US003657.
XX
PR 24-MAR-1994; 94US-00217186.
PR 17-JUN-1994; 94US-00261160.
PR 15-AUG-1994; 94US-00290381.
(LUDW-) LUDWIG INST CANCER RES.
PA (UYOX-) UNIV OXFORD.
PA (UYLE-) RIJKSUNIV LEIDEN.
PI Townsend A, Bastin J, Boon-Palleur T, Van Der Bruggen P, Coulie P;
Gajewski T, Melief CJ, Visseren MW, Kast WM;
XX WPI; 1995-344584/44.
XX
XX Isolated peptide(s) which complex with HLA-A2 - used as immunogens for
the prodn. of antibodies, or as targets for the generation of cytolytic T
cell clones.
XX
XX Claim 15; Page 23; 44pp; English.
XX
XX The peptides given in AAR79845-47 represent tumour rejection antigens
derived from MAGE tumour rejection precursor. These peptides form a
strong complex with HLA-2 which may be used diagnostically and as an
immunogen in the production of antibodies. They may also be used as
targets for the generation of cytolytic T cell clones. This cytolytic T
cell clone is used to treat a cancerous condition characterised by the
fact that the cancer cells present the HLA-2/ peptide complex on their

```

CC surface
XX Sequence 9 AA;
SQ Query Match 100.0%; Score 54; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FIEGYCTPE 9
Db 1 FIEGYCTPE 9

RESULT 2
AA71492
ID AAY71492 standard; peptide; 9 AA.
XX
XX
AC AAY71492;
XX
DT 12-OCT-2000 (first entry)
XX
DE Human MAGE-A10 nonapeptide-3.
XX
DE MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
KW immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
KW cancer; TNF; tumour necrosis factor; vaccine; cytostatic.
XX
OS Homo sapiens.
XX
XX WO200032769-A2.
XX
XX 08-JUN-2000.
XX
XX 26-NOV-1999; 99WO-IB002018.
XX
XX 27-NOV-1998; 98GB-00026143.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
XX WPI; 2000-412317/35.
XX
XX Novel polypeptides expressed in tumor cells useful for treating cancers
PT have an ability to complex with a major histocompatibility complex
PT molecule and comprises a specific unbroken amino acid sequence.
XX
XX Claim 5; Page 36; 80pp; English.
XX
XX The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
CC decapeptide sequences, that function as tumour rejection antigens (TRAs).
CC These peptides are capable of forming a complex with major
CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
CC Antigen), that are recognised by T-lymphocytes and elicit an immune
CC response from cytolytic T-lymphocytes (CTL). They function as an immune
CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
CC therapy and diagnosis of tumours and are effective in controlling or
CC preventing tumour growth. The present peptide sequence is the human MAGE-
CC A10 nonapeptide-3, that corresponds to residues 235-243 of the MAGE-A10
CC protein. This peptide can serve as a tumour rejection antigen (TRA) and
CC in combination with adjuvants, can produce vaccines useful for treating a
CC variety of tumours that express MAGE-A10
XX
XX Sequence 9 AA;
XX Query Match 100.0%; Score 54; DB 3; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FIEGYCTPE 9
Db 1 FIEGYCTPE 9

us-09-856-812b-49.rag
RESULT 3
ADI47251
ID ADI47251 standard; peptide; 9 AA.
XX
XX
AC ADI47251;
XX
DT 22-APR-2004 (first entry)
XX
DE Anti-cancer HLA-A2 complex associated peptide seq id 18.
XX
KW cytostatic; gene therapy; cancer; cytolytic T cell; HLA-A2.
XX
OS Synthetic.
XX
XX US6682731-B1.
XX
XX 27-JAN-2004.
XX
XX 23-MAR-2000; 2000US-00533499.
XX
XX 24-MAR-1994; 94US-00217186.
XX
XX 24-MAR-1994; 94US-00217188.
XX
XX 17-JUN-1994; 94US-00261160.
XX
XX 15-AUG-1994; 94US-00290381.
XX
XX 06-FEB-1997; 97US-00722115.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX (UYOX-) UNIV OXFORD.
XX
XX (UYLE-) RIJKSUNIV LEIDEN.
XX
XX Townsend A, Bastin J, Boon-Falleur T, Van Der Bruggen P, Coulie P;
XX Gajewski T, Mellief CJM, Visseren MJW, Kast MW;
XX WPI; 2004-118569/12.
XX
XX Treating a subject with a cancerous condition by administering cytolytic
PT T cells specific for the complexes to lyse the cancer cells.
XX
XX Example 13; SEQ ID NO 19; 27pp; English.
XX
XX The invention describes a method of treating a subject with a cancerous
CC condition comprising administering cytolytic T cells specific for the
CC complexes to lyse the cancer cells of the subject. The cancer cells
CC present complexes of HLA-A2 molecules and a peptide with a fully defined
CC sequence comprising 9 amino acids. The method is useful for treating a
CC subject with a cancerous condition. This is the amino acid sequence of a
CC HLA-A2 complex associated peptide.
XX
XX Sequence 9 AA;
XX Query Match 100.0%; Score 54; DB 8; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FIEGYCTPE 9
Db 1 FIEGYCTPE 9

RESULT 4
AA71485
ID AAY71485 standard; protein; 369 AA.
XX
XX
AC AAY71485;
XX
XX 12-OCT-2000 (first entry)
XX
XX Human MAGE-A10 protein.
XX
XX MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
KW

```

KW immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
 KW cancer; TNF; tumour necrosis factor; cytostatic.
 XX
 OS Homo sapiens.
 PN WO200032769-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 26-NOV-1999; 99WO-IB002018.
 XX
 PR 27-NOV-1998; 98GB-00026143.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
 XX
 DR WPI: 2000-412317/35.
 XX
 DR N-PSDB; AAD01311, AAD01312, AAD01313.
 XX
 PT Novel polypeptides expressed in tumor cells useful for treating cancers
 PT have an ability to complex with a major histocompatibility complex
 PT molecule and comprises a specific unbroken amino acid sequence.
 XX
 PS Claim 1; Fig 7; 80pp; English.
 XX
 CC The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
 CC decapeptide sequences, that function as tumour rejection antigens (TRAs).
 CC These peptides are capable of forming a complex with major
 CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
 CC Antigen), that are recognised by T-lymphocytes and elicit an immune
 CC response from cytolytic T-lymphocytes (CTL). They function as an immune
 CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
 CC therapy and diagnosis of tumours and are effective in controlling or
 CC preventing tumour growth. The present sequence is the human MAGE-A10
 CC protein, comprising nonapeptides and decapeptides, that serve as tumour
 CC rejection antigens (TRAs). The novel TRAs encoded by MAGE-A10 is
 CC identified using melanoma cell line (UBI751-MEL), stimulated by
 CC autologous CTL clone (447A/5) to produce TNF (tumour necrosis factor).
 CC Expression of MAGE-A10 has been detected in a variety of tumours like
 CC melanomas, carcinomas of the head and neck, bladder and prostate,
 CC myelomas and lung cancer. The only normal tissue expressing MAGE-A10 is
 CC the testis
 XX
 SQ Sequence 369 AA;
 Query Match 100.0%; Score 54; DB 3; Length 369;
 Best Local Similarity 100.0%; Pred. No. 0.89; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FIEGYCTPE 9
 Db |||||
 235 FIEGYCTPE 243
 RESULT 5
 AAB80297
 ID AAB80297 standard; protein; 369 AA.
 XX
 AC AAB80297;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human prostate cancer antigen #25.
 XX
 KW Immunosuppressive; nootropic; neuroprotective; antiviral; vulnery;
 KW anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant;
 KW immune disorder; cardiovascular disorder; neurological disease;
 KW infection; cancer; cytostatic; antiarthritic; antirheumatic;
 KW antiasthmatic; anticonvulsant; vasotropic; vulnery; human;
 KW secreted protein; prostate cancer antigen.
 XX
 OS Homo sapiens.

XX WO200107476-A1.
 PN
 XX
 PD 01-FEB-2001.
 XX
 PF 20-JUL-2000; 2000WO-US019666.
 XX
 PR 21-JUL-1999; 99US-0144972P.
 PR 13-AUG-1999; 99US-0148681P.
 PR 17-AUG-1999; 99US-0149173P.
 PR 06-OCT-1999; 99US-0158004P.
 PR 05-APR-2000; 2000US-0194689P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 XX
 PI Rosen CA, Birse C;
 XX
 DR WPI: 2001-138554/14.
 DR N-PSDB; AAF72765.
 XX
 PT New nucleic acid molecule encoding human secreted prostate cancer
 PT antigens, useful for the diagnosis and treatment of disorders such as
 PT cancer, leukemia and autoimmune disease.
 XX
 PS Claim 11; Page 399-400; 433pp; English.
 XX
 CC The present invention relates to human secreted prostate cancer antigen
 CC coding sequences (AAF72741-AAF72789) and proteins (AAB80273-AAB80321).
 CC The coding sequences and proteins of the present invention are useful for
 CC preventing, treating or ameliorating a medical condition; and for the
 CC diagnosis and treatment of diseases and disorders. Diseases and disorders
 CC that can be diagnosed and treated include (auto)immune diseases (e.g.
 CC graft versus host disease and rheumatoid arthritis), inflammatory and
 CC allergic disorders (e.g. asthma), hyperproliferative disorders (e.g.
 CC cancers and leukemias), cardiovascular disorders (e.g. heart attacks and
 CC arrhythmias), cerebrovascular disorders (e.g. stroke), arterial occlusive
 CC disorders (e.g. arteriosclerosis), angiogenesis related disorders (e.g.
 CC retinopathy and keloid scars), ocular disorders (e.g. glaucoma),
 CC neurological disorders (e.g. Alzheimer's, Parkinson's disease, epilepsy
 CC and Creutzfeld-Jakob disease) and infections caused by bacteria, fungi,
 CC viruses or parasites. They may also be useful for wound healing,
 CC epithelial cell proliferation, supporting cell culture, tissue
 CC regeneration, birth control and as a food additive or preservative
 XX
 SQ Sequence 369 AA;
 Query Match 100.0%; Score 54; DB 4; Length 369;
 Best Local Similarity 100.0%; Pred. No. 0.89; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FIEGYCTPE 9
 Db |||||
 235 FIEGYCTPE 243
 RESULT 6
 ABR48215
 ID ABR48215 standard; protein; 369 AA.
 XX
 AC ABR48215;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Human bladder cancer associated protein sequence SEQ ID NO:149.
 XX
 KW Human; bladder cancer; cytostatic; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 PN WO2003003906-A2.
 XX
 PD 16-JAN-2003.

XX 03-JUL-2002; 2002WO-US021338.
 PF
 XX
 PR 03-JUL-2001; 2001US-0302814P.
 PR 03-AUG-2001; 2001US-0310099P.
 PR 08-NOV-2001; 2001US-0343705P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 12-APR-2002; 2002US-0372246P.
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 PA Mack DH, Aziz N;
 XX
 PI WPI; 2003-201532/19.
 XX N-PSDB; ACC51029.
 DR
 DR
 XX
 PT Detecting a bladder cancer-associated transcript in a cell from a
 PT patient, comprises contacting a biological sample from the patient with a
 PT bladder cancer-associated polynucleotide or antibody.
 XX
 PS Claim 10; Page 282; 307pp; English.
 XX
 CC The present invention describes a method for detecting a bladder cancer-
 CC associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with a polynucleotide
 CC that selectively hybridizes to a sequence that is 80 % identical to a
 CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
 CC encode the human bladder cancer-associated proteins given in ABR48146 to
 CC ABR48242). Bladder cancer-associated sequences from the present invention
 CC have cytostatic activities, and can be used in antisense gene therapy and
 CC in vaccine production. The method can be used for detecting a bladder
 CC cancer-associated transcript in a cell from a patient. The method is
 CC useful in diagnosing or treating bladder cancer and in screening for
 CC compounds that modulate bladder cancer, such as hormones or antibodies.
 CC The nucleic acid molecules from the present invention may be used in
 CC various screening and diagnostic methods, and for gene therapy, vaccine
 CC and/or antisense/inhibition applications
 XX
 SQ Sequence 369 AA;
 Query Match 100.0%; Score 54; DB 6; Length 369;
 Best Local Similarity 100.0%; Pred. No. 0.89;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FIEGYCTPE 9
 |||||
 Db 235 FIEGYCTPE 243
 RESULT 7
 ABUS6516
 ID ABUS6516 standard; protein; 369 AA.
 XX
 AC ABUS6516;
 XX
 DT 02-APR-2003 (first entry)
 XX
 XX Lung cancer-associated polypeptide #109.
 XX
 KW Lung cancer-associated polypeptide; cytostatic; emphysema;
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX
 OS Unidentified.
 OS
 XX
 PN WO200286443-A2.
 XX
 XX 31-OCT-2002.
 PD
 XX
 PF 18-APR-2002; 2002WO-US012476.
 XX

PR 18-APR-2001; 2001US-0284770P.
 PR 10-MAY-2001; 2001US-0290492P.
 PR 09-NOV-2001; 2001US-0339245P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 29-NOV-2001; 2001US-0334370P.
 PR 12-APR-2002; 2002US-0372246P.
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Aziz N, Murray R;
 XX
 XX WPI; 2003-093161/08.
 DR N-PSDB; ABX76240.
 XX
 XX
 PT Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased
 PT expression in lung cancer.
 XX
 PS Claim 27; Page 276-277; 453pp; English.
 XX
 CC The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridizes
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung cancer-
 CC associated polynucleotides and polypeptides are used for identifying a
 CC compound that modulates a lung cancer-associated polypeptide, for
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung
 CC cancer in a patient and for treating a mammal having lung cancer by
 CC administering a modulatory compound identified. The methods are useful
 CC for treating lung cancer, such as small cell lung cancer, non-small cell
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, asthma and
 CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, fibrosis,
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
 CC for diagnostic purposes and as targets for screening for therapeutic
 CC compounds that modulate lung cancer, such as antibodies. Sequences
 CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
 CC invention
 XX
 SQ Sequence 369 AA;
 Query Match 100.0%; Score 54; DB 6; Length 369;
 Best Local Similarity 100.0%; Pred. No. 0.89;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FIEGYCTPE 9
 |||||
 Db 235 FIEGYCTPE 243
 RESULT 8
 ABO58424
 ID ABO58424 standard; protein; 383 AA.
 XX
 AC ABO58424;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 XX Human genome derived single exon protein #4658.
 XX
 KW Human; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.
 XX
 OS Homo sapiens.
 OS
 XX
 PN US2003194704-A1.
 XX
 XX 16-OCT-2003.
 PD
 XX
 PF 03-APR-2002; 2002US-00029386.
 XX

PR 03-APR-2002; 2002US-00029386.
XX (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
XX
PI Penn SG, Rank DR, Hanzel DK;
XX WPI; 2004-119264/12.
XX
XX New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX
XX Claim 45; SEQ ID NO 32058; 80pp; English.
XX
CC The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridizes under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subsequence, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterizing
CC alternative splicing events, in detecting and characterizing gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe protein of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
XX SEQ Sequence 393 AA;

Query Match 100.0%; Score 54; DB 8; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.92;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FIEGYCTPE 9
DB 256 FIEGYCTPE 264
|||||
|||||

RESULT 9
AAY37790
ID AAY37790 standard; protein; 91 AA.
XX AC
XX AAY37790;
XX
DT 07-OCT-1999 (first entry)
XX
DE Chlamydia trachomatis cellular envelope protein.

XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis;
KW Bartholinitis; pneumopathy; venereal lymphogranulomatosis.
XX Chlamydia trachomatis.
OS
XX WO9928475-A2.
XX PN
XX 10-JUN-1999.
XX PD
XX 27-NOV-1998; 98WO-IB001939.
PF
XX 28-NOV-1997; 97FR-00015041.
PR 17-DEC-1997; 97FR-00016034.
PR 04-NOV-1998; 98US-0107077P.
XX
XX (GEST) GENSET.
XX Griffais R;
XX WPI; 1999-371125/31.
XX
XX Genome sequence of Chlamydia trachomatis.
XX
XX Disclosure; Page 1373; 1755pp; English.
XX
CC AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome
CC of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as
CC vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences
CC can also be used to control growth of the microorganism. Chlamydia
CC trachomatis is responsible for a large number of diseases, e.g. eye
CC diseases such as conventional trachoma, nonendemic trachoma,
CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
CC perihepatitis, Bartholinitis; pneumopathy in breast feeding infants; and
CC venereal lymphogranulomatosis. The polypeptides of the invention may be
CC of use in treating these diseases
XX
XX Sequence 91 AA;

Query Match 75.9%; Score 41; DB 2; Length 91;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 IEGYCTPE 9
DB 30 MEGYCSPE 37
:|||||
:

RESULT 10
AAU86754
ID AAU86754 standard; protein; 277 AA.
XX
XX AAU86754;
XX
DT 21-MAY-2002 (first entry)
XX
DE Novel human connective tissue related polypeptide #320.
XX
KW Human; connective tissue related disorder; cancer; cytostatic.
XX
XX Homo sapiens.
XX
XX WO200155343-A1.
XX PN
XX 02-AUG-2001.
XX PD
XX 17-JAN-2001; 2001WO-US001322.
PF
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0198874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234977P.
PR 25-SEP-2000; 2000US-0234988P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246529P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251983P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-565190/63.
XX N-PSDB; ABK41932.
DR
DR Nucleic acid encoding novel connective tissue associated polypeptides,
XX used in diagnosing, preventing, treating or ameliorating a disorder such
PT as cancer or rheumatoid arthritis.
XX

PS Claim 11; SEQ ID NO 819; 673pp; English.

XX The present invention relates to the isolation of novel human connective

CC tissue related polypeptides and the polynucleotide (cDNA and genomic)

CC sequences encoding them. The sequences of the invention are useful in the

CC diagnosis, treatment, prevention and/or prognosis of diseases associated

CC with connective tissue(s), including cancer. The polynucleotide sequences

CC of the invention are also useful in gene therapy. AAU86435-AAU86923

CC represent the novel human connective tissue related polypeptides. Note:

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 277 AA;

Query Match 74.1%; Score 40; DB 4; Length 277;

Best Local Similarity 77.8%; Pred. No. 1.5e+02;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTGEGCTPE 9

Db :|||||

199 WIEGYCTVE 207

RESULT 11

ADB60088

ID ADB60088 standard; protein; 277 AA.

XX AC

AC ADB60088;

XX AC

DT 04-DEC-2003 (first entry)

XX

DE Connective tissue antigen (CTA) #320.

XX

KW cytostatic; neuroprotective; nootropic; antiparkinsonian; cardiovascular;

KW antiarteriosclerotic; immunosuppressive; antirheumatic; antiarthritic;

KW antiinflammatory; antiallergic; antiaesthetic; dermatological;

KW nephrotoxic; virucide; fungicide; antibacterial; antiparasitic;

KW gene therapy; ds; connective tissues disorder; rheumatoid arthritis;

KW systemic lupus erythematosus; scleroderma; Sjogren's syndrome; cancer;

KW cancer metastasis; neoplasia; leukemia; neurodegenerative disorder;

KW Alzheimer's disease; Parkinson's disease; cardiovascular disease;

KW atherosclerosis; myocarditis; cardiopulmonary bypass complication;

KW autoimmune disease; multiple sclerosis; allergic reaction; asthma;

KW rhinitis; eczema; inflammatory condition; Crohn's disease; nephritis;

KW gastrointestinal disorder; inflammatory bowel disease;

KW organ transplant rejection; immune system disorder; Bruton's disease;

KW X-linked lymphoproliferative syndrome;

KW B-cell lymphoproliferative disorder; HIV; AIDS; infection;

KW chromosome identification; chromosome mapping; connective tissue antigen;

KW CTA.

XX

OS Homo sapiens.

XX

XX

PN US2003054375-A1.

XX

PD

PD

XX

XX 20-MAR-2003.

XX

XX

XX 07-MAR-2002; 2002US-00092154.

XX

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 18-AUG-2000; 2000US-0225759P.

PR 22-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226688P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-SEP-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.

PR 08-SEP-2000; 2000US-0231413P.

PR 08-SEP-2000; 2000US-0231414P.

PR 08-SEP-2000; 2000US-0232080P.

PR 12-SEP-2000; 2000US-0231988P.

PR 14-SEP-2000; 2000US-0232397P.

PR 14-SEP-2000; 2000US-0232398P.

PR 14-SEP-2000; 2000US-0232399P.

PR 14-SEP-2000; 2000US-0232400P.

PR 14-SEP-2000; 2000US-0232401P.

PR 14-SEP-2000; 2000US-0233063P.

PR 14-SEP-2000; 2000US-0233064P.

PR 14-SEP-2000; 2000US-0233065P.

PR 21-SEP-2000; 2000US-0234223P.

PR 21-SEP-2000; 2000US-0234274P.

PR 25-SEP-2000; 2000US-0234997P.

PR 25-SEP-2000; 2000US-0234998P.

PR 26-SEP-2000; 2000US-0235484P.

PR 27-SEP-2000; 2000US-0235834P.

PR 27-SEP-2000; 2000US-0235836P.

PR 29-SEP-2000; 2000US-0236327P.

PR 29-SEP-2000; 2000US-0236367P.

PR 29-SEP-2000; 2000US-0236368P.

PR 29-SEP-2000; 2000US-0236369P.

PR 29-SEP-2000; 2000US-0236370P.

PR 02-OCT-2000; 2000US-0236802P.

PR 02-OCT-2000; 2000US-0237037P.

PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.

PR 02-OCT-2000; 2000US-0237040P.

PR 13-OCT-2000; 2000US-0239935P.

PR 13-OCT-2000; 2000US-0239937P.

PR 20-OCT-2000; 2000US-0240960P.

PR 20-OCT-2000; 2000US-0241221P.

PR 20-OCT-2000; 2000US-0241785P.

PR 20-OCT-2000; 2000US-0241786P.

PR 20-OCT-2000; 2000US-0241787P.

PR 20-OCT-2000; 2000US-0241808P.

PR 20-OCT-2000; 2000US-0241809P.

PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
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PR 08-NOV-2000; 2000US-0246525P.
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PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
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PR 17-NOV-2000; 2000US-0249207P.
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PR 17-NOV-2000; 2000US-0249209P.
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PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
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PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764847.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Barash SC;
XX
XX WPI; 2003-634869/60.
XX N-PSDB; ADB59599.
XX
XX New connective tissue-related polypeptides and polynucleotides, useful
XX for treating, preventing and/or prognosing e.g. disorders of connective
XX tissue, (e.g. rheumatoid arthritis), cancers, cancer metastases and/or
XX neoplasias.
XX
XX Claim 11; SEQ ID NO 819; 248pp; English.
XX
XX The invention describes an isolated nucleic acid molecule (I), which
XX comprises a sequence that is at least 95 % identical to a connective
XX tissue-related polynucleotide encoding connective tissue antigens (CTA).
XX The polypeptide or polynucleotide is useful for preventing, treating, or
XX ameliorating medical conditions in a mammal. The connective tissue
XX polypeptides, polynucleotides and antibodies are particularly useful for
XX treating, preventing and/or prognosing disorders of connective tissues

CC (e.g. rheumatoid arthritis, discoid and systemic lupus erythematosus,
CC scleroderma, or Sjogren's syndrome), cancers, cancer metastases and/or
CC neoplasias (e.g. leukaemia), neurodegenerative disorders (e.g.
CC Alzheimer's disease, or Parkinson's disease), cardiovascular diseases
CC (e.g. atherosclerosis, myocarditis or cardiopulmonary bypass
CC complications), autoimmune diseases (e.g. systemic lupus erythematosus,
CC rheumatoid arthritis, or multiple sclerosis), allergic reactions (e.g.

Query Match 74.1%; Score 40; DB 7; Length 277;

Best Local Similarity 77.8%; Pred. No. 1.5e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 1;

QY 1 FIEGYCTPE 9

Db 199 WIEGYCTVE 207

RESULT 12

AAB19380

ID AAB19380 standard; protein; 489 AA.

XX AC AAB19380;

XX DT 06-MAR-2001 (first entry)

XX DE Amino acid sequence of a human lipoxigenase protein.

XX KW Human; lipoxigenase; leukotriene; lipid; chemotactic agent; inflammation;

XX KW smooth muscle contraction; asthma; eye disease; arthritis; lung disease;

XX KW cancer; acne; psoriasis.

XX OS Homo sapiens.

XX PN WO200061765-A2.

XX PD 19-OCT-2000.

XX PF 12-APR-2000; 2000WO-US009657.

XX PR 12-APR-1999; 99US-0128817P.

XX PR 24-AUG-1999; 99US-0150454P.

XX PA (LEXI-) LEXICON GENETICS INC.

XX PI Turner CA, Zambrowicz B, Nehls M, Friedrich G, Sands AT;

XX DR WPI; 2000-665134/64.

XX DR N-PSDB; AAC61748.

XX PT Novel polynucleotides encoding human lipoxigenase proteins useful for

XX PT producing transgenic animals preferably mouse.

XX PS Claim 3; Page 60-61; 83pp; English.

XX AAB19379-92 represent novel human lipoxigenase proteins. Lipoxigenases
XX oxidise lipids to produce leukotrienes. Leukotrienes bind cognate
XX receptors and trigger biological effects. Leukotrienes influence a
XX variety of biological processes, and can serve as, inter alia, potent
XX chemotactic agents and mediators of inflammation, smooth muscle
XX contractions, etc. . Lipoxigenases and leukotrienes are implicated in a
XX variety of diseases and disorders, such as asthma, eye diseases,
XX arthritis, lung disease, cancer, acne, psoriasis, etc

XX SQ Sequence 489 AA;

Query Match 74.1%; Score 40; DB 3; Length 489;

Best Local Similarity 77.8%; Pred. No. 2.6e+02;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIEGYCTPE 9

Db 104 WIEGYCTVE 112


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RESULT 13
AAB19383
ID AAB19383 standard; protein; 615 AA.
XX AC AAB19383;
XX DT 06-MAR-2001 (first entry)
XX DE Amino acid sequence of a human lipoxigenase protein.
XX KW Human; lipoxigenase; leukotriene; lipid; chemotactic agent; inflammation;
XX KW smooth muscle contraction; asthma; eye disease; arthritis; lung disease;
XX KW cancer; acne; psoriasis.
XX OS Homo sapiens.
XX PN WO200061765-A2.
XX PD 19-OCT-2000.
XX PF 12-APR-2000; 2000WO-US009657.
XX PR 12-APR-1999; 99US-0128817P.
XX PR 24-AUG-1999; 99US-0150454P.
XX PA (LEXI-) LEXICON GENETICS INC.
XX PI Turner CA, Zambrowicz B, Nehls M, Friedrich G, Sands AT;
XX WPI; 2000-665134/64.
XX DR N-PSDB; AAC61751.
XX PT Novel polynucleotides encoding human lipoxigenase proteins useful for
XX PT producing transgenic animals preferably mouse.
XX PS Claim 3; Page 66-67; 83pp; English.
XX CC AAB19379-92 represent novel human lipoxigenase proteins. Lipoxigenases
XX CC oxidise lipids to produce leukotrienes. Leukotrienes bind cognate
XX CC receptors and trigger biological effects. Leukotrienes influence a
XX CC variety of biological processes, and can serve as, inter alia, potent
XX CC chemotactic agents and mediators of inflammation, smooth muscle
XX CC contractions, etc. . Lipoxigenases and leukotrienes are implicated in a
XX CC variety of diseases and disorders, such as asthma, eye diseases,
XX CC arthritis, lung disease, cancer, acne, psoriasis, etc
XX SQ Sequence 615 AA;
Query Match 74.1%; Score 40; DB 3; Length 615;
Best Local Similarity 77.8%; Pred. No. 3.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FIEGYCTPE 9
Db 104 WIEGYCTVE 112
:|||||
RESULT 14
AAB19391
ID AAB19391 standard; protein; 645 AA.
XX AC AAB19391;
XX DT 06-MAR-2001 (first entry)
XX DE Amino acid sequence of a human lipoxigenase protein.
XX KW Human; lipoxigenase; leukotriene; lipid; chemotactic agent; inflammation;
XX KW smooth muscle contraction; asthma; eye disease; arthritis; lung disease;
XX KW cancer; acne; psoriasis.
XX OS Homo sapiens.
```

```
XX WO200061765-A2.
XX 19-OCT-2000.
XX 12-APR-2000; 2000WO-US009657.
XX 12-APR-1999; 99US-0128817P.
XX 24-AUG-1999; 99US-0150454P.
XX (LEXI-) LEXICON GENETICS INC.
XX Turner CA, Zambrowicz B, Nehls M, Friedrich G, Sands AT;
XX WPI; 2000-665134/64.
XX DR N-PSDB; AAC61759.
XX PT Novel polynucleotides encoding human lipoxigenase proteins useful for
XX PT producing transgenic animals preferably mouse.
XX PS Claim 3; Page 77-79; 83pp; English.
XX CC AAB19379-92 represent novel human lipoxigenase proteins. Lipoxigenases
XX CC oxidise lipids to produce leukotrienes. Leukotrienes bind cognate
XX CC receptors and trigger biological effects. Leukotrienes influence a
XX CC variety of biological processes, and can serve as, inter alia, potent
XX CC chemotactic agents and mediators of inflammation, smooth muscle
XX CC contractions, etc. . Lipoxigenases and leukotrienes are implicated in a
XX CC variety of diseases and disorders, such as asthma, eye diseases,
XX CC arthritis, lung disease, cancer, acne, psoriasis, etc
XX SQ Sequence 645 AA;
Query Match 74.1%; Score 40; DB 3; Length 645;
Best Local Similarity 77.8%; Pred. No. 3.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FIEGYCTPE 9
Db 260 WIEGYCTVE 268
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ABM84236
ID ABM84236 standard; protein; 671 AA.
XX AC ABM84236;
XX 18-NOV-2004 (first entry)
XX Human diagnostic and therapeutic pprotein SEQ ID NO:4485.
XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX Homo sapiens.
XX WO2004023973-A2.
XX 25-MAR-2004.
XX 12-SEP-2003; 2003WO-US028227.
XX 12-SEP-2002; 2002US-0410259P.
XX 12-SEP-2002; 2002US-0410260P.
XX (INCY-) INCYTE CORP.
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
XX Harthorne TA, Suchorski MT, Altus CM, Pitts SJ, Elder LV;
XX Mooney EM, Deleane AM, Panesar IS, Banville SC, Reddy TP;
XX Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
XX Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
XX Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
```

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;

DR WPI; 2004-329368/30.
DR N-PSDB; ACN42888.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

XX
PS Claim 27; Page; 190pp; English.

XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX
SQ Sequence 671 AA;

Query Match 74.1%; Score 40; DB 8; Length 671;
Best Local Similarity 77.8%; Pred. NO. 3.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIEGYCTPE 9

Db :|||||
104 WIEGYCTVE 112

Search completed: March 17, 2006, 23:27:39
Job time : 124 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:34:23 ; Search time 28.3333 Seconds
(without alignments)
26.262 Million cell updates/sec

Title: US-09-856-812B-49

Perfect score: 54

Sequence: 1 FIEGYCTPE 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.*
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6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	54	100.0	369	1	US-08-773-870-4
3	40	74.1	489	2	US-09-547-435-4
4	40	74.1	615	2	US-09-547-435-10
5	40	74.1	645	2	US-09-547-435-26
6	40	74.1	711	2	US-09-547-435-2
7	40	74.1	771	2	US-09-547-435-28
8	40	74.1	867	2	US-09-547-435-24
9	39	72.2	133	2	US-09-543-681A-6889
10	39	72.2	226	2	US-09-268-364-2
11	39	72.2	603	2	US-09-198-452A-1011
12	39	72.2	612	2	US-09-438-185A-942
13	39	72.2	727	2	US-09-252-991A-18812
14	38	70.4	141	2	US-09-252-991A-20786
15	38	70.4	724	2	US-09-252-991A-30884
16	37	68.5	208	2	US-09-902-540-13701
17	37	68.5	312	2	US-09-949-016-9383
18	36	66.7	207	2	US-09-248-796A-16052
19	36	66.7	319	2	US-09-949-016-8188
20	36	66.7	346	2	US-09-468-433C-22
21	36	66.7	410	2	US-09-489-039A-9449
22	35	64.8	225	2	US-09-270-767-32487
23	35	64.8	225	2	US-09-270-767-47704
24	35	64.8	280	2	US-09-292-858B-5
25	35	64.8	282	2	US-09-292-858B-4
26	35	64.8	287	2	US-09-107-532A-5182
27	35	64.8	303	2	US-09-949-016-9089

28 35 64.8 306 2 US-09-457-046B-22 Sequence 22, Appl
29 35 64.8 306 2 US-09-866-570B-22 Sequence 22, Appl
30 35 64.8 358 2 US-09-949-016-10216 Sequence 10216, A
31 35 64.8 433 2 US-09-614-912-168 Sequence 168, App
32 35 64.8 1621 2 US-08-972-927-3 Sequence 3, Appl1
33 34 63.0 132 2 US-09-252-991A-18884 Sequence 18884, A
34 34 63.0 172 2 US-09-328-352-8130 Sequence 8130, Ap
35 34 63.0 196 2 US-09-252-991A-31920 Sequence 31920, A
36 34 63.0 198 1 US-08-097-827-2 Sequence 2, Appl1
37 34 63.0 198 1 US-08-494-574-2 Sequence 2, Appl1
38 34 63.0 210 2 US-09-583-110-2852 Sequence 2852, Ap
39 34 63.0 231 2 US-09-543-681A-5953 Sequence 5953, Ap
40 34 63.0 286 2 US-09-583-110-5194 Sequence 5194, Ap
41 34 63.0 291 2 US-09-107-433-5198 Sequence 5198, Ap
42 34 63.0 320 2 US-09-949-016-10187 Sequence 10187, A
43 34 63.0 413 2 US-09-602-472A-4 Sequence 4, Appl1
44 34 63.0 457 2 US-09-602-472A-2 Sequence 2, Appl1
45 34 63.0 473 2 US-09-538-092-1353 Sequence 1353, Ap

ALIGNMENTS

RESULT 1

US-09-533-499B-19

; Sequence 19, Application US/09533499B

; Patent No. 6682731

; GENERAL INFORMATION:

; APPLICANT: Townsend, Alan; Bastin, Judy; Boon-Palleur, Thierry; van der
; Bruggen, Pierre; Coullie, Pierre; Gajewski, Thomas; Melief,
; Cornelis J.M.; Visseren, M.W.; Kast, W.M.

; TITLE OF INVENTION: ISOLATED PEPTIDES DERIVED FROM MAGE TUMOR
; REJECTION ANTIGEN PRECURSORS WHICH COMPLEX WITH
; HLA-A2 MOLECULES

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fulbright & Jaworski LLP

; STREET: 666 Fifth Avenue

; CITY: New York City

; STATE: New York

; COUNTRY: USA

; ZIP: 10103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/533,499B

; FILING DATE: 23-Mar-2000

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/722,115

; FILING DATE: February 6, 1997

; APPLICATION NUMBER: 08/290,381

; FILING DATE: 15-August-1994

; APPLICATION NUMBER: 08/261,160

; FILING DATE: 17-June-1994

; APPLICATION NUMBER: 08/217,186

; FILING DATE: 24-March-1994

; APPLICATION NUMBER: 08/217,188

; FILING DATE: 24-March-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, No. 6682731man D.

; REGISTRATION NUMBER: 30,946

; REFERENCE/DOCKET NUMBER: LUD 5327.3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 318-3168

; TELEFAX: (212) 318-3400

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-533-499B-19

Query Match      100.0%; Score 54; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FIEGYCTPE 9
Db      1 FIEGYCTPE 9

RESULT 2
US-08-773-870-4
; Sequence 4, Application US/08773870
; Patent No. 5912143
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN WAGE-LIKE PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/773,870
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0179 US
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 533511
US-08-773-870-4

Query Match      100.0%; Score 54; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FIEGYCTPE 9
Db      235 FIEGYCTPE 243

RESULT 3
US-09-547-435-4
; Sequence 4, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-10

Query Match      74.1%; Score 40; DB 2; Length 615;
Best Local Similarity 77.8%; Pred. No. 69;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FIEGYCTPE 9
Db      104 WIEGYCTVE 112

RESULT 4
US-09-547-435-10
; Sequence 10, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-10

Query Match      74.1%; Score 40; DB 2; Length 615;
Best Local Similarity 77.8%; Pred. No. 69;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FIEGYCTPE 9
Db      104 WIEGYCTVE 112

RESULT 5
US-09-547-435-26
; Sequence 26, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-10

Query Match      74.1%; Score 40; DB 2; Length 615;
Best Local Similarity 77.8%; Pred. No. 69;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FIEGYCTPE 9
Db      104 WIEGYCTVE 112

RESULT 6
US-09-547-435-26
; Sequence 26, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-10

Query Match      74.1%; Score 40; DB 2; Length 615;
Best Local Similarity 77.8%; Pred. No. 69;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FIEGYCTPE 9
Db      104 WIEGYCTVE 112

RESULT 7
US-09-547-435-26
; Sequence 26, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-10

Query Match      74.1%; Score 40; DB 2; Length 615;
Best Local Similarity 77.8%; Pred. No. 69;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FIEGYCTPE 9
Db      104 WIEGYCTVE 112

RESULT 8
US-09-547-435-26
; Sequence 26, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-10

Query Match      74.1%; Score 40; DB 2; Length 615;
Best Local Similarity 77.8%; Pred. No. 69;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FIEGYCTPE 9
Db      104 WIEGYCTVE 112

RESULT 9
US-09-547-435-26
; Sequence 26, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-10

Query Match      74.1%; Score 40; DB 2; Length 615;
Best Local Similarity 77.8%; Pred. No. 69;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FIEGYCTPE 9
Db      104 WIEGYCTVE 112

RESULT 10
US-09-547-435-26
; Sequence 26, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-10

Query Match      74.1%; Score 40; DB 2; Length 615;
Best Local Similarity 77.8%; Pred. No. 69;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FIEGYCTPE 9
Db      104 WIEGYCTVE 112

RESULT 11
US-09-547-435-26
; Sequence 26, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-10

Query Match      74.1%; Score 40; DB 2; Length 615;
Best Local Similarity 77.8%; Pred. No. 69;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FIEGYCTPE 9
Db      104 WIEGYCTVE 112

RESULT 12
US-09-547-435-26
; Sequence 26, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls,
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; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-26

Query Match 74.1%; Score 40; DB 2; Length 645;
Best Local Similarity 77.8%; Pred. No. 73;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 FIEGYCTPE 9
:|||||
Db 260 WIEGYCTVE 268

RESULT 6

US-09-547-435-2
; Sequence 2, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-2

Query Match 74.1%; Score 40; DB 2; Length 711;
Best Local Similarity 77.8%; Pred. No. 80;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 FIEGYCTPE 9
:|||||
Db 104 WIEGYCTVE 112

RESULT 7

US-09-547-435-28
; Sequence 28, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 771
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-547-435-28

Query Match 74.1%; Score 40; DB 2; Length 771;
Best Local Similarity 77.8%; Pred. No. 88;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIEGYCTPE 9
:|||||
Db 260 WIEGYCTVE 268

RESULT 8

US-09-547-435-24
; Sequence 24, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 867
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-24

Query Match 74.1%; Score 40; DB 2; Length 867;
Best Local Similarity 77.8%; Pred. No. 99;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIEGYCTPE 9
:|||||
Db 260 WIEGYCTVE 268

RESULT 9

US-09-543-681A-6889
; Sequence 6889, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6889
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6889

Query Match 72.2%; Score 39; DB 2; Length 133;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IEGYCTPE 9
:|||||
Db 63 VERYCTPE 70

RESULT 10

US-09-268-364-2
; Sequence 2, Application US/09268364A
; Patent No. 6204063

; GENERAL INFORMATION:

; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; APPLICANT: Lightner, Jonathan
; APPLICANT: Odell, Joan

; TITLE OF INVENTION: PLANT GLYCOLYSIS AND RESPIRATION ENZYMES
; FILE REFERENCE: BB-1154

; CURRENT APPLICATION NUMBER: US/09/268,364A

; CURRENT FILING DATE: 1999-03-15

; EARLIER APPLICATION NUMBER: 60/079,387

; EARLIER FILING DATE: March 16, 1998

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 2

; LENGTH: 226

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: (49)..(50)

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: (54)..(55)

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: (58)

US-09-268-364-2

Query Match 72.2%; Score 39; DB 2; Length 226;

Best Local Similarity 100.0%; Pred. No. 36;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYCTPE 9

|||||

Db 211 GYCTPE 216

RESULT 11

US-09-198-452A-1011

; Sequence 1011, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffois, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 1011

; LENGTH: 603

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-1011

Query Match 72.2%; Score 39; DB 2; Length 603;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYCTPE 9

|||||

Db 182 GYCTPE 187

RESULT 12

US-09-438-185A-942

; Sequence 942, Application US/09438185A

; Patent No. 6822071

; GENERAL INFORMATION:

; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald

; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence

; FILE REFERENCE: 018941-000411US

; CURRENT APPLICATION NUMBER: US/09/438,185A

; CURRENT FILING DATE: 2002-03-13

; PRIOR APPLICATION NUMBER: US 60/108,279

; PRIOR FILING DATE: 1998-11-12

; PRIOR APPLICATION NUMBER: US 60/128,606

; PRIOR FILING DATE: 1999-04-08

; NUMBER OF SEQ ID NOS: 1074

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 942

; LENGTH: 612

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

; FEATURE:

; OTHER INFORMATION: Cpn0940

US-09-438-185A-942

Query Match 72.2%; Score 39; DB 2; Length 612;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYCTPE 9

|||||

Db 191 GYCTPE 196

RESULT 13

US-09-252-991A-18812

; Sequence 18812, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 18812

; LENGTH: 727

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-18812

Query Match 72.2%; Score 39; DB 2; Length 727;

Best Local Similarity 62.5%; Pred. No. 1.2e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIEGYCTP 8

|||||

Db 361 FVSGYCSP 368

RESULT 14

US-09-252-991A-20786

; Sequence 20786, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

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; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20786
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20786

Query Match          70.4%; Score 38; DB 2; Length 141;
Best Local Similarity 63.8%; Pred. No. 33;
Matches 7; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY      1 FIEGYC--TPE 9
Db      95 FLDGYCIITPE 105

RESULT 15
US-09-252-991A-30884
; Sequence 30884, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30884
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30884

Query Match          70.4%; Score 38; DB 2; Length 724;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 EGYCTPE 9
Db      563 EGYCRPE 569

Search completed: March 17, 2006, 23:36:21
Job time : 30.3333 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:35:13 ; Search time 98.3333 Seconds
(without alignments)
38.242 Million cell updates/sec

Title: US-09-856-812b-49
Perfect score: 54
Sequence: 1 FIEGYCTPE 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:
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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	369	4	US-10-036-542-84
2	54	100.0	369	4	US-10-188-832-149
3	54	100.0	369	5	US-10-658-884-4
4	54	100.0	369	5	US-10-756-149-4721
5	54	100.0	383	4	US-10-029-386-32058
6	40	74.1	277	3	US-09-764-847-819
7	40	74.1	277	4	US-10-092-154-819
8	40	74.1	489	4	US-10-422-264-4
9	40	74.1	618	4	US-10-422-264-10
10	40	74.1	635	4	US-10-425-115-193718
11	40	74.1	645	4	US-10-422-264-26
12	40	74.1	711	3	US-09-862-658-2
13	40	74.1	711	4	US-10-175-696-23
14	40	74.1	711	4	US-10-422-264-2
15	40	74.1	711	4	US-10-275-998-3
16	40	74.1	711	4	US-10-776-871-23
17	40	74.1	717	4	US-10-369-493-5773
18	40	74.1	771	4	US-10-422-264-28
19	40	74.1	867	4	US-10-422-264-24
20	40	74.1	1045	4	US-10-425-115-193717
21	40	74.1	1306	4	US-10-425-115-193709
22	40	74.1	1762	4	US-10-425-115-193719
23	39	72.2	130	4	US-10-282-122A-68941
24	39	72.2	143	4	US-10-767-701-38991
25	39	72.2	226	3	US-09-756-998-2
26	39	72.2	468	4	US-10-425-115-193423
27	39	72.2	484	4	US-10-437-963-107560

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28 39 72.2 493 4 US-10-425-114-58902 Sequence 58902, A
29 39 72.2 603 4 US-10-289-762-1011 Sequence 1011, Ap
30 39 72.2 674 4 US-10-425-115-284028 Sequence 284028,
31 38 70.4 54 4 US-10-029-386-32779 Sequence 32779, A
32 38 70.4 130 4 US-10-424-599-164220 Sequence 164220,
33 38 70.4 314 4 US-10-425-114-67858 Sequence 67858, A
34 38 70.4 347 4 US-10-425-115-236312 Sequence 236312,
35 37 68.5 115 4 US-10-425-115-332470 Sequence 332470,
36 37 68.5 156 5 US-10-450-763-57015 Sequence 57015, A
37 37 68.5 313 5 US-10-774-355A-2232 Sequence 2232, A
38 37 68.5 315 4 US-10-437-963-150636 Sequence 150636,
39 37 68.5 403 4 US-10-424-599-190863 Sequence 190863,
40 37 68.5 532 5 US-10-473-127-746 Sequence 746, App
41 37 68.5 532 5 US-10-473-127-747 Sequence 747, App
42 37 68.5 584 4 US-10-437-963-191207 Sequence 191207,
43 37 68.5 810 4 US-10-425-115-193712 Sequence 193712,
44 37 68.5 890 4 US-10-437-963-150639 Sequence 150639,
45 37 68.5 944 4 US-10-437-963-192627 Sequence 192627,

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ALIGNMENTS

RESULT 1

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US-10-036-542-84
; Sequence 84, Application US/10036542
; Publication No. US20030083481A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
; FILE REFERENCE: PA002PI
; CURRENT APPLICATION NUMBER: US/10/036,542
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: PCT/US00/19666
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/144,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/148,681
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/149,173
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/158,004
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/194,689
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-036-542-84

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Query Match 100.0%; Score 54; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 FIEGYCTPE 9

Db 235 FIEGYCTPE 243

RESULT 2

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US-10-188-832-149
; Sequence 149, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer

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; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/189,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 149
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-149

Query Match      100.0%; Score 54; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FIEGYCTPE 9
Db      235 FIEGYCTPE 243

RESULT 3
US-10-658-884-4
; Sequence 4, Application US/10658884
; Publication No. US20050019304A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: NOVEL HUMAN MAGE-LIKE PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/658,884
; FILING DATE: 09-Sep-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/773,870
; FILING DATE: 27-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0179 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
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; LIBRARY: GenBank
; CLONE: 533511
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-658-884-4

Query Match      100.0%; Score 54; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FIEGYCTPE 9
Db      235 FIEGYCTPE 243

RESULT 4
US-10-756-149-4721
; Sequence 4721, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4721
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-4721

Query Match      100.0%; Score 54; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FIEGYCTPE 9
Db      235 FIEGYCTPE 243

RESULT 5
US-10-029-386-32058
; Sequence 32058, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AROMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32058
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AF134576.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
; OTHER INFORMATION: SWISSPROT HIT: P43363, EVALUAE 0.00e+00
US-10-029-386-32058
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Query Match 100.0%; Score 54; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FIEGYCTPE 9
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Db 256 FIEGYCTPE 264

RESULT 6
US-09-764-847-819
; Sequence 819, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; PRIOR APPLICATION DATA REMOVED - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 819
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (223)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (224)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (232)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (256)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (257)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-847-819

Query Match 74.1%; Score 40; DB 3; Length 277;
Best Local Similarity 77.8%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIEGYCTPE 9
:|||||||
Db 199 WIEGYCTVE 207

RESULT 7
US-10-092-154-819
; Sequence 819, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 819
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (223)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: misc_feature
; LOCATION: (224)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: misc_feature
; LOCATION: (232)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: misc_feature
; LOCATION: (256)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: misc_feature
; LOCATION: (257)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-092-154-819

Query Match 74.1%; Score 40; DB 4; Length 277;
Best Local Similarity 77.8%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIEGYCTPE 9
:|||||||
Db 199 WIEGYCTVE 207

RESULT 8
US-10-422-264-4
; Sequence 4, Application US/10422264
; Publication No. US20030172391A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20030172391A1el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/10/422,264
; CURRENT FILING DATE: 2003-04-23
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-422-264-4

Query Match 74.1%; Score 40; DB 4; Length 489;
Best Local Similarity 77.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIEGYCTPE 9
:|||||||
Db 104 WIEGYCTVE 112

RESULT 9
US-10-422-264-10
; Sequence 10, Application US/10422264
; Publication No. US20030172391A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20030172391A1el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/10/422,264
; CURRENT FILING DATE: 2003-04-23
; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-422-264-10

Query Match 74.1%; Score 40; DB 4; Length 615;
Best Local Similarity 77.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIEGYCTPE 9
:|||||
Db 104 WIEGYCTVE 112

RESULT 10
US-10-425-115-193718
; Sequence 193718, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(S3222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 193718
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_108252C.1.pep
US-10-425-115-193718

Query Match 74.1%; Score 40; DB 4; Length 638;
Best Local Similarity 87.5%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 IEGYCTPE 9
:|||||
Db 408 IEGYCTKE 415

RESULT 11
US-10-422-264-26
; Sequence 26, Application US/10422264
; Publication No. US20030172391A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20030172391A1 Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: 7705,0009-00000
; CURRENT APPLICATION NUMBER: US/10/422,264
; CURRENT FILING DATE: 2003-04-23
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-422-264-26

Query Match 74.1%; Score 40; DB 4; Length 645;
Best Local Similarity 77.8%; Pred. No. 2.3e+02;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FIEGYCTPE 9
:|||||
Db 260 WIEGYCTVE 268

RESULT 12
US-09-862-658-2
; Sequence 2, Application US/09862658
; Patent No. US20020137101A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 46638, A NOVEL HUMAN LIPOXYGENASE FAMILY
; FILE REFERENCE: 10448-053001
; CURRENT APPLICATION NUMBER: US/09/862,658
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/205,675
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-862-658-2

Query Match 74.1%; Score 40; DB 3; Length 711;
Best Local Similarity 77.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIEGYCTPE 9
:|||||
Db 104 WIEGYCTVE 112

RESULT 13
US-10-175-696-23
; Sequence 23, Application US/10175696
; Publication No. US20030092658A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-193001
; CURRENT APPLICATION NUMBER: US/10/175,696
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 10/067,668
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/266,140
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/823,901
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US01/10720
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/193,920
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/862,658
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US01/16380
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/205,675
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/882,837
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: PCT/US01/19319
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/211,727
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 23
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-175-696-23

Query Match      74.1%; Score 40; DB 4; Length 711;
Best Local Similarity 77.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FIEGYCTPE 9
Db      104 WIEGYCTVE 112

RESULT 14
US-10-422-264-2
; Sequence 2, Application US/10422264
; Publication No. US20030172391A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20030172391A1el Lipoxxygenase Proteins and Polynucleotides
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/10/422,264
; CURRENT FILING DATE: 2003-04-23
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-422-264-2

Query Match      74.1%; Score 40; DB 4; Length 711;
Best Local Similarity 77.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FIEGYCTPE 9
Db      104 WIEGYCTVE 112

RESULT 15
US-10-275-998-3
; Sequence 3, Application US/10275998
; Publication No. US20040023354A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DAS, Debopriya
; APPLICANT: REDDY, Roopa
; APPLICANT: YAO, Monique G.
; APPLICANT: NGUYEN, Darniel B.
; APPLICANT: LU, Yan
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: YUE, Henry
; APPLICANT: KHAN, Farrah A.
; APPLICANT: GANDHI, Aameena R.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LAL, Preeti
; APPLICANT: KEARNEY, Liam
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: DING, Li
; APPLICANT: THORNTON, Michael
; TITLE OF INVENTION: LIPID METABOLISM ENZYMES
; FILE REFERENCE: PI-0095 USN
; CURRENT APPLICATION NUMBER: US/10/275,998
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 01/15210
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; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/203,511
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/207,903
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/210,150
; PRIOR FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: US 60/213,392
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023354A1 7473234CD1
US-10-275-998-3

Query Match      74.1%; Score 40; DB 4; Length 711;
Best Local Similarity 77.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FIEGYCTPE 9
Db      104 WIEGYCTVE 112

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5: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	66.7	151	7	US-11-103-957-72 Sequence 72, Appl
2	36	66.7	295	7	US-11-096-568A-5906 Sequence 5906, Ap
3	36	66.7	302	7	US-11-165-226-127 Sequence 127, App
4	36	66.7	413	7	US-11-096-568A-5905 Sequence 5905, Ap
5	36	66.7	414	7	US-11-096-568A-5904 Sequence 5904, Ap
6	34	63.0	15	7	US-11-106-932-130 Sequence 130, App
7	34	63.0	19	7	US-11-129-741-3677 Sequence 3677, Ap
8	34	63.0	30	7	US-11-106-932-41 Sequence 41, Appl
9	34	63.0	120	7	US-11-096-568A-4895 Sequence 4895, Ap
10	34	63.0	150	7	US-11-096-568A-4894 Sequence 4894, Ap
11	34	63.0	218	7	US-11-096-568A-17864 Sequence 17864, A
12	34	63.0	253	7	US-11-096-568A-24694 Sequence 24694, A
13	34	63.0	258	7	US-11-096-568A-32629 Sequence 32629, A
14	34	63.0	267	7	US-11-096-568A-17863 Sequence 17863, A
15	34	63.0	269	7	US-11-096-568A-29824 Sequence 29824, A
16	34	63.0	278	7	US-11-096-568A-24693 Sequence 24693, A
17	34	63.0	294	7	US-11-096-568A-5167 Sequence 5167, Ap
18	34	63.0	297	7	US-11-096-568A-7083 Sequence 7083, Ap
19	34	63.0	303	7	US-11-096-568A-27931 Sequence 27931, A
20	34	63.0	307	7	US-11-096-568A-24692 Sequence 24692, A
21	34	63.0	323	7	US-11-096-568A-5166 Sequence 5166, Ap
22	34	63.0	327	7	US-11-096-568A-15669 Sequence 15669, A
23	34	63.0	334	7	US-11-096-568A-27492 Sequence 27492, A
24	34	63.0	334	7	US-11-096-568A-29004 Sequence 29004, A
25	34	63.0	334	7	US-11-096-568A-29823 Sequence 29823, A

ALIGNMENTS

RESULT 1

US-11-103-957-72
; Sequence 72, Application US/11103957
; Publication No. US20050281847A1
; GENERAL INFORMATION: Francois-Xavier Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Verlant, Vincent Georges Christian Louis
; TITLE OF INVENTION: Vaccine Composition
; FILE REFERENCE: B45261
; CURRENT APPLICATION NUMBER: US/11/103,957
; PRIOR FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: US/10/467,534
; PRIOR FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: PCT/EP02/01356
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103169.9
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-11-103-957-72

Query Match 66.7%; Score 36; DB 7; Length 151;
Best Local Similarity 62.5%; Pred. No. 15;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 IEQYCTPE 9
:|:|:|:
Db 90 MEGHCSP 97

RESULT 2

US-11-096-568A-5906
; Sequence 5906, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION: Alexander, Nickolai et al.
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471

```
; SEQ ID NO 5906
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Glycine max
; NAME/KEY: misc feature
; LOCATION: (1)-(295)
; OTHER INFORMATION: Ceres Seq. ID no. 14312303
US-11-096-568A-5906

Query Match      66.7%; Score 36; DB 7; Length 295;
Best Local Similarity 71.4%; Pred. No. 28;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 EGYCTPE 9
DB      121 QGYCAPE 127

RESULT 3
US-11-165-226-127
; Sequence 127, Application US/11165226
; Publication No. US20050287627A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Process for producing dipeptides or dipeptide derivatives
; FILE REFERENCE: 4093-13
; CURRENT APPLICATION NUMBER: US/11/165,226
; PRIOR FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: JP2004-189007
; PRIOR FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 127
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Mesorhizobium loti MAF303099
US-11-165-226-127

Query Match      66.7%; Score 36; DB 7; Length 302;
Best Local Similarity 62.5%; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 IEGYCTPE 9
DB      159 VMGFCTPE 166

RESULT 4
US-11-096-568A-5905
; Sequence 5905, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 5905
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Glycine max
; NAME/KEY: misc feature
; LOCATION: (1)-(413)
; OTHER INFORMATION: Ceres Seq. ID no. 14312302
US-11-096-568A-5905

Query Match      66.7%; Score 36; DB 7; Length 413;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 EGYCTPE 9
DB      239 QGYCAPE 245

RESULT 5
US-11-096-568A-5904
; Sequence 5904, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 5904
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Glycine max
; NAME/KEY: misc feature
; LOCATION: (1)-(414)
; OTHER INFORMATION: Ceres Seq. ID no. 14312301
US-11-096-568A-5904

Query Match      66.7%; Score 36; DB 7; Length 414;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 EGYCTPE 9
DB      240 QGYCAPE 246

RESULT 6
US-11-106-932-130
; Sequence 130, Application US/11106932
; Publication No. US20050260697A1
; GENERAL INFORMATION:
; APPLICANT: WANG, KA-WANG KEVIN
; APPLICANT: HAYES, RONALD
; APPLICANT: LIU, MING CHEN
; APPLICANT: OLI, MONIKA
; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
; FILE REFERENCE: 5853-549-1
; CURRENT APPLICATION NUMBER: US/11/106,932
; CURRENT FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 130
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-106-932-130

Query Match      63.0%; Score 34; DB 7; Length 15;
Best Local Similarity 83.3%; Pred. No. 4;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GYCTPE 9
DB      3 GYCAPE 8

RESULT 7
US-11-129-741-3677
; Sequence 3677, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
```


APPLICANT: YUEN, KWOK YUNG
APPLICANT: WOO, CHIU YAT PATRICK
APPLICANT: LAU, KAR PUI SUSANNA
APPLICANT: CHAN, KWOK HUNG
APPLICANT: POON, LIT MAN
APPLICANT: PEIRIS, JOSEPH S.M.
APPLICANT: GUAN, YI
TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
TITLE OF INVENTION: INFECTION AND USES THEREOF
FILE REFERENCE: V0690.0044
CURRENT FILING DATE: 2005-05-16
PRIOR APPLICATION NUMBER: 10/895,064
PRIOR FILING DATE: 2004-07-21
NUMBER OF SEQ ID NOS: 4257
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3677
LENGTH: 19
TYPE: PRT
ORGANISM: Corononavirus-HKU1
US-11-129-741-3677

Query Match 63.0%; Score 34; DB 7; Length 19;
Best Local Similarity 62.5%; Pred. No. 5.4;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FIEGYCTP 8
: |||||
Db 4 YINGCYCP 11

RESULT 8
US-11-106-932-41
Sequence 41, Application US/11106932
Publication No. US20050260697A1
GENERAL INFORMATION:
APPLICANT: WANG, KA-WANG KEVIN
APPLICANT: HAYES, RONALD
APPLICANT: LIU, MING CHEN
APPLICANT: OLI, MONIKA
TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING
FILE REFERENCE: 5853-549-1
CURRENT APPLICATION NUMBER: US/11/106,932
CURRENT FILING DATE: 2005-04-15
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn version 3.2
SEQ ID NO 41
LENGTH: 30
TYPE: PRT
ORGANISM: Mus musculus
US-11-106-932-41

Query Match 63.0%; Score 34; DB 7; Length 30;
Best Local Similarity 83.3%; Pred. No. 8.1;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GYCTPE 9
|||
Db 18 GYCAPE 23

RESULT 9
US-11-096-568A-4895
Sequence 4895, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 4895
LENGTH: 120
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(120)
OTHER INFORMATION: Ceres Seq. ID no. 14304946
US-11-096-568A-4895

Query Match 63.0%; Score 34; DB 7; Length 120;
Best Local Similarity 83.3%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GYCTPE 9
|||
Db 68 GYCAPE 73

RESULT 10
US-11-096-568A-4894
Sequence 4894, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 4894
LENGTH: 150
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(150)
OTHER INFORMATION: Ceres Seq. ID no. 14304945
US-11-096-568A-4894

Query Match 63.0%; Score 34; DB 7; Length 150;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GYCTPE 9
|||
Db 98 GYCAPE 103

RESULT 11
US-11-096-568A-17864
Sequence 17864, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 17864
LENGTH: 218
TYPE: PRT
ORGANISM: Zea mays subsp. mays

Query Match 63.0%; Score 34; DB 7; Length 218;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GYCTPE 9
|||
Db 98 GYCAPE 103

US-11-096-568A-17864
Sequence 17864, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01

```
Query Match      63.0%; Score 34; DB 7; Length 218;
Best Local Similarity 83.3%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      4 GYCTPE 9
      |||||
Db      5 GYCAPE 10

RESULT 12
US-11-096-568A-24694
; Sequence 24694, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 24694
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(253)
; OTHER INFORMATION: Ceres Seq. ID no. 12443276
US-11-096-568A-24694

Query Match      63.0%; Score 34; DB 7; Length 253;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      4 GYCTPE 9
      |||||
Db      68 GYCAPE 73

RESULT 13
US-11-096-568A-32629
; Sequence 32629, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32629
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(258)
; OTHER INFORMATION: Ceres Seq. ID no. 13593696
US-11-096-568A-32629

Query Match      63.0%; Score 34; DB 7; Length 258;
Best Local Similarity 83.3%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      4 GYCTPE 9
      |||||
Db      124 GYCAPE 129

RESULT 14
US-11-096-568A-17863
```

```
; Sequence 17863, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17863
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(267)
; OTHER INFORMATION: Ceres Seq. ID no. 12361288
US-11-096-568A-17863

Query Match      63.0%; Score 34; DB 7; Length 267;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      4 GYCTPE 9
      |||||
Db      54 GYCAPE 59

RESULT 15
US-11-096-568A-29824
; Sequence 29824, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 29824
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(269)
; OTHER INFORMATION: Ceres Seq. ID no. 4931039
US-11-096-568A-29824

Query Match      63.0%; Score 34; DB 7; Length 269;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      4 GYCTPE 9
      |||||
Db      122 GYCAPE 127

Search completed: March 17, 2006, 23:42:01
Job time : 12.6667 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:28:08 ; Search time 19.3333 Seconds
(without alignments)
44.791 Million cell updates/sec

Title: US-09-856-812b-49

Perfect score: 54

Sequence: 1 FIEGYCTPE 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	369	2	138659 melanoma antigen MAGE-10 - human
2	41	75.9	150	2	15K cysteine-rich
3	40	74.1	717	2	hypothetical prote
4	40	74.1	915	2	hypothetical prote
5	39	72.2	151	2	15K cysteine-rich
6	39	72.2	427	2	serine/threonine k
7	39	72.2	603	2	exonuclease ABC,
8	39	72.2	603	2	excinuclease ABC,
9	38	70.4	114	2	hypothetical prote
10	38	70.4	358	2	hypothetical prote
11	38	70.4	398	2	probable argg prot
12	38	70.4	399	2	arginosuccinate sy
13	38	70.4	435	2	NADH-ubiquinone ox
14	38	70.4	683	2	probable oligopept
15	37	68.5	389	2	hypothetical prote
16	37	68.5	606	2	probable membrane
17	36	66.7	150	2	probable 15kda cys
18	36	66.7	152	2	15K cysteine-rich
19	36	66.7	157	2	hypothetical prote
20	36	66.7	177	2	oxidoreductase wit
21	36	66.7	188	2	probable oxidoredu
22	36	66.7	220	2	hypothetical prote
23	36	66.7	319	2	melanoma antigen M
24	36	66.7	416	2	hypothetical prote
25	36	66.7	416	2	hypothetical prote
26	36	66.7	531	2	T02264
27	36	66.7	1230	2	T19899
28	36	66.7	1234	2	T30515
29	35	64.8	130	2	B64426

30	35	64.8	134	2	H65131	hypothetical 14.6
31	35	64.8	248	2	T41608	hypothetical prote
32	35	64.8	275	2	G91156	hypothetical prote
33	35	64.8	275	2	D86002	hypothetical prote
34	35	64.8	389	2	AG2260	DNA mismatch repai
35	35	64.8	391	2	T29277	hypothetical prote
36	35	64.8	521	2	S51682	dnak-type molecula
37	35	64.8	667	2	T40727	probable chloride
38	35	64.8	673	1	D1MSR1	protein-arginine d
39	35	64.8	1623	2	T01369	ABC transporter At
40	34	63.0	103	2	AD0258	hypothetical phage
41	34	63.0	122	2	G82955	hypothetical prote
42	34	63.0	161	2	E75043	conserved hypotet
43	34	63.0	166	2	B56279	carbon-monoxide de
44	34	63.0	167	2	E83743	4-hydroxybenzoyl-C
45	34	63.0	170	2	H83404	probable ferredoxi

ALIGNMENTS

RESULT 1

I38659

melanoma antigen MAGE-10 - human

C:Species: Homo sapiens (man)

C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004

C:Accession: I38659

R:De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; B.

oon, T.

Immunogenetics 40, 360-369, 1994

A>Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fam

A:Reference number: I38659; MUID:95012457; PMID:7927540

A:Accession: I38659

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-369 <RES>

A:Cross-references: UNIPROT:P43363; UNIPARC:UPI00000000C57; EMBL:U10685; NID:9533510; PI

C:Genetics:

A:Gene: GDB:MAGEA10; MAGE10

A:Cross-references: GDB:331126

A:Map position: Xq28-Xq28

A:Introns: #status absent

C:Superfamily: tumor associated protein MAGE

Query Match 100.0%; Score 54; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FIEGYCTPE 9

DB 235 FIEGYCTPE 243

RESULT 2

JT0420

15K cysteine-rich outer membrane protein - Chlamydia trachomatis (serotype L)

C:Species: Chlamydia trachomatis

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C:Accession: JT0420; D43584; F00088; S18982; S24278

R:Clarke, I.N.; Ward, M.E.; Lambden, P.R.

Gene 71, 307-314, 1988

A>Title: Molecular cloning and sequence analysis of a developmentally regulated cysteine

A:Reference number: JT0419; MUID:89138006; PMID:3066701

A:Accession: JT0420

A:Molecule type: DNA

A:Residues: 1-150 <CLA>

A:Cross-references: UNIPROT:P18587; UNIPARC:UPI0000128474; GB:M35148; GB:M23180; GB:M351

A>Note: serotype L1

R:de la Maza, L.M.; Fielder, T.J.; Carlson, E.J.; Markoff, B.A.; Peterson, E.M.

Infect. Immun. 59, 1196-1201, 1991

A>Title: Sequence diversity of the 60-kilodalton protein and of a putative 15-kilodalton

A:Reference number: A43584; MUID:91147205; PMID:1997423

A:Accession: D43584

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-150
A;Cross-references: UNIPARC:UPI0000128474; EMBL:X54390; NID:g40766; PIDN:CAA38262.1; PID
A;Note: serotype L3
R;Lambden, P.R.; Everson, J.S.; Ward, M.E.; Clarke, I.N.
Gene 87, 105-112, 1990
A;Title: Sulfur-rich proteins of Chlamydia trachomatis: developmentally regulated transcr
A;Reference number: JQ0514; MUID:90236284; PMID:2332164
A;Accession: PQ0088
A;Molecule type: mRNA
A;Residues: 1-47 <LAM>
A;Cross-references: UNIPARC:UPI00001791C8
C;Genetics:
A;Gene: Srp
C;Superfamily: Chlamydia 15K cysteine-rich outer membrane protein
C;Keywords: membrane protein

Query Match 75.9%; Score 41; DB 2; Length 150;
Best Local Similarity 75.0%; Pred. No. 3.7;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 IEQYCTPE 9
:|||||
DB 89 MEGYCSP 96

RESULT 3
T28829
hypothetical protein F37C12.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28829
R;Fulton, L.
submitted to the EMBL Data Library, March 1994
A;Description: The sequence of C. elegans cosmid F37C12.
A;Reference number: Z20530
A;Accession: T28829
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-717 <FUL>
A;Cross-references: UNIPROT:Q02121; UNIPARC:UPI0000176212; EMBL:U00033; PIDN:AAC48292.1;
A;Experimental source: strain Bristol N2; clone F37C12
C;Genetics:
A;Gene: CESP:F37C12.7
A;Map position: 3
A;Introns: 83/3; 343/3; 663/1
C;Superfamily: human long-chain-fatty-acid-CoA ligase; acetate-CoA ligase homology
F;149-699/Domain: acetate-CoA ligase homology <ACL>

Query Match 74.1%; Score 40; DB 2; Length 717;
Best Local Similarity 62.5%; Pred. No. 24;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FIEGYCTP 8
:|||||
DB 415 YLEGYCSP 422

RESULT 4
T26695
hypothetical protein Y38H6C.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26695
R;White, S.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z20255
A;Accession: T26695
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-915 <WIL>
A;Cross-references: UNIPROT:Q9XX53; UNIPARC:UPI0000061285; EMBL:AL031630; PIDN:CAA20985.1

A;Experimental source: clone Y38H6C
C;Genetics:
A;Gene: CESP:Y38H6C.5
A;Map position: 5
A;Introns: 41/2; 150/1; 174/3; 440/3; 697/1; 706/3

Query Match 74.1%; Score 40; DB 2; Length 915;
Best Local Similarity 77.8%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FIEGYCTPE 9
:|||||
DB 573 FTEGRCCTPE 581

RESULT 5
E43584
15K cysteine-rich outer membrane protein - Chlamydia trachomatis (serotype E)
C;Species: Chlamydia trachomatis
C;Date: 12-Jan-1993 #sequence_revision 12-Jan-1993 #text_change 09-Jul-2004
C;Accession: E43584; S18980; S24276
R;de la Maza, L.M.; Fielder, T.J.; Carlson, E.J.; Markoff, B.A.; Peterson, E.M.
Infect. Immun. 59, 1196-1201, 1991
A;Title: Sequence diversity of the 60-kilodalton protein and of a putative 15-kilodalton
A;Reference number: A43584; MUID:91147205; PMID:1997423
A;Accession: E43584
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-151
A;Cross-references: UNIPROT:P26757; UNIPARC:UPI0000128472; EMBL:X54389; NID:g40763; PIDN:
C;Superfamily: Chlamydia 15K cysteine-rich outer membrane protein
C;Keywords: membrane protein

Query Match 72.2%; Score 39; DB 2; Length 151;
Best Local Similarity 75.0%; Pred. No. 8.6;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 IEQYCTPE 9
:|||||
DB 90 IEHCSP 97

RESULT 6
AC1875
serine/threonine kinase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AC1875
R;Kansko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpko, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC1875
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-427 <KUR>
A;Cross-references: UNIPROT:Q8YZC9; UNIPARC:UPI00000CDDA9; GB:BA000019; PIDN:BA072506.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr0548

Query Match 72.2%; Score 39; DB 2; Length 427;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 EGYCTPE 9
:|||||
DB 338 EGYCAPE 344

RESULT 7

B86608
excinnulease ABC, subunit C [imported] - Chlamydothila pneumoniae (strain J138)
C:Species: Chlamydothila pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: B86608
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ie
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: B86608
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-603 <STO>
A:Cross-references: UNIPROT:Q9ZG96; UNIPARC:UPI0000137ED6; GB:BA0000008; NID:g8979314; PI
A:Experimental source: strain J138
C:Genetics:
A:Gene: uvrC
C:Superfamily: excinnulease ABC chain C

Query Match 72.2%; Score 39; DB 2; Length 603;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYCTPE 9
Db 182 GYCTPE 187

RESULT 8
F72017
excinnulease ABC, chain C CP0921 [imported] - Chlamydothila pneumoniae (strains CWL029 a
C:Species: Chlamydothila pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: F72017; B81522
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: F72017
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-603 <ARN>
A:Cross-references: UNIPROT:Q9ZG96; UNIPARC:UPI0000137ED6; GB:AE001673; GB:AE001363; NID
A:Experimental source: strain CWL029
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: B81522
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-603 <REA>
A:Cross-references: UNIPARC:UPI0000137ED6; GB:AE002251; GB:AE002161; NID:g7189833; PIDN:
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: uvrC; CP0921
C:Superfamily: excinnulease ABC chain C

Query Match 72.2%; Score 39; DB 2; Length 603;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYCTPE 9
Db 182 GYCTPE 187

RESULT 9
A83300
hypothetical protein PA2762 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C:Accession: A83300
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; B.
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lin,
L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: A83300
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <STO>
A:Cross-references: UNIPROT:Q9I081; UNIPARC:UPI00000C57BF; GB:AE004704; GB:AE004091; NI
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2762

Query Match 70.4%; Score 38; DB 2; Length 114;
Best Local Similarity 63.6%; Pred. No. 10;
Matches 7; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 1 FIEGYC--TPE 9
Db 68 FLDGYCIITPE 78

RESULT 10
C95898
hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid pSym
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: C95898
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herna
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing end
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: C95898
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <KUR>
A:Cross-references: UNIPROT:Q92W94; UNIPARC:UPI00000CB52A; GB:AL591985; PIDN:CAC48851.1,
A:Experimental source: strain 1021, megaplasmid pSymB
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hehault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Welle, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMB20469
A:Genome: plasmid

Query Match 70.4%; Score 38; DB 2; Length 358;
Best Local Similarity 62.5%; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIEGYCTP 8
Db 101 FVEGFCLP 108

RESULT 11
E70621
probable argG protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: E70621
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998

A:Authors: Sqaers, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: E70621
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-398 <COL>
A:Cross-references: UNIPROT:P94993; UNIPARC:UPI000012618B; GB:285982; GB:AL123456; NID:9
A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: argG
C:Superfamily: argininosuccinate synthase

Query Match 70.4%; Score 38; DB 2; Length 398;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FIEGYCTP 8
| | | | |
Db 68 FAEGYCLP 75

RESULT 12
F87085
argininosuccinate synthase [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: F87085
R:Colo, S.T.; Eglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: F87085
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-399 <STO>
A:Cross-references: UNIPROT:Q9CC10; UNIPARC:UPI000012618A; GB:AL450380; NID:gl3093294; F
C:Genetics:
A:Gene: argG
C:Superfamily: argininosuccinate synthase

Query Match 70.4%; Score 38; DB 2; Length 399;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FIEGYCTP 8
| | | | |
Db 69 FAEGYCLP 76

RESULT 13
F82821
NADH-ubiquinone oxidoreductase, NQO4 subunit XF0308 [imported] - Xylella fastidiosa (str
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 12-Jul-2004
C:Accession: F82821
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: F82821
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-435 <SIM>
A:Cross-references: UNIPROT:Q9PGJ2; UNIPARC:UPI00000C237B; GB:AE003884; GB:AE003849; NID
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Artuda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, C.Y.
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
P.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawas
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silve
M.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0308
C:Superfamily: [Nife]-hydrogenase-3-type complex, large subunit/NADH:quinone oxidoreduct

Query Match 70.4%; Score 38; DB 2; Length 435;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FIEGYCTP 8
| | | | |
Db 357 FSEGYCVP 364

RESULT 14
D83481
probable oligopeptidase PA1304 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: D83481
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Li
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lin,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: D83481
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-683 <STO>
A:Cross-references: UNIPROT:Q9I440; UNIPARC:UPI00000C52FF; GB:AE004560; GB:AE004091; NID
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1304
C:Superfamily: prolyl oligopeptidase

Query Match 70.4%; Score 38; DB 2; Length 683;
Best Local Similarity 85.7%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 EGYCTPE 9
| | | | |
Db 522 EGYCRPE 528

RESULT 15
T05814
hypothetical protein T5K18.90 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T05814
R:Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; B.
submitted to the Protein Sequence Database, April 1998
A:Reference number: Z15453
A:Accession: T05814
A:Molecule type: DNA
A:Residues: 1-389 <BEV>
A:Cross-references: UNIPROT:O65702; UNIPARC:UPI00000A8969; EMBL:AL022580
A:Experimental source: cultivar Columbia; BAC clone T5K18
C:Genetics:
A:Map position: 4
A:Introns: 20/3; 56/3; 147/2; 175/3
A:Note: T5K18.90

Query Match 68.5%; Score 37; DB 2; Length 389;
 Best Local Similarity 75.0%; Pred. No. 47;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 IEGYCTPE 9
 Db 301 IQRVCTPE 308

Search completed: March 17, 2006, 23:34:53
 Job time : 22.3333 secs

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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:21:42 ; Search time 123 Seconds
(without alignments)
51.624 Million cell updates/sec

Title: US-09-856-812B-49
Perfect score: 54
Sequence: 1 FIEGYCTPE 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	369	1 MAGAA_HUMAN	P43363 homo sapien
2	42	77.8	375	2 Q61X69 CAEBR	Q61X69 caenorhabdi
3	41	75.9	150	1 CRPL_CHLTR	P18587 chlamydia t
4	41	75.9	752	2 Q6F1E9 MESFL	Q6F1E9 mesoplasma
5	40	74.1	417	2 Q5NIN2 FRATT	Q5NIN2 francisella
6	40	74.1	709	2 Q4F3J0 USTMA	Q4F3J0 ustilago ma
7	40	74.1	711	1 LOXE3_HUMAN	Q9BYJ1 homo sapien
8	40	74.1	731	2 Q20121 CAEBR	Q20121 caenorhabdi
9	40	74.1	731	2 Q20121 CAEBR	Q20121 caenorhabdi
10	40	74.1	915	2 Q9XX53 CAEBR	Q9XX53 caenorhabdi
11	40	74.1	1032	2 Q6CB13 YARLI	Q6CB13 yarrowia li
12	39	72.2	101	2 Q9K1R0 STRCO	Q9K1R0 streptomyce
13	39	72.2	130	2 Q4V1S0 BACCZ	Q4V1S0 bacillus ce
14	39	72.2	151	1 CRPE_CHLTR	P26757 chlamydia t
15	39	72.2	295	2 Q4HPC6 CAMUP	Q4HPC6 campylobact
16	39	72.2	394	2 Q7Q520 GIALA	Q7Q520 giardia lam
17	39	72.2	427	2 Q8YZC9 ANASP	Q8YZC9 anabaena sp
18	39	72.2	484	2 Q6L566 ORYSA	Q6L566 oryza sativ
19	39	72.2	603	1 UVRC_CHLNP	Q9Z6W6 chlamydia p
20	39	72.2	1101	2 Q8AEV2 BACTN	Q8AEV2 bacteroides
21	38	70.4	114	2 Q4LNE4 BURKH	Q4LNE4 burkholderi
22	38	70.4	114	2 Q8BE03 PSRPK	Q8BE03 pseudomonas
23	38	70.4	114	2 Q9T081 PSEAE	Q9T081 pseudomonas
24	38	70.4	358	2 Q2AW94 RHIME	Q2AW94 rhizobium m
25	38	70.4	398	1 ASSY_MYCPA	P63643 mycobacteri
26	38	70.4	398	1 ASSY_MYCPA	P61525 mycobacteri
27	38	70.4	399	1 ASSY_MYCTU	P63642 mycobacteri
28	38	70.4	399	1 ASSY_MYCTU	Q9CC10 mycobacteri
29	38	70.4	435	2 Q5GX74 XANOR	Q5GX74 xanthomonas
30	38	70.4	435	2 Q4UWB5_XANCP	Q4UWB5 xanthomonas
31	38	70.4	435	2 Q87EQ2_XYLFT	Q87EQ2 xyella fas

32	38	70.4	435	2 Q9PGJ2_XYLFA	Q9PGJ2 xyella fas
33	38	70.4	435	2 Q8P7T5_XANCP	Q8P7T5 xanthomonas
34	38	70.4	435	2 Q8PJ43_XANAC	Q8PJ43 xanthomonas
35	38	70.4	628	2 Q57689_BRARE	Q57689 brachydanio
36	38	70.4	630	2 Q6P932_BRARE	Q6P932 brachydanio
37	38	70.4	640	2 Q6V7Q1_9VIRU	Q6V7Q1 staphylococ
38	38	70.4	640	2 Q4Z9Z4_9VIRU	Q4Z9Z4 bacteriophag
39	38	70.4	683	2 Q9I440_PSEAE	Q9I440 pseudomonas
40	38	70.4	758	2 Q4N8F5_THPEA	Q4N8F5 theileria p
41	38	70.4	761	2 Q4UH63_THPEA	Q4UH63 theileria p
42	38	70.4	2813	1 VWF_MOUSE	Q8C1Z8 mus musculu
43	37	68.5	187	2 Q8BM55_BACFR	Q8BM55 bacteroides
44	37	68.5	191	2 Q8F5Z1_CAEBR	Q8F5Z1 caenorhabdi
45	37	68.5	193	2 Q8STG0_CAEBR	Q8STG0 caenorhabdi

ALIGNMENTS

RESULT 1
MAGAA_HUMAN
ID MAGAA_HUMAN STANDARD; PRT; 369 AA.
AC P43363;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Melanoma-associated antigen 10 (MAGE-10 antigen).
GN Name=MAGE10; Synonyms=MAGE10;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95012457; PubMed=7927540;
RA de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,
RA de Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C.,
RA Brasseur R., Chomez P., de Backer O., Cavenne W., Boon T.;
RT "Structure, chromosomal localization, and expression of 12 genes of
the MAGE family";
RL Immunogenetics 40:360-369(1994).

[2]
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX TISSUE=Skin;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Sutterch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Not known, though may play a role in embryonal
development and tumor transformation or aspects of tumor
progression.
CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
such as melanoma, head and neck squamous cell carcinoma, lung
carcinoma and breast carcinoma, but not in normal tissues except
for testes and placenta.

```
CC -!- SIMILARITY: Contains 1 MAGE domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U10685; AA68869.1; -; Genomic_DNA.
DR EMBL; BC004105; AA04105.1; -; mRNA.
DR PIR; I38659; I38659.
DR Ensembl; ENSG00000124260; Homo sapiens.
DR HGNC; HGNC:6797; MAGEA10.
DR H-InvDB; HIX0017116; -.
DR MIM; 300343; -.
DR InterPro; IPR002190; MAGE.
DR PANTHER; PTHR11736; MAGE; 2.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
KW Antigen; Multigene family; Tumor antigen.
FT DOMAIN 134 333
FT COMBIAS 54 62 Poly-Ser.
SQ SEQUENCE 369 AA; 40767 MW; 16FA3301CAB716A6 CRC64;
Query Match 100.0%; Score 54; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.24; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;
QY 1 FIEGYCTPE 9
DB 235 FIEGYCTPE 243
RESULT 2
Q61X69 CAEBR PRELIMINARY; PRT; 375 AA.
AC Q61X69-
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG04102.
GN Name=CBG04102;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAC01000016; CAE60488.1; -; Genomic_DNA.
DR InterPro; IPR009676; DUF1265.
DR Pfam; PF06887; DUF1265; 1.
KW Hypothetical protein.
SQ SEQUENCE 375 AA; 43246 MW; F7377D02FA868628 CRC64;
Query Match 77.8%; Score 42; DB 2; Length 375;
Best Local Similarity 77.8%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 FIEGYCTPE 9
DB 105 FSAGYCTPE 113
RESULT 3
CRPL_CHLTR
ID CRPL CHLTR STANDARD; PRT; 150 AA.
AC P18587;
DT 01-NOV-1990 (Rel. 16, Created)
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DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE 15 kDa cysteine-rich outer membrane protein, serovars L1/L3.
GN Name=crpa;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LL/440/LN;
RX MEDLINE=89138006; PubMed=3066701; DOI=10.1016/0378-1119(88)90047-9;
RA Clarke I.N., Ward M.E., Lambden P.R.;
RT "Molecular cloning and sequence analysis of a developmentally
RT regulated cysteine-rich outer membrane protein from Chlamydia
RT trachomatis";
RL Gene 71:307-314(1988).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=L3/404;
RX MEDLINE=91147205; PubMed=1997423;
RA de la Maza L.M., Fiedler T.J., Carlson E.J., Markoff B.A.,
RA Peterson E.M.;
RT "Sequence diversity of the 60-kilodalton protein and of a putative 15-
RT kilodalton protein between the trachoma and lymphogranuloma venereum
RT biovars of Chlamydia trachomatis";
RL Infect. Immun. 59:1196-1201(1991).
CC -!- FUNCTION: Associated with differentiation of reticulate bodies
CC (RBs) into elementary bodies (EBs). It is necessary for structural
CC integrity of the EBs outer envelope.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; M35148; AAA23120.1; -; Genomic_DNA.
DR EMBL; X54390; CAA38262.1; -; Genomic_DNA.
DR PIR; JTO420; JTO420.
DR InterPro; IPR008436; CRPA.
DR Pfam; PF05745; CRPA; 1.
KW Membrane; Outer membrane.
SQ SEQUENCE 150 AA; 15836 MW; 104D384C2332DB65 CRC64;
Query Match 75.9%; Score 41; DB 1; Length 150;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 IEGYCTPE 9
DB 89 MEGYCSP 96
RESULT 4
Q6F1E9 MESEFL PRELIMINARY; PRT; 752 AA.
AC Q6F1E9-
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Alpha glucosidase/alpha-xylosidase.
GN OrderedLocustNames=Mf1317;
OS Mesoplasma florum (Acholeplasma florum).
OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
OC Entomoplasmataceae; Mesoplasma.
OX NCBI_TaxID=2151;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LI / ATCC 33453;
RA Birren B.W., Stange-Thomann N., Hafez N., Decaprio D., Fisher S.,
RA Butler J., Elkins T., Kodira C.D., Major J., Wang S., Nicol R.,
RA Nusbaum C.;
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RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017263; AAT75674.1; -; Genomic DNA.
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR000322; Glyco_hydro_31.
DR Pfam; PF01055; Glyco_hydro_31; 1.
KW Complete proteome.
SQ SEQUENCE 752 AA; 87288 MW; 30048E1E2A6ECC84 CRC64;

Query Match 75.9%; Score 41; DB 2; Length 752;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IEGYCTP 8
Db 146 LEGYCTP 152

RESULT 5
Q5NIN2 FRATT PRELIMINARY; PRT; 417 AA.
AC Q5NIN2;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE NADH dehydrogenase I, D subunit (EC 1.6.5.3).
GN Name=nuoD; OrderedLocNames=FT0034;
OS Francisella tularensis (subsp. tularensis).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Thiotrichales;
OC Francisellaceae; Francisella.
OX NCBI_TaxID=119856;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCHU S4 / Schu 4;
EX PubMed=15660799; DOI=10.1038/ngl499;
RA Larsson P., Oyston P.C.F., Chain P., Chu M.C., Duffield M.,
Raxwalia H.-H., Garcia E., Haelethorp G., Johansson D., Isherwood K.E.,
Karp P.D., Larsson E., Liu Y., Michell S., Prior J., Prior R.,
RA Malfatti S., Sjoestedt A., Svensson K., Thompson N., Vergez L.,
RA Wagg J.K., Wren B.W., Lindler L.E., Andersson S.G.E., Forsman M.,
RA Titball R.W.;
RT "The complete genome sequence of Francisella tularensis, the causative
agent of tularemia."
RL Nat. Genet. 37:153-159 (2005).
DR EMBL; AJ749949; CAG44667.1; -; Genomic DNA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0016651; F:oxidoreductase activity, acting on NADH or . . .; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR010219; NuoD.
DR Pfam; PF00346; Complex1_49kDa; 1.
DR TIGRFAM; TIGR01962; NuoD; 1.
DR PROSITE; PS00535; COMPLEX1_49K; 1.
KW Complete proteome; Oxidoreductase.
SQ SEQUENCE 417 AA; 47572 MW; F907A3D76D5D562B CRC64;

Query Match 74.1%; Score 40; DB 2; Length 417;
Best Local Similarity 77.8%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FIEGYCTPE 9
Db 339 FSEGYCTTE 347

RESULT 6
Q4P3J0 USTMA
ID Q4P3J0 USTMA PRELIMINARY; PRT; 709 AA.
AC Q4P3J0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

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DE Hypothetical protein.
GN ORFNames=UM05323.1;
OS Ustilago maydis 521.
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=237631;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=521;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachanteang P., Baldwin J., Barry A.,
RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Bouhgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Doris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyalteen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Jones C., Kamal M., Kamat A., Kamyseslis M., Karlson E.,
RA Jaffe D., Jones C., Kamal M., Hughes L., Hulme W., Hueby E., Iliev I.,
RA Kellis C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokvitsang T., Lokvitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
RA Mesirov J., Mihaliev A., Mihova T., Mikkelson T., Mlenga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Piganoni B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond P.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherga N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann M., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tensing P., Tesfaye S., Theodore J., Thoulucsang Y., Topham K.,
RA Towey S., Tsamila T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Ustilago maydis."
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AACP01000191; EAK96572.1; -; Genomic DNA.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF00319; SRP-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00066; MADS_BOX_2; 1.
DR DNA-binding; Hypothetical protein; Nuclear protein; Transcription;
KW Transcription regulation.
SQ SEQUENCE 709 AA; 74669 MW; D60B150C0C10A784 CRC64;

Query Match 74.1%; Score 40; DB 2; Length 709;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IEGYCTP 8
Db 59 IDGYCTP 65

RESULT 7
LOX3_HUMAN

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ID LOXE3 HUMAN STANDARD; PRT; 711 AA.
AC Q9BYJ1; Q9H4P2; Q9HC22;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Epidermis-type lipoxigenase 3 (EC 1.13.11.-) (e-LOX-3).
GN Name=ALOXE3;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21248677; PubMed=11350124; DOI=10.1006/geno.2001.6519;
RA Krieg P., Marks F., Fuerstenberger G.;
RT "A gene cluster encoding human epidermis-type lipoxigenases at
RT chromosome 17p13.1: cloning, physical mapping, and expression.";
RL Genomics 73:323-330 (2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Brash A.R., Boeglin W.E.;
RT "Human epidermal lipoxigenase, ortholog of mouse Alox3.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Krieg P., Fuerstenberger G.;
RT "cDNA cloning, genomic structure, and chromosomal localization of
RT human epidermis-type lipoxigenase-3";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP VARIANTS NCIE SER-396 AND PHE-500.
RX MEDLINE=21634626; PubMed=1173004; DOI=10.1093/hmg/11.1.107;
RA Jobard F., Lefevre C., Karaduman A., Blanchet-Bardon C., Emre S.,
RA Weissenbach J., Ozguc M., Lathrop M., Prud'homme J.-F., Fischer J.;
RT "Lipoxigenase-3 (ALOXE3) and 12(R)-lipoxigenase (ALOX12B) are mutated
RT in non-bullous congenital ichthyosiform erythroderma (NCIE) linked to
RT chromosome 17p13.1.";
RL Hum. Mol. Genet. 11:107-113 (2002).
CC -!- FUNCTION: Introduces molecular oxygen into polyunsaturated fatty
CC acids. Exact substrate is not known.
CC -!- COFACTOR: Iron (By similarity).
CC -!- PATHWAY: Leukotrienes biosynthesis.
CC -!- TISSUE SPSCIFICITY: Predominantly expressed in skin.
CC -!- DISEASE: Defects in ALOXE3 are a cause of nonbullous congenital
CC ichthyosiform erythroderma (NCIE) [MIM:242100]. NCIE is
CC characterized by prominent erythroderma and fine white,
CC superficial, semiadherent scales. As many as 90% of affected
CC individuals present at birth as collodion babies. Patients suffer
CC from palmoplantar keratoderma, often with painful fissures,
CC digital contractures, and loss of pulp volume. In half of the
CC cases, a nail dystrophy including ridging, subungual
CC hyperkeratosis, or hypoplasia has been described.
CC -!- SIMILARITY: Belongs to the lipoxigenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
CC
CC EMBL; AJ305020; CAC34518.1; -; Genomic_DNA.
DR EMBL; AJ305021; CAC34518.1; JOINED; Genomic_DNA.
DR EMBL; AJ305023; CAC34518.1; JOINED; Genomic_DNA.
DR EMBL; AJ305025; CAC34518.1; JOINED; Genomic_DNA.
DR EMBL; AF182218; AAG16899.1; -; mRNA.
DR EMBL; AJ268499; CAC12843.1; -; mRNA.
DR HSSP; P12530; ILOX.
DR Ensembl; ENSG00000179148; Homo sapiens.
DR HGNC; HGNC:13743; ALOXE3.
DR MIM; 607206; -.
DR MIM; 242100; -.

DR InterPro; IPR008976; Lipase_LipOase.
DR InterPro; IPR000907; LipOase.
DR InterPro; IPR001024; LipOase_LH2.
DR InterPro; IPR001885; Mammal_LipOase.
DR PANTHER; PTHR11771; Lipoxigenase; 1.
DR Pfam; PF00305; Lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR PRINTS; PR00467; MAMLIPOXGNASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
KW Dioxygenase; Disease mutation; Iron; Leukotriene biosynthesis;
KW Metal-binding; Oxidoreductase.
FT DOMAIN 2 119 PLAT.
FT METAL 408 408 Iron (By similarity).
FT METAL 413 413 Iron (By similarity).
FT METAL 588 588 Iron (By similarity).
FT METAL 711 711 Iron (By similarity).
FT VARIANT 396 396 R -> S (in NCIE).
FT /FTID=VAR_015175.
FT VARIANT 500 500 V -> F (in NCIE).
FT /FTID=VAR_015176.
FT CONFLICT 155 155 C -> R (in Ref. 3).
FT CONFLICT 194 194 F -> L (in Ref. 2).
SQ SEQUENCE 711 AA; 80543 MW; BDED1B4ED5CF6783 CRC64;

Query Match 74.1%; Score 40; DB 1; Length 711;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIEGYCTPE 9
DB 104 WIEGYCTVE 112

RESULT 8
O61MS4 CAEBR PRELIMINARY; PRT; 731 AA.
ID O61MS4 CAEBR PRELIMINARY; PRT; 731 AA.
AC O61MS4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG08359.
GN Name=CBG08359; briggae.
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC family.
CC EMBL; CAAC0100035; CAE63810.1; -; Genomic_DNA.
DR GO; GO:0003824; P:catalytic activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 2.
DR PRINTS; PR00154; AMPBINDING.
DR PROSITE; PS00455; AMP BINDING; 1.
KW Hypothetical protein.
SQ SEQUENCE 731 AA; 81445 MW; C071504A05B95631 CRC64;

Query Match 74.1%; Score 40; DB 2; Length 731;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 FIEGYCTP 8
Db 429 YLEGYCSP 436

RESULT 9
Q20121 CAEBL
ID Q20121 CAEBL PRELIMINARY; PRT; 731 AA.
AC Q20121;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
GN ORFNames=F37C12.7;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
RL Science 282:2012-2018(1998).
CC -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
family.
DR EMBL; U048033; AAC48292.3; -; Genomic_DNA.
DR PIR; T28829; T28829.
DR Ensembl; F37C12.7; Caenorhabditis elegans.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0008152; P: metabolism; IEA.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 2.
DR PRINTS; PR00154; AMPBINDING.
DR PROSITE; PS00455; AMP_BINDING; 1.
SQ Complete proteome; Hypothetical protein.
KW SEQUENCE 731 AA; 81253 MW; 1F317B9D899C5F5C0 CRC64;

Query Match 74.1%; Score 40; DB 2; Length 731;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FIEGYCTP 8
Db 429 YLEGYCSP 436

RESULT 10
Q9XX53 CAEBL
ID Q9XX53 CAEBL PRELIMINARY; PRT; 915 AA.
AC Q9XX53;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein Y38H6C.5.
GN ORFNames=Y38H6C.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AL031630; CAA20985.1; -; Genomic_DNA.
DR FIR; T26695; T26695.
DR Ensembl; Y38H6C.5; Caenorhabditis elegans.
```

```
DR WormBase; WBGene00012618; Y38H6C.5.
DR WormPep; Y38H6C.5; CE19099.
DR GO; GO:0003676; F: nucleic acid binding; IEA.
DR InterPro; IPR005162; Retrotrans_gag.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF03732; Retrotrans_gag; 1.
DR Pfam; PF00098; ZF-CCHC; 1.
DR PRINTS; PR00939; C2HCZNFINGER.
DR SMART; SM00343; Znf_C2HC; 1.
DR PROSITE; PS0158; ZF_CCHC; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 915 AA; 103082 MW; 748243692E007281 CRC64;

Query Match 74.1%; Score 40; DB 2; Length 915;
Best Local Similarity 77.8%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FIEGYCTP 9
Db 573 FTEGRCTP 581

RESULT 11
Q6CB13 YARLI
ID Q6CB13 YARLI PRELIMINARY; PRT; 1032 AA.
AC Q6CB13;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Similar to tr|Q06593|Saccharomyces cerevisiae YPR194C.
GN OrderedLocusNames=YALI0C184919;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Boissans A., Boyer J., Cattolico L., Confanioli F., de Darivar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
DR EMBL; CR382129; CAG82299.1; -; Genomic_DNA.
DR InterPro; IPR004648; Oligopept_transp.
DR InterPro; IPR004813; Tetrapept_transp.
DR Pfam; PF03169; OPT; 1.
DR TIGRFAMs; TIGR00727; ISP4 OPT; 1.
DR TIGRFAMs; TIGR00728; OPT_sfam; 1.
KW Complete proteome.
SQ SEQUENCE 1032 AA; 116472 MW; 1F98CC166E54A454 CRC64;

Query Match 74.1%; Score 40; DB 2; Length 1032;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 IEGYCTP 9
Db 832 IEIGCTP 839

RESULT 12
```

```
Q9KYR0_STRCO PRELIMINARY; PRT; 101 AA.
ID Q9KYR0_STRCO PRELIMINARY; PRT; 101 AA.
AC Q9KYR0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein SC05705.
DE OrderedLocusNames=SC05705; ORFNames=SC5H4.29;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieffer H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Frazer A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieffer T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939124; CAB91141.1; -; Genomic_DNA.
DR InterPro; IPR007393; DUF448.
DR Pfam; PF04296; DUF448; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 101 AA; 11028 MW; 9E87AF940CC4671D CRC64;

Query Match 72.2%; Score 39; DB 2; Length 101;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 IEQGYCTPE 9
:|||||
DB 33 VEGHCTPD 40

RESULT 13
Q4VIS0_BACCZ PRELIMINARY; PRT; 130 AA.
ID Q4VIS0_BACCZ PRELIMINARY; PRT; 130 AA.
AC Q4VIS0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Uncharacterized protein.
DE ORFNames=pe33L466_0179;
OS Bacillus cereus (strain ZK).
OG Plasmid pe33L466.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E33L;
RG Joint Genome Institute Microbial Sequencing, Finishing and Annotation
RG Team;
RT "Complete genome sequence of Bacillus cereus E33L.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E33L;
RG Joint Genome Institute Microbial Sequencing, Finishing and Annotation
RG Team;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000040; AAY60337.1; -; Genomic_DNA.
KW Plasmid.
SQ SEQUENCE 130 AA; 14934 MW; A5E709BEC334CEC4 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 130;
Best Local Similarity 87.5%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 IEQGYCTPE 9
|||||
DB 12 IEGETCTPE 19

RESULT 14
CRPE_CHLTR STANDARD; PRT; 151 AA.
ID CRPE_CHLTR STANDARD; PRT; 151 AA.
AC P26757;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 15 kDa cysteine-rich outer membrane protein, serovar E.
GN Name=crpA;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=BOUR / Serovar E;
RX MEDLINE=91147205; PubMed=1997423;
RA de la Maza L.M., Fiedler T.J., Carlson E.J., Markoff B.A.,
RA Peterson E.M.;
RA "Sequence diversity of the 60-kilodalton protein and of a putative 15-
RT kilodalton protein between the trachoma and lymphogranuloma venereum
RT biovars of Chlamydia trachomatis.";
RL Infect. Immun. 59:1196-1201(1991).
CC -!- FUNCTION: Associated with differentiation of reticulate bodies
CC (RBs) into elementary bodies (EBs). It is necessary for structural
CC integrity of the EBs outer envelope.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X54389; CAA38260.1; -; Genomic_DNA.
DR PIR; E43584; E43584.
DR InterPro; IPR008436; CRPA.
DR Pfam; PF05745; CRPA; 1.
KW Membrane; Outer membrane.
SQ SEQUENCE 151 AA; 16020 MW; C6CA7DFB8FC0C354 CRC64;

Query Match 72.2%; Score 39; DB 1; Length 151;
Best Local Similarity 75.0%; Pred. No. 54;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 IEQGYCTPE 9
|||||
DB 90 IEHGCSPPE 97

RESULT 15
Q4HPC6_CAMUP PRELIMINARY; PRT; 295 AA.
ID Q4HPC6_CAMUP PRELIMINARY; PRT; 295 AA.
AC Q4HPC6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Uncharacterized BCR.
GN Name=pvds; ORFNames=CUP1104;
OS Campylobacter upsaliensis RM3195.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=306264;
RN [1]
```

```

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RM3195;
RA Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Rasako D.A.,
RA Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,
RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,
RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,
RA Nelson K.E.;
RT "Major structural and novel potential virulence mechanisms from the
RT genomes of multiple Campylobacter species.";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAFJ01000009; EAL52696.1; -; Genomic DNA.
SQ SEQUENCE 295 AA; 34325 MW; 8080FC4E77AC96EA CRC64;

Query Match 72.2%; Score 39; DB 2; Length 295;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FIEGYCTPE 9
   :: |||||
Db 121 YWVGCTPE 129

Search completed: March 17, 2006, 23:33:55
Job time : 130 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:21:17 ; Search time 118 Seconds
(without alignments)
33.512 Million cell updates/sec

Title: US-09-856-812B-50

Perfect score: 45

Sequence: 1 GLEGAQAPL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003s.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	2 AAR79846	Aar79846 Tumour re
2	45	100.0	9	8 ADI47252	Adi47252 Anti-canc
3	45	100.0	369	3 AAY71485	Aay71485 Human MAG
4	45	100.0	369	4 AAB80297	Aab80297 Human pro
5	45	100.0	369	6 ABR48215	Abr48215 Human bla
6	45	100.0	369	6 ABUS6516	Abu56516 Lung can
7	45	100.0	383	8 ABO58424	Abos58424 Human gen
8	39	86.7	759	9 ABM96962	Abm96962 M. xanthu
9	38	84.4	310	4 AAO00093	Aao00093 Human pol
10	38	84.4	415	7 ABO82077	Abos82077 Pseudomon
11	36	80.0	183	8 ADX73183	Adx73183 Plant ful
12	36	80.0	349	7 ADF04756	Adf04756 Bacterial
13	36	80.0	360	7 ADC00950	Adc00950 Enterohae
14	36	80.0	588	4 AAU35412	Aau35412 Haemophil
15	36	80.0	588	6 ABU30211	Abu30211 Protein e
16	36	80.0	591	6 ABM68497	Abm68497 Photorhab
17	36	80.0	598	6 ABUS0576	Abu50576 Protein e
18	36	80.0	949	4 ABG03771	Abg03771 Novel hum
19	35	77.8	9	3 AAY71493	Aay71493 Human MAG
20	35	77.8	89	4 AAM18722	Aam18722 Peptide #
21	35	77.8	89	4 ABB37797	Abb37797 Peptide #
22	35	77.8	89	4 AAM31192	Aam31192 Peptide #
23	35	77.8	89	4 ABB23072	Abb23072 Protein #
24	35	77.8	89	4 AAM70900	Aam70900 Human bon

ALIGNMENTS

RESULT 1

AAR79846

ID AAR79846 standard; peptide; 9 AA.

XX AAR79846;

DT 08-MAY-1996 (first entry)

DE Tumour rejection antigen peptide #10.

KW Tumour rejection antigen; MAGE tumour rejection precursor; complex;

KW HLA-2; immunogen; antibody; cytolytic T cell clone.

OS Synthetic.

PN WO9525740-A1.

XX 28-SEP-1995.

PF 22-MAR-1995; 95WO-US003657.

PR 24-MAR-1994; 94US-00217186.

PR 17-JUN-1994; 94US-00261160.

PR 15-AUG-1994; 94US-00290381.

PA (LUDW-) LUDWIG INST CANCER RES.

PA (UYOX-) UNIV OXFORD.

PA (UYLE-) RIJKSUNIV LEIDEN.

PI Townsend A, Bastin J, Boon-Falleur T, Van Der Bruggen P, Coulie P;

PI Gajewski T, Melief CJ, Visseren MW, Kast WM;

PI WPI; 1995-344584/44.

DR Isolated peptide(s) which complex with HLA-A2 - used as immunogens for the prodn. of antibodies, or as targets for the generation of cytolytic T cell clones.

XX Claim 15; Page 23; 44pp; English.

XX The peptides given in AAR79845-47 represent tumour rejection antigens derived from MAGE tumour rejection precursor. These peptides form a strong complex with HLA-2 which may be used diagnostically and as an immunogen in the production of antibodies. They may also be used as targets for the generation of cytolytic T cell clones. This cytolytic T cell clone is used to treat a cancerous condition characterised by the fact that the cancer cells present the HLA-2/ peptide complex on their

```

CC surface
XX Sequence 9 AA;
SQ

Query Match      100.0%; Score 45; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLEGAQAPL 9
DB      1 GLEGAQAPL 9
      |||||
RESULT 2
ADI47252
ID ADI47252 standard; peptide; 9 AA.
XX
AC ADI47252;
XX
XX 22-APR-2004 (first entry)
XX
XX Anti-cancer HLA-A2 complex associated peptide seq id 19.
DE
XX cytostatic; gene therapy; cancer; cytolytic T cell; HLA-A2.
XX
XX Synthetic.
XX
XX US6682731-B1.
XX
XX 27-JAN-2004.
XX
XX 23-MAR-2000; 2000US-00533499.
XX
XX 24-MAR-1994; 94US-00217186.
PR 24-MAR-1994; 94US-00217188.
PR 17-JUN-1994; 94US-00261160.
PR 15-AUG-1994; 94US-00290381.
PR 06-FEB-1997; 97US-00722115.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
PA (UYOX-) UNIV OXFORD.
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
XX Townsend A, Bastin J, Boon-Falleur T, Van Der Bruggen P, Coulie P;
PI Gajewski T, Melief CUM, Visseren MJW, Kast MW;
PI
XX WPI; 2004-118569/12.
XX
XX Treating a subject with a cancerous condition by administering cytolytic
PT T cells specific for the complexes to lyse the cancer cells.
XX
XX Example 13; SEQ ID NO 20; 27pp; English.
XX
XX The invention describes a method of treating a subject with a cancerous
CC condition comprising administering cytolytic T cells specific for the
CC complexes to lyse the cancer cells of the subject. The cancer cells
CC present complexes of HLA-A2 molecules and a peptide with a fully defined
CC sequence comprising 9 amino acids. The method is useful for treating a
CC subject with a cancerous condition. This is the amino acid sequence of a
CC HLA-A2 complex associated peptide.
XX
SQ Sequence 9 AA;

Query Match      100.0%; Score 45; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLEGAQAPL 9
DB      1 GLEGAQAPL 9
      |||||
RESULT 3
ADI47252
ID ADI47252 standard; peptide; 9 AA.
XX
AC ADI47252;
XX
XX 22-APR-2004 (first entry)
XX
XX Anti-cancer HLA-A2 complex associated peptide seq id 19.
DE
XX cytostatic; gene therapy; cancer; cytolytic T cell; HLA-A2.
XX
XX Synthetic.
XX
XX US6682731-B1.
XX
XX 27-JAN-2004.
XX
XX 23-MAR-2000; 2000US-00533499.
XX
XX 24-MAR-1994; 94US-00217186.
PR 24-MAR-1994; 94US-00217188.
PR 17-JUN-1994; 94US-00261160.
PR 15-AUG-1994; 94US-00290381.
PR 06-FEB-1997; 97US-00722115.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
PA (UYOX-) UNIV OXFORD.
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
XX Townsend A, Bastin J, Boon-Falleur T, Van Der Bruggen P, Coulie P;
PI Gajewski T, Melief CUM, Visseren MJW, Kast MW;
PI
XX WPI; 2004-118569/12.
XX
XX Treating a subject with a cancerous condition by administering cytolytic
PT T cells specific for the complexes to lyse the cancer cells.
XX
XX Example 13; SEQ ID NO 20; 27pp; English.
XX
XX The invention describes a method of treating a subject with a cancerous
CC condition comprising administering cytolytic T cells specific for the
CC complexes to lyse the cancer cells of the subject. The cancer cells
CC present complexes of HLA-A2 molecules and a peptide with a fully defined
CC sequence comprising 9 amino acids. The method is useful for treating a
CC subject with a cancerous condition. This is the amino acid sequence of a
CC HLA-A2 complex associated peptide.
XX
SQ Sequence 9 AA;

Query Match      100.0%; Score 45; DB 3; Length 369;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLEGAQAPL 9
DB      24 GLEGAQAPL 32
      |||||
RESULT 4
AAB80297
ID AAB80297 standard; protein; 369 AA.
XX
AC AAB80297;
XX
XX 24-APR-2001 (first entry)
XX
DT

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AAY71485
ID AAY71485 standard; protein; 369 AA.
XX
AC AAY71485;
XX
XX 12-OCT-2000 (first entry)
XX
XX Human MAGE-A10 protein.
XX
XX MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
KW immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
KW cancer; TNF; tumour necrosis factor; cytostatic.
XX
XX Homo sapiens.
OS
XX WO200032769-A2.
FN
XX 08-JUN-2000.
PD
XX 26-NOV-1999; 99WO-IB002018.
PP
XX 27-NOV-1998; 98GB-00026143.
PR
XX (LUDW-) LUDWIG INST CANCER RES.
PA
XX Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
PI
XX WPI; 2000-412317/35.
DR
XX N-PSDB; AAD01311, AAD01312, AAD01313.
DR
XX Novel polypeptides expressed in tumor cells useful for treating cancers
PT have an ability to complex with a major histocompatibility complex
PT molecule and comprises a specific unbroken amino acid sequence.
XX
XX Claim 1; Fig 7; 80pp; English.
XX
XX The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
CC decapeptide sequences, that function as tumour rejection antigens (TRA8).
CC These peptides are capable of forming a complex with major
CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
CC Antigen), that are recognised by T-lymphocytes and elicit an immune
CC response from cytolytic T-lymphocytes (CTL). They function as an immune
CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
CC therapy and diagnosis of tumours and are effective in controlling or
CC preventing tumour growth. The present sequence is the human MAGE-A10
CC protein, comprising nonapeptides and decapeptides, that serve as tumour
CC rejection antigens (TRA8). The novel TRA8 encoded by MAGE-A10 is
CC identified using melanoma cell line (JBI751-MEL), stimulated by
CC autologous CTL clone (447A/5) to produce TNF (tumour necrosis factor).
CC Expression of MAGE-A10 has been detected in a variety of tumours like
CC melanomas, carcinomas of the head and neck, bladder and prostate.
CC myelomas and lung cancer. The only normal tissue expressing MAGE-A10 is
CC the testis
XX
SQ Sequence 369 AA;

Query Match      100.0%; Score 45; DB 3; Length 369;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLEGAQAPL 9
DB      24 GLEGAQAPL 32
      |||||
RESULT 4
AAB80297
ID AAB80297 standard; protein; 369 AA.
XX
AC AAB80297;
XX
XX 24-APR-2001 (first entry)
XX
DT

```

XX DE Human prostate cancer antigen #25.
 XX DE Immunosuppressive; neuroprotective; antiviral; vulnery;
 KW anticonvulsant; antibacterial; antifungal; antiparasitic; cardiac;
 KW immune disorder; cardiovascular disorder; neurological disease;
 KW infection; cancer; cytostatic; antiarthritic; antirheumatic;
 KW antasthmatic; anticonvulsant; vasotropic; vulnery; human;
 KW secreted protein; prostate cancer antigen.
 XX OS Homo sapiens.
 XX PN WO200107476-A1.
 XX PD 01-FEB-2001.
 XX PF 20-JUL-2000; 2000WO-US019666.
 XX PR 21-JUL-1999; 99US-0144972P.
 PR 13-AUG-1999; 99US-014681P.
 PR 17-AUG-1999; 99US-0149173P.
 PR 06-OCT-1999; 99US-0158004P.
 PR 05-APR-2000; 2000US-0194689P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 XX PI Rosen CA, Birse C;
 XX WPI: 2001-138554/14.
 DR N-PSDB; AAF72765.
 XX PS Claim 11; Page 399-400; 433pp; English.
 CC The present invention relates to human secreted prostate cancer antigen
 CC coding sequences (AAF72741-AAF72789) and proteins (AAB80273-AAB80321).
 CC The coding sequences and proteins of the present invention are useful for
 CC preventing, treating or ameliorating a medical condition; and for the
 CC diagnosis and treatment of diseases and disorders. Diseases and disorders
 CC that can be diagnosed and treated include (auto)immune diseases (e.g.
 CC graft versus host disease and rheumatoid arthritis), inflammatory and
 CC allergic disorders (e.g. asthma), hyperproliferative disorders (e.g.
 CC cancers and leukemias), cardiovascular disorders (e.g. heart attacks and
 CC arrhythmias), cerebrovascular disorders (e.g. stroke), arterial occlusive
 CC disorders (e.g. arteriosclerosis), angiogenesis related disorders (e.g.
 CC retinopathy and keloid scars), ocular disorders (e.g. glaucoma),
 CC neurological disorders (e.g. Alzheimer's, Parkinson's disease, epilepsy
 CC and Creutzfeld-Jakob disease) and infections caused by bacteria, fungi,
 CC viruses or parasites. They may also be useful for wound healing,
 CC epithelial cell proliferation, supporting cell culture, tissue
 CC regeneration, birth control and as a food additive or preservative
 XX Sequence 369 AA;
 SQ Query Match 100.0%; Score 45; DB 4; Length 369;
 Best Local Similarity 100.0%; Pred. No. 5.1; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Indels 0; Indels 0; Gaps 0;
 QY 1 GLEGAQAFL 9
 DB 24 GLEGAQAFL 32
 RESULT 5
 ABR48215
 ID ABR48215 standard; protein; 369 AA.
 XX AC ABR48215;
 XX KW Lung cancer-associated polypeptide #109.
 KW Lung cancer-associated polypeptide; cytostatic; emphysema;
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;

DT 12-JUN-2003 (first entry)
 XX DE Human bladder cancer associated protein sequence SEQ ID NO:149.
 XX KW Human; bladder cancer; cytostatic; gene therapy; vaccine.
 XX OS Homo sapiens.
 XX PN WO2003003906-A2.
 XX PD 16-JAN-2003.
 XX PF 03-JUL-2002; 2002WO-US021338.
 XX PR 03-JUL-2001; 2001US-0302814P.
 PR 03-AUG-2001; 2001US-0310099P.
 PR 08-NOV-2001; 2001US-0343705P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 12-APR-2002; 2002US-0372246P.
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 XX Mack DH, Aziz N;
 XX WPI: 2003-201532/19.
 DR N-PSDB; ACC51029.
 XX PT Detecting a bladder cancer-associated transcript in a cell from a
 PT patient, comprises contacting a biological sample from the patient with a
 PT bladder cancer-associated polynucleotide or antibody.
 XX Claim 10; Page 282; 307pp; English.
 CC The present invention describes a method for detecting a bladder cancer-
 CC associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with a polynucleotide
 CC that selectively hybridises to a sequence that is 80 % identical to a
 CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
 CC encode the human bladder cancer-associated proteins given in ABR48146 to
 CC ABR48242). Bladder cancer-associated sequences from the present invention
 CC have cytostatic activities, and can be used in antisense gene therapy and
 CC in vaccine production. The method can be used for detecting a bladder
 CC cancer-associated transcript in a cell from a patient. The method is
 CC useful in diagnosing or treating bladder cancer and in screening for
 CC compounds that modulate bladder cancer, such as hormones or antibodies.
 CC The nucleic acid molecules from the present invention may be used in
 CC various screening and diagnostic methods, and for gene therapy, vaccine
 CC and/or antisense/inhibition applications
 XX Sequence 369 AA;
 SQ Query Match 100.0%; Score 45; DB 6; Length 369;
 Best Local Similarity 100.0%; Pred. No. 5.1; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Indels 0; Indels 0; Gaps 0;
 QY 1 GLEGAQAFL 9
 DB 24 GLEGAQAFL 32
 RESULT 6
 ABUS6516
 ID ABUS6516 standard; protein; 369 AA.
 XX AC ABUS6516;
 XX XX 02-APR-2003 (first entry)
 DE Lung cancer-associated polypeptide #109.
 KW Lung cancer-associated polypeptide; cytostatic; emphysema;
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;

KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX Unidentified.
OS
XX WO200286443-A2.
PN
PD 31-OCT-2002.
XX
XX 18-APR-2002; 2002WO-US012476.
XX
XX 18-APR-2001; 2001US-0284770P.
PR
XX 10-MAY-2001; 2001US-0290492P.
PR
XX 09-NOV-2001; 2001US-0339245P.
PR
XX 13-NOV-2001; 2001US-0350666P.
PR
XX 29-NOV-2001; 2001US-0334370P.
PR
XX 12-APR-2002; 2002US-0372246P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX
PI Aziz N, Murray R;
XX
XX WPI; 2003-093161/08.
DR
XX N-PSDB; ABX76240.
XX
XX Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
XX Claim 27; Page 276-277; 453pp; English.
XX
XX The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridizes
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
CC invention
XX
XX Sequence 369 AA;
SQ
Query Match 100.0%; Score 45; DB 6; Length 369;
Best Local Similarity 100.0%; Pred. No. 5.1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLEGAQAPL 9
Db 24 GLEGAQAPL 32
RESULT 7
ABO58424
ID ABO58424 standard; protein; 383 AA.
XX
AC ABO58424;
XX
XX 29-JUL-2004 (first entry)
DT
XX Human genome derived single exon protein #4658.
DE
XX

KW Human; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
XX
XX Homo sapiens.
XX
XX US2003194704-A1.
PN
XX 16-OCT-2003.
PD
XX
XX 03-APR-2002; 2002US-00029386.
PF
XX
XX 03-APR-2002; 2002US-00029386.
PR
XX (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANK/) HANKEL D K.
XX
XX Penn SG, Rank DR, Hanzel DK;
PI
XX WPI; 2004-119264/12.
DR
XX
XX New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX
XX Claim 45; SEQ ID NO 32058; 80pp; English.
PS
XX The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridizes under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subsequence, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe protein of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
XX Sequence 383 AA;
SQ
Query Match 100.0%; Score 45; DB 8; Length 383;
Best Local Similarity 100.0%; Pred. No. 5.3; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLEGAQAPL 9
Db 45 GLEGAQAPL 53

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RESULT 8
ABM96962
ID ABM96962 standard; protein; 759 AA.
XX AC ABM96962;
XX AC ABM96962;
XX DT 02-JUN-2005 (first entry)
XX DE M. xanthus protein sequence, seq id 16161.
XX KW Transgenic plant; DNA replication; gene regulation; gene expression.
XX OS Myxococcus xanthus.
XX PN US6833447-B1.
XX PD 21-DEC-2004.
XX PF 10-JUL-2001; 2001US-00902540.
XX PR 10-JUL-2000; 2000US-0217883P.
XX PA (MONS ) MONSANTO TECHNOLOGY LLC.
XX PI Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;
XX DR WPI; 2005-028716/03.
XX CC New substantially purified Myxococcus xanthus nucleic acid molecule
PT encoding a nitrite reductase, useful for determining gene expression,
PT identifying mutations in a gene of interest, and for constructing
PT mutations in a gene of interest.
XX PS Example 2; SEQ ID NO 16161; 25pp; English.
XX CC The invention relates to a substantially purified nucleic acid molecule
CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
CC recombinant DNA construct for expression of a nitrite reductase gene in a
CC plant cell, and a plant cell comprising the recombinant DNA construct.
CC The nucleic acid is useful for determining gene expression, identifying
CC mutations in a gene of interest, and for constructing mutations in a gene
CC of interest. Sequences given in records for SEQ IDs 9692-16825 represent
CC a group of 7134 Myxococcus xanthus proteins and peptides. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
XX SQ Sequence 759 AA;
Query Match 86.7%; Score 39; DB 9; Length 759;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLEGAQAP 8
Db 353 GMEGAQAP 360
RESULT 9
AAO00093
ID AAO00093 standard; protein; 310 AA.
XX AC AAO00093;
XX DT 06-NOV-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 13985.
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.

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XX OS Homo sapiens.
XX PN WO200164835-A2.
XX PD 07-SEP-2001.
XX PF 26-FEB-2001; 2001WO-US004927.
XX PR 28-FEB-2000; 2000US-00515126.
XX PR 18-MAY-2000; 2000US-00577409.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX DR WPI; 2001-514838/56.
XX DR N-PSDB; AAI80024.
XX PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX PS Claim 20; SEQ ID NO 13985; 1399pp + Sequence Listing; English.
XX CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 310 AA;
Query Match 84.4%; Score 38; DB 4; Length 310;
Best Local Similarity 77.8%; Pred. No. 90;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLEGAQAPL 9
Db 83 GLEGSQGPL 91
RESULT 10
ABO82077
ID ABO82077 standard; protein; 415 AA.
XX AC ABO82077;
XX DT 29-JUL-2004 (first entry)
XX DE Pseudomonas aeruginosa polypeptide #14252.
XX KW Pseudomonas aeruginosa polypeptide #14252.
XX OS Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX PN Pseudomonas aeruginosa.
XX PN US6551795-B1.
XX PD 22-APR-2003.
XX PF 18-FEB-1999; 99US-00252991.
XX PR 18-FEB-1998; 98US-0074788P.
XX PR 27-JUL-1998; 98US-0094190P.
XX PA (GENO-) GENOME THERAPEUTICS CORP.

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XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX WPI; 2003-615309/58.
 DR N-PSDB; ABD15648.
 XX Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX Disclosure; SEQ ID NO 30823; 455pp; English.
 XX The invention relates to *Pseudomonas aeruginosa* polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-*P. aeruginosa* drugs, as templates for recombinant
 CC production of *P. aeruginosa*-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of *P. aeruginosa*-caused
 CC infection, and in detection of *P. aeruginosa* sequences or other sequences
 CC of *Pseudomonas* species using biochip technology. Sequences AB067826-
 CC AB084396 represent *P. aeruginosa* polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX Sequence 415 AA;
 SQ

Query Match 84.4%; Score 38; DB 7; Length 415;
 Best Local Similarity 77.8%; Pred. No. 1.2e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGQAQPL 9
 Db 269 GLEGAGPL 277
 |||||
 |||||

RESULT 11
 ADX73183
 ID ADX73183 standard; protein; 183 AA.
 XX
 AC ADX73183;
 DT 21-APR-2005 (first entry)
 XX Plant full length insert polypeptide seqid 42549.
 XX plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.
 XX Unidentified.
 OS
 XX US2004034888-A1.
 PN
 XX 19-FEB-2004.
 PD
 XX 28-APR-2003; 2003US-00425114.
 XX
 PF 06-MAY-1999; 99US-00304517.
 XX
 PR 05-NOV-2001; 2001US-00985678.
 XX
 XX (LIU/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 XX

(SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAO/) CAO Y.
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 PI WPI; 2004-180133/17.
 XX New recombinant DNA construct, useful for improving plant tolerance to
 XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 PT
 PS Claim 1; SEQ ID NO 42549; 15pp; English.
 XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.
 XX Sequence 183 AA;
 SQ

Query Match 80.0%; Score 36; DB 8; Length 183;
 Best Local Similarity 77.8%; Pred. No. 1.3e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGQAQPL 9
 Db 72 GRGQAQPL 80
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 |||||

RESULT 12
 ADF04756
 ID ADF04756 standard; protein; 349 AA.
 XX
 AC ADF04756;
 XX 12-FEB-2004 (first entry)
 DT
 XX Bacterial polypeptide #869.
 DE
 XX *Proteus mirabilis* infection; bacterial infection; antibacterial;
 KW immunostimulant.
 KW
 XX *Proteus mirabilis*.
 OS
 XX US6605709-B1.
 PN
 XX 12-AUG-2003.
 PD
 XX 05-APR-2000; 2000US-00543681.
 XX
 PF 09-APR-1999; 99US-0128706P.
 XX
 PR (GENO-) GENOME THERAPEUTICS CORP.
 PA
 XX Breton GL;
 PI
 XX WPI; 2003-895291/82.
 DR

DR N-PSDB; ADF00584.
XX New Proteus mirabilis polypeptides and polynucleotides, useful as
PT reagents for diagnosis of bacterial disease, as components of
PT antibacterial vaccines, as targets for antibacterial drugs, or as
PT biocontrol agents for plants.
PS Disclosure; SEQ ID NO 5041; 870pp; English.
XX
CC The invention relates to new Proteus mirabilis polypeptides and
CC polynucleotides. The invention also relates to antibodies against the
CC polypeptides, methods for producing the polypeptides, a method of
CC generating vaccines for immunising an individual against P. mirabilis, a
CC method for evaluating a compound for the ability to bind a P. mirabilis
CC polypeptide and a method for screening test compounds for anti-bacterial
CC activity. The polypeptides and polynucleotides are useful as molecular
CC targets for diagnosing, preventing and treating pathological conditions
CC resulting from bacterial infection, as reagents for diagnosis of
CC bacterial diseases, as components of antibacterial vaccines, as targets
CC for antibacterial drugs or as bio-control agents for plants. This
CC sequence represents a Proteus mirabilis polypeptide of the invention.
XX
SQ Sequence 349 AA;

Query Match 80.0%; Score 36; DB 7; Length 349;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
DB 92 GLQGSQSPL 100
||:|:|:|

RESULT 13
ADC00950
ID ADC00950 standard; protein; 360 AA.
XX AC ADC00950;
XX DT 04-DEC-2003 (first entry)
XX DE Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 995.
XX KW enterohaemorrhagic; anti-bacterial.
XX OS Escherichia coli; O157:H7.
XX FN JP2002355074-A.
XX PD 10-DEC-2002.
XX PF 24-JAN-2002; 2002JP-00015959.
XX PR 24-JAN-2001; 2001JP-00112010.
XX PA (UYTS-) UNIV TSUKUBA.
XX WPI; 2003-451640/43.
XX
PT Enterohaemorrhagic Escherichia coli O157:H7-specific nucleic acid molecule
PT and a polypeptide and its use, a polypeptide, a vector and a host cell.
XX
PS Claim 3; SEQ ID NO 995; 2067pp; Japanese.
XX
CC The invention relates to a novel enterohaemorrhagic Escherichia coli
CC O157:H7-specific nucleic acid molecule. A polynucleotide of the invention
CC has anti-bacterial activity. The polypeptide can be used in detection
CC and/or treatment of O157:H7 infection. The nucleotide sequence of the
CC genome of Enterohaemorrhagic E coli O157:H7 was determined. The present
CC sequence represents an E. coli O157:H7-specific polypeptide of the
CC invention.
XX
SQ Sequence 360 AA;

Query Match 80.0%; Score 36; DB 7; Length 360;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
DB 104 GLQGSQSPL 112
||:|:|:|

RESULT 14
AAU35412
ID AAU35412 standard; protein; 588 AA.
XX AC AAU35412;
XX DT 14-FEB-2002 (first entry)
XX DE Haemophilus influenzae cellular proliferation protein #53.
XX KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.
XX OS Haemophilus influenzae.
XX PN WO200170955-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009180.
XX PR 21-MAR-2000; 2000US-0191078P.
XX PR 23-MAY-2000; 2000US-0206848P.
XX PR 26-MAY-2000; 2000US-0207272P.
XX PR 23-OCT-2000; 2000US-0242578P.
XX PR 27-NOV-2000; 2000US-0253625P.
XX PR 22-DEC-2000; 2000US-0257931P.
XX PR 16-FEB-2001; 2001US-0269308P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;
PI Yamamoto RT, Xu HH;
XX WPI; 2001-611495/70.
XX DR N-PSDB; AAS53271.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 11005; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 588 AA;

Query Match 80.0%; Score 36; DB 4; Length 588;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
||| |:
DB 361 GLEGVQSPI 369

RESULT 15

ABU30211
ID ABU30211 standard; protein; 588 AA.

XX AC ABU30211;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #15738.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Haemophilus influenzae.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

XX DR N-PSDB; ACA34081.

XX PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 58135; 1766pp; English.

XX CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 588 AA;

Query Match 80.0%; Score 36; DB 6; Length 588;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9

DB 361 GLEGVQSPI 369

Search completed: March 17, 2006, 23:27:45
Job time : 124 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:34:23 ; Search time 28.3333 Seconds
(without alignments)
26.262 Million cell updates/sec

Title: US-09-856-812B-50
Perfect score: 45
Sequence: 1 GLEGAQAPL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA*
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2: /cgn2_6/ptodata/1/1aa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/H COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/PCITUS COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	9	2	US-09-533-499B-20
2	45	100.0	369	1	US-08-773-870-4
3	39	86.7	759	2	US-09-902-540-16161
4	38	84.4	415	2	US-09-252-991A-30823
5	36	80.0	349	2	US-09-543-681A-5041
6	35	77.8	1023	2	US-09-514-907A-6
7	35	77.8	1023	2	US-09-896-994-6
8	35	77.8	1023	2	US-10-040-722-2
9	35	77.8	1212	2	US-09-090-535-1
10	35	77.8	1212	2	US-09-090-535-2
11	35	77.8	1212	2	US-09-090-535-3
12	35	77.8	1212	2	US-09-090-535-4
13	34	75.6	9	1	US-08-217-188A-15
14	34	75.6	9	1	US-08-687-228-15
15	34	75.6	9	1	US-08-667-725B-15
16	34	75.6	9	2	US-09-007-748-15
17	34	75.6	175	2	US-09-902-540-14835
18	34	75.6	314	1	US-08-928-615-2
19	34	75.6	314	2	US-09-166-448-2
20	34	75.6	314	2	US-09-348-933-2
21	34	75.6	314	2	US-09-697-884-2
22	34	75.6	314	2	US-09-392-714-30
23	34	75.6	314	2	US-09-396-315-2
24	34	75.6	314	2	US-09-849-602-29
25	34	75.6	314	2	US-09-692-401-2
26	34	75.6	371	2	US-09-902-540-9910
27	34	75.6	424	2	US-09-489-039A-13454

28	34	75.6	599	2	US-09-543-681A-4524	Sequence 4524, Ap
29	34	75.6	682	2	US-09-798-791-2	Sequence 2, Appli
30	33	73.3	145	2	US-09-732-210-619	Sequence 619, App
31	33	73.3	146	2	US-08-858-207A-494	Sequence 494, App
32	33	73.3	146	2	US-09-732-210-609	Sequence 609, App
33	33	73.3	146	2	US-09-583-110-4126	Sequence 4126, Ap
34	33	73.3	150	2	US-09-732-210-620	Sequence 620, App
35	33	73.3	151	2	US-09-732-210-622	Sequence 622, App
36	33	73.3	151	2	US-09-107-532A-4906	Sequence 4906, Ap
37	33	73.3	151	2	US-09-134-000C-5804	Sequence 5804, Ap
38	33	73.3	155	2	US-09-107-433-3548	Sequence 3548, Ap
39	33	73.3	187	2	US-09-270-767-36102	Sequence 36102, A
40	33	73.3	187	2	US-09-270-767-51319	Sequence 51319, A
41	33	73.3	324	2	US-09-902-540-12246	Sequence 12246, A
42	33	73.3	343	2	US-09-948-094-2	Sequence 9727, Ap
43	33	73.3	343	2	US-10-037-417-130	Sequence 2, Appli
44	33	73.3	343	2	US-09-328-352-5272	Sequence 130, App
45	33	73.3	453	2		Sequence 5272, Ap

ALIGNMENTS

RESULT 1

US-09-533-499B-20
; Sequence 20, Application US/09533499B
; Patent No. 6682731
; GENERAL INFORMATION:

APPLICANT: Townsend, Alan; Bastin, Judy; Boon-Falleur, Thierry; van der
Bruggen, Pierre; Coullie, Pierre; Gajewski, Thomas; Melief,
Cornelis J.M.; Visseren, M.W.; Kast, W.M.
TITLE OF INVENTION: ISOLATED PEPTIDES DERIVED FROM MAGE TUMOR
REJECTION ANTIGEN PRECURSORS WHICH COMPLEX WITH
HLA-A2 MOLECULES

NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/533,499B
FILING DATE: 23-Mar-2000
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/722,115
FILING DATE: February 6, 1997
APPLICATION NUMBER: 08/290,381
FILING DATE: 15-August-1994
APPLICATION NUMBER: 08/261,160
FILING DATE: 17-June-1994
APPLICATION NUMBER: 08/217,186
FILING DATE: 24-March-1994
APPLICATION NUMBER: 08/217,188
FILING DATE: 24-March-1994

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6682731man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5327.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 318-3400
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid

;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-533-499B-20

Query Match 100.0%; Score 45; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
| | | | | | | | | |
Db 1 GLEGAQAPL 9

RESULT 2
US-08-773-870-4
; Sequence 4, Application US/08773870
; Patent No. 5912143
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MAGR-LIKE PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/773,870
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0179 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 533511
US-08-773-870-4

Query Match 100.0%; Score 45; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
| | | | | | | | | |
Db 24 GLEGAQAPL 32

RESULT 3
US-09-902-540-16161
; Sequence 16161, Application US/09902540

; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16161
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16161

Query Match 86.7%; Score 39; DB 2; Length 759;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLEGAQAP 8
| : | | | | | | | |
Db 353 GMEGAQAP 360

RESULT 4
US-09-252-991A-30823
; Sequence 30823, Application US/09252991A
; Patent No. 6851795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30823
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30823

Query Match 84.4%; Score 38; DB 2; Length 415;
Best Local Similarity 77.8%; Pred. No. 34;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
| | | | | : | | | |
Db 269 GLEGAEGPL 277

RESULT 5
US-09-543-681A-5041
; Sequence 5041, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344

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; SEQ ID NO 5041
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5041

Query Match      80.0%; Score 36; DB 2; Length 349;
Best Local Similarity 66.7%; Pred. No. 66;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLEGAQAAPL 9
Db      92 GLGQSQSP 100

RESULT 6
US-09-514-907A-6
; Sequence 6, Application US/09514907A
; Patent No. 6567705
; GENERAL INFORMATION:
; APPLICANT: Kenneth B. Stokes
; Jos,e Morissette
; TITLE OF INVENTION: SYSTEMS FOR ENHANCING CARDIAC SIGNAL
; SENSING BY CARDIAC PACEMAKERS THROUGH
; GENETIC TREATMENT
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6567705ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/514,907A
; FILING DATE: 08-Feb-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1023 amino acids
; STRANDEDNESS: single
; TOPOLOGY: unknown
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-514-907A-6

Query Match      77.8%; Score 35; DB 2; Length 1023;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 GLEGAQAAPL 9
Db      276 GLEGGQTPI 284

RESULT 7
US-09-896-994-6
; Sequence 6, Application US/09896994
; Patent No. 6665563
; GENERAL INFORMATION:
; APPLICANT: Ken Stokes
```

```
; Jos,e Morissette
; TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC
; SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREAT
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6665563ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/896,994
; FILING DATE: 02-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/514,907
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1023 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-896-994-6

Query Match      77.8%; Score 35; DB 2; Length 1023;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 GLEGAQAAPL 9
Db      276 GLEGGQTPI 284

RESULT 8
US-10-040-722-2
; Sequence 2, Application US/10040722
; Patent No. 6844483
; GENERAL INFORMATION:
; APPLICANT: Ruiz-Opazo, Nelson
; TITLE OF INVENTION: METHOD OF ASSAYING MODULATORS OF
; TITLE OF INVENTION: HYPERTENSION
; FILE REFERENCE: 50047/006003
; CURRENT APPLICATION NUMBER: US/10/040,722
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 09/653,030
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 60/152,011
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1023
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-040-722-2

Query Match      77.8%; Score 35; DB 2; Length 1023;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
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Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
|||||:
Db 276 GLEGGQTPI 284

RESULT 9
US-09-090-535-1
; Sequence 1, Application US/09090535A
; Patent No. 6309874
; GENERAL INFORMATION:
; APPLICANT: BELUSA, Roger
; TITLE OF INVENTION: SELECTION MARKER
; FILE REFERENCE: BELUSA 09/090,535
; CURRENT APPLICATION NUMBER: US/09/090,535A
; CURRENT FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: US 60/048,601
; EARLIER FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1212
; TYPE: PRT
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (43)
; OTHER INFORMATION: Xaa is any amino acid.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1103)
; OTHER INFORMATION: Xaa is any amino acid.
US-09-090-535-1

Query Match 77.8%; Score 35; DB 2; Length 1212;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
|||||:
Db 355 GLEGGQTPI 363

RESULT 10
US-09-090-535-2
; Sequence 2, Application US/09090535A
; Patent No. 6309874
; GENERAL INFORMATION:
; APPLICANT: BELUSA, Roger
; TITLE OF INVENTION: SELECTION MARKER
; FILE REFERENCE: BELUSA 09/090,535
; CURRENT APPLICATION NUMBER: US/09/090,535A
; CURRENT FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: US 60/048,601
; EARLIER FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1212
; TYPE: PRT
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (43)
; OTHER INFORMATION: Xaa is any amino acid.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1103)
; OTHER INFORMATION: Xaa is any amino acid.
US-09-090-535-2

Query Match 77.8%; Score 35; DB 2; Length 1212;

Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
|||||:
Db 355 GLEGGQTPI 363

RESULT 11
US-09-090-535-3
; Sequence 3, Application US/09090535A
; Patent No. 6309874
; GENERAL INFORMATION:
; APPLICANT: BELUSA, Roger
; TITLE OF INVENTION: SELECTION MARKER
; FILE REFERENCE: BELUSA 09/090,535
; CURRENT APPLICATION NUMBER: US/09/090,535A
; CURRENT FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: US 60/048,601
; EARLIER FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1212
; TYPE: PRT
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (43)
; OTHER INFORMATION: Xaa is any amino acid.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1103)
; OTHER INFORMATION: Xaa is any amino acid.
US-09-090-535-3

Query Match 77.8%; Score 35; DB 2; Length 1212;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
|||||:
Db 355 GLEGGQTPI 363

RESULT 12
US-09-090-535-4
; Sequence 4, Application US/09090535A
; Patent No. 6309874
; GENERAL INFORMATION:
; APPLICANT: BELUSA, Roger
; TITLE OF INVENTION: SELECTION MARKER
; FILE REFERENCE: BELUSA 09/090,535
; CURRENT APPLICATION NUMBER: US/09/090,535A
; CURRENT FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: US 60/048,601
; EARLIER FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1212
; TYPE: PRT
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (43)
; OTHER INFORMATION: Xaa is any amino acid.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1103)
; OTHER INFORMATION: Xaa is any amino acid.
US-09-090-535-4

Query Match 77.8%; Score 35; DB 2; Length 1212;

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Query Match 77.8%; Score 35; DB 2; Length 1212;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
Db 355 GLEGGQTPI 363

RESULT 13
US-08-217-188A-15
; Sequence 15, Application US/08217188A
; Patent No. 5554724
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,226
; FILING DATE: 25-JULY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5686068man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5447
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-687-226-15

Query Match 75.6%; Score 34; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAP 8
Db 1 GLVGAQAP 8

RESULT 15
US-08-667-725B-15
; Sequence 15, Application US/08667725B
; Patent No. 6063900
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,725B
; FILING DATE: 21 June 1996
; CLASSIFICATION: 530

Query Match 75.6%; Score 34; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAP 8
Db 1 GLVGAQAP 8

RESULT 14
US-08-687-226-15
; Sequence 15, Application US/08687226
; Patent No. 5686068
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.; Visseren, M. W.;
; APPLICANT: van der Burg, Sjoerd; van der Bruggen, Pierre;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Derived From
; TITLE OF INVENTION: Mage-2, Cytolytic T Cells Specific To Complexes Of
; TITLE OF INVENTION: Peptides And HLA-A2 Molecules, And Uses Thereof
```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6063900man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340.1 DIV (081585)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-667-725B-15

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Query Match      75.6%; Score 34; DB 2; Length 9;
Best Local Similarity 87.5%; Pred. NO. 4.6e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 GLEGAQAP 8
Db      1 GLVGAQAP 8

```

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Search completed: March 17, 2006, 23:36:22
Job time : 29.3333 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:35:13 ; Search time 98.3333 Seconds
(without alignments)
38.242 Million cell updates/sec

Title: US-09-856-812B-50

Perfect score: 45

Sequence: 1 GLEGAQAAPL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	369	4	US-10-036-542-84
2	45	100.0	369	4	US-10-188-832-149
3	45	100.0	369	5	US-10-658-884-4
4	45	100.0	369	5	US-10-756-149-4721
5	45	100.0	383	4	US-10-029-386-32058
6	37	82.2	75	4	US-10-424-599-268960
7	36	80.0	97	4	US-10-437-963-139267
8	36	80.0	183	4	US-10-425-114-42549
9	36	80.0	588	3	US-09-815-242-11005
10	36	80.0	588	4	US-10-282-122A-58135
11	36	80.0	598	4	US-10-282-122A-78500
12	36	80.0	949	5	US-10-450-763-34130
13	35	77.8	89	3	US-09-864-761-38370
14	35	77.8	114	4	US-10-080-170-612
15	35	77.8	114	4	US-10-080-170-612
16	35	77.8	114	4	US-10-468-356-612
17	35	77.8	196	4	US-10-424-599-222287
18	35	77.8	225	4	US-10-425-114-65434
19	35	77.8	307	4	US-10-425-114-64885
20	35	77.8	751	3	US-09-925-298-745
21	35	77.8	751	4	US-10-102-806-745
22	35	77.8	1023	3	US-09-896-994-6
23	35	77.8	1023	4	US-10-040-722-2
24	35	77.8	1023	4	US-10-408-765A-30
25	35	77.8	1023	4	US-10-408-765A-31
26	35	77.8	1023	5	US-10-685-237-6
27	35	77.8	1023	5	US-10-852-840-6

28 35 77.8 1023 5 US-10-489-740-171 Sequence 171, App
29 34 75.6 9 4 US-10-219-850-16 Sequence 16, Appl
30 34 75.6 9 4 US-10-353-678-22 Sequence 22, Appl
31 34 75.6 9 4 US-10-149-135-141 Sequence 141, App
32 34 75.6 9 4 US-10-149-135-338 Sequence 338, App
33 34 75.6 9 4 US-10-149-135-1379 Sequence 1379, Ap
34 34 75.6 9 4 US-10-149-135-1550 Sequence 1550, Ap
35 34 75.6 9 4 US-10-149-135-2056 Sequence 2056, Ap
36 34 75.6 9 4 US-10-149-135-2111 Sequence 2111, Ap
37 34 75.6 9 4 US-10-777-053-866 Sequence 866, App
38 34 75.6 9 4 US-10-837-217-866 Sequence 866, App
39 34 75.6 10 4 US-10-149-135-142 Sequence 142, App
40 34 75.6 10 4 US-10-149-135-339 Sequence 339, App
41 34 75.6 10 4 US-10-149-135-1411 Sequence 1411, Ap
42 34 75.6 10 4 US-10-149-135-1582 Sequence 1582, Ap
43 34 75.6 11 4 US-10-149-135-88 Sequence 88, Appl
44 34 75.6 11 4 US-10-149-135-284 Sequence 284, App
45 34 75.6 11 4 US-10-149-135-1324 Sequence 1324, Ap

ALIGNMENTS

RESULT 1

US-10-036-542-84

; Sequence 84, Application US/10036542

; Publication No. US20030083481A1

; GENERAL INFORMATION:

; APPLICANT: Birse et al.

; TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins

; FILE REFERENCE: PA002P1

; CURRENT APPLICATION NUMBER: US/10/036,542

; CURRENT FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: PCT/US00/19666

; PRIOR FILING DATE: 2000-07-20

; PRIOR APPLICATION NUMBER: 60/144,972

; PRIOR FILING DATE: 1999-07-21

; PRIOR APPLICATION NUMBER: 60/148,681

; PRIOR FILING DATE: 1999-08-13

; PRIOR APPLICATION NUMBER: 60/149,173

; PRIOR FILING DATE: 1999-08-17

; PRIOR APPLICATION NUMBER: 60/158,004

; PRIOR FILING DATE: 1999-10-06

; PRIOR APPLICATION NUMBER: 60/194,689

; PRIOR FILING DATE: 2000-04-05

; NUMBER OF SEQ ID NOS: 157

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 84

; LENGTH: 369

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-036-542-84

Query Match

Best Local Similarity 100.0%; Score 45; DB 4; Length 369;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLEGAQAAPL 9

|||||

Db 24 GLEGAQAAPL 32

RESULT 2

US-10-188-832-149

; Sequence 149, Application US/10188832

; Publication No. US20040076955A1

; GENERAL INFORMATION:

; APPLICANT: Mack, David H.

; APPLICANT: Aziz, Natasha

; APPLICANT: Eos Biotechnology, Inc.

; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions

; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder

; TITLE OF INVENTION: Cancer

FILE REFERENCE: 018501-002330US
CURRENT APPLICATION NUMBER: US/10/188,832
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US 60/302,814
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: US 60/310,099
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/343,705
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/372,246
PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 207
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 149
LENGTH: 369
TYPE: PRT
ORGANISM: Homo sapiens
US-10-188-832-149

Query Match 100.0%; Score 45; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
DB 24 GLEGAQAPL 32

RESULT 3

US-10-658-884-4
Sequence 4, Application US/10658884
Publication No. US20050019304A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MAGE-LIKE PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/658,884
FILING DATE: 09-Sep-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/773,870
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0179 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:

LIBRARY: GenBank
CLONE: 533511
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-658-884-4

Query Match 100.0%; Score 45; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
DB 24 GLEGAQAPL 32

RESULT 4

US-10-756-149-4721
Sequence 4721, Application US/10756149
Publication No. US20050181375A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
FILE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4721
LENGTH: 369
TYPE: PRT
ORGANISM: Homo sapiens
US-10-756-149-4721

Query Match 100.0%; Score 45; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
DB 24 GLEGAQAPL 32

RESULT 5

US-10-029-386-32058
Sequence 32058, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 32058
LENGTH: 383
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AF134576.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
OTHER INFORMATION: SWISSPROT HIT: P43363, EVALUATION 0.00e+00
US-10-029-386-32058


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Query Match      100.0%; Score 45; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLEGAQAPL 9
      |||||
DB      45 GLEGAQAPL 53

RESULT 6
US-10-424-599-268960
; Sequence 268960, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 268960
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_84893C.1.pap
US-10-424-599-268960

Query Match      82.2%; Score 37; DB 4; Length 75;
Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 GLEGAQAPL 9
      |||||
DB      60 GLKGQAPL 68

RESULT 7
US-10-437-963-139267
; Sequence 139267, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 139267
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(97)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_40576C.1.pap
US-10-437-963-139267

Query Match      80.0%; Score 36; DB 4; Length 97;
Best Local Similarity 87.5%; Pred. No. 55;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LEGAQAPL 9
      |||||
DB      62 LEGAQAPL 69

RESULT 8
US-10-425-114-42549
; Sequence 42549, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 42549
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700262287_FLI.pap
US-10-425-114-42549

Query Match      80.0%; Score 36; DB 4; Length 183;
Best Local Similarity 77.8%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 GLEGAQAPL 9
      |||||
DB      72 GRGGAQAPL 80

RESULT 9
US-09-815-242-11005
; Sequence 11005, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
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; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 11005
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-815-242-11005

Query Match 80.0%; Score 36; DB 3; Length 588;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
Db 361 GLEGVQSPI 369

RESULT 10
US-10-282-122A-58135
; Sequence 58135, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Lianguu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58135
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-282-122A-58135

Query Match 80.0%; Score 36; DB 4; Length 588;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
Db 361 GLEGVQSPI 369

RESULT 11
US-10-282-122A-78500
; Sequence 78500, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Lianguu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78500
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Yersinia pestis
US-10-282-122A-78500

Query Match 80.0%; Score 36; DB 4; Length 598;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
Db 360 GLEGVQSPI 368

RESULT 12
US-10-450-763-34130
; Sequence 34130, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763

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; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 34130
; TYPE: PRT
; LENGTH: 949
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (169)..(182)
; OTHER INFORMATION: PROTEIN ZINC-FINGER METAL-BINDI domain identified by eMATRIX,
; OTHER INFORMATION: accession number PD00066, p-value=1.391e-11, raw score of 13.92
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (151)..(203)
; OTHER INFORMATION: Zinc finger, C2H2 type domain identified by Pfam, accession
; OTHER INFORMATION: name zf-C2H2, E-value=6.6e-10, Pfam score of 46.3
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(949)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-34130

Query Match      80.0%; Score 36; DB 5; Length 949;
Best Local Similarity 77.8%; Pred. No. 5.7e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GLEGAQAPL 9
DB      820 GLRGGAQPL 828

RESULT 13
US-09-864-761-38370
; Sequence 38370, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmics-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38370
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004904.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 8.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 6.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.4
; OTHER INFORMATION: SWISSPROT HIT: P50997, EVALUE 5.00e-36
; OTHER INFORMATION: EST_HUMAN HIT: AU124927.1, EVALUE 1.00e-34
US-09-864-761-38370

Query Match      77.8%; Score 35; DB 3; Length 89;
Best Local Similarity 66.7%; Pred. No. 77;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 GLEGAQAPL 9
DB      24 GLEGGQTPI 32

RESULT 14
US-10-080-170-612
; Sequence 612, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 612
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-612

Query Match      77.8%; Score 35; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LEGAQAP 8
DB      104 LEGAQAP 110
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RESULT 15
US-10-080-170-612
; Sequence 612, Application US/10080170
; Publication No. US20040121322A9
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 612
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-612

Query Match      77.8%; Score 35; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LEGAQAP 8
      |||||
Db      104 LEGAQAP 110

Search completed: March 17, 2006, 23:41:23
Job time : 99.3333 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:36:38 ; Search time 11.6667 Seconds
(without alignments)
22.081 Million cell updates/sec

Title: US-09-856-812B-50
Perfect score: 45
Sequence: 1 GLEGAQAPL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New.*
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4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	77.8	1023	6	US-10-821-234-1377 Sequence 1377, Ap
2	34	75.6	9	7	US-11-026-403-22 Sequence 22, Appl
3	34	75.6	251	7	US-11-096-568A-10274 Sequence 10274, A
4	34	75.6	260	7	US-11-245-400-43 Sequence 43, Appl
5	34	75.6	300	7	US-11-096-568A-10273 Sequence 10273, A
6	34	75.6	314	6	US-10-510-101-69 Sequence 69, Appl
7	34	75.6	314	7	US-11-155-288-6 Sequence 6, Appli
8	34	75.6	682	7	US-11-039-756-2 Sequence 2, Appli
9	33	73.3	280	7	US-11-096-568A-6822 Sequence 6822, Ap
10	33	73.3	343	7	US-11-080-991-86 Sequence 86, Appl
11	33	73.3	343	7	US-11-019-711-130 Sequence 130, Appl
12	33	73.3	393	6	US-10-821-234-1043 Sequence 1043, Ap
13	33	73.3	749	7	US-11-052-554A-148 Sequence 148, Appl
14	32	71.1	144	6	US-10-467-657-7734 Sequence 7734, Ap
15	32	71.1	144	7	US-11-194-246-420 Sequence 420, Appl
16	32	71.1	149	7	US-11-098-686-11221 Sequence 11221, A
17	32	71.1	735	7	US-11-087-099-4908 Sequence 4908, Ap
18	31	68.9	177	7	US-11-234-424-18 Sequence 18, Appl
19	31	68.9	184	6	US-10-131-826A-76 Sequence 76, Appl
20	31	68.9	184	6	US-10-973-115B-76 Sequence 76, Appl
21	31	68.9	250	6	US-10-528-000-1 Sequence 1, Appli
22	31	68.9	326	6	US-10-330-773-169 Sequence 169, Appl
23	31	68.9	341	7	US-11-142-700-12 Sequence 12, Appl
24	31	68.9	391	6	US-10-467-657-5988 Sequence 5988, Ap
25	31	68.9	517	7	US-11-096-568A-20651 Sequence 20651, A

ALIGNMENTS

RESULT 1

US-10-821-234-1377
; Sequence 1377, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1377
; LENGTH: 1023
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1377

Query Match 77.8%; Score 35; DB 6; Length 1023;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
Db 276 GLEGGQTPI 284

RESULT 2

US-11-026-403-22
; Sequence 22, Application US/11026403
; Publication No. US20060002946A1
; GENERAL INFORMATION:
; APPLICANT: Gallichan, Scott
; APPLICANT: Uger, Bob
; APPLICANT: Salha, Danielle
; TITLE OF INVENTION: Targeted Immunogens
; FILE REFERENCE: API-03-19-US
; CURRENT APPLICATION NUMBER: US/11/026,403
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: US 60/533,728
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patent in version 3.3

Sequence 20650, A
Sequence 368, Appl
Sequence 10, Appl
Sequence 18, Appl
Sequence 33917, A
Sequence 1443, Ap
Sequence 33916, A
Sequence 34032, A
Sequence 28146, A
Sequence 14789, A
Sequence 34031, A
Sequence 28145, A
Sequence 1445, Ap
Sequence 33915, A
Sequence 29, Appl
Sequence 34030, A
Sequence 10, Appl
Sequence 28144, A
Sequence 14788, A

26 31 68.9 525 7 US-11-096-568A-20650
27 31 68.9 618 6 US-10-501-035-368
28 31 68.9 665 6 US-10-491-468-10
29 31 68.9 793 7 US-11-142-700-18
30 31 68.9 861 7 US-11-096-568A-33917
31 31 68.9 862 7 US-11-051-720-1443
32 31 68.9 881 7 US-11-096-568A-33916
33 31 68.9 925 7 US-11-096-568A-34032
34 31 68.9 960 7 US-11-096-568A-28146
35 31 68.9 961 7 US-11-096-568A-14789
36 31 68.9 967 7 US-11-096-568A-34031
37 31 68.9 973 7 US-11-096-568A-28145
38 31 68.9 1007 7 US-11-051-720-1445
39 31 68.9 1069 7 US-11-096-568A-33915
40 31 68.9 1081 7 US-11-142-700-29
41 31 68.9 1084 7 US-11-142-700-24
42 31 68.9 1084 7 US-11-096-568A-34030
43 31 68.9 1086 7 US-11-142-700-10
44 31 68.9 1088 7 US-11-096-568A-28144
45 31 68.9 1094 7 US-11-096-568A-14788

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; SEQ ID NO 22
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide (MAGE-A3 24) derived from cancer-testis antigen
US-11-026-403-22

Query Match          75.6%; Score 34; DB 7; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAP 8
   |||||||
Db 1 GLVGQAQAP 8

RESULT 3
US-11-096-568A-10274
; Sequence 10274, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 10274
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(251)
; OTHER INFORMATION: Ceres Seq. ID no. 13585435
US-11-096-568A-10274

Query Match          75.6%; Score 34; DB 7; Length 251;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEGAQAAPL 9
   :|||:|
Db 1 MEGAEAPL 8

RESULT 4
US-11-245-400-43
; Sequence 43, Application US/11245400
; Publication No. US20060040357A1
; GENERAL INFORMATION:
; APPLICANT: Bandaru, Rajasekhara
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Encoding Melanoma
; TITLE OF INVENTION: Associated Antigen Molecules, Aminotransferase
; TITLE OF INVENTION: Molecules, ATPase Molecules, Acyltransferase Molecules,
; TITLE OF INVENTION: Pyridoxal-Phosphate Dependant Enzyme Molecules and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/247400
; CURRENT APPLICATION NUMBER: US/11/245,400
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US/10/164,966
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 10/034,864
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/258,517
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 09/996,194
; PRIOR FILING DATE: 2001-11-28
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; PRIOR APPLICATION NUMBER: 60/250,348
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/250,073
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/253,878
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,338
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/908,928
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/220,465
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MAGE family PFAM consensus domain
US-11-245-400-43
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Query Match          75.6%; Score 34; DB 7; Length 260;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAP 8
   |||||||
Db 22 GLVGQAQAP 29
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RESULT 5
US-11-096-568A-10273
; Sequence 10273, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 10273
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(300)
; OTHER INFORMATION: Ceres Seq. ID no. 13585434
US-11-096-568A-10273
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Query Match          75.6%; Score 34; DB 7; Length 300;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEGAQAAPL 9
   :|||:|
Db 50 MEGAEAPL 57
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```
RESULT 6
US-10-510-101-69
; Sequence 69, Application US/10510101
; Publication No. US20060018915A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Ishioka, Glenn
; APPLICANT: Fikes, John
; APPLICANT: Tangri, Shabnam
; APPLICANT: Sette, Alessandro
```

;
; TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
; FILE REFERENCE: 2060.009PC05
; CURRENT APPLICATION NUMBER: US/10/510,101
; CURRENT FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: US 60/413,471
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 10/116,118
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-510-101-69

Query Match 75.6%; Score 34; DB 6; Length 314;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAP 8
|||
Db 24 GLVGAQAP 31

RESULT 7
US-11-155-288-6
; Sequence 6, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANK 050A
; CURRENT APPLICATION NUMBER: US/11/155,288
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-6

Query Match 75.6%; Score 34; DB 7; Length 314;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAP 8
|||
Db 24 GLVGAQAP 31

RESULT 8
US-11-039-756-2
; Sequence 2, Application US/11039756
; Publication No. US20050278806A1
; GENERAL INFORMATION:
; APPLICANT: HEYER, ARND G.
; APPLICANT: REHM, JOCHEN
; APPLICANT: WENDENBURG, REGINA
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES HAVING
; TITLE OF INVENTION: FRUCTOSYLTRANSFERASE ACTIVITY, AND THEIR USE
; FILE REFERENCE: MPG-9
; CURRENT APPLICATION NUMBER: US/11/039,756
; CURRENT FILING DATE: 2005-01-19
; PRIOR APPLICATION NUMBER: US 09/798,791
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: PCT/EP99/06319
; PRIOR FILING DATE: 1999-08-27

;
; PRIOR APPLICATION NUMBER: DE 198 40 028.4
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 682
; TYPE: PRT
; ORGANISM: Aspergillus sydowi
US-11-039-756-2

Query Match 75.6%; Score 34; DB 7; Length 682;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
|:|:|:|
Db 288 GVEGAVAPI 296

RESULT 9
US-11-096-568A-6822
; Sequence 6822, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6822
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(280)
; OTHER INFORMATION: Ceres Seq. ID no. 15168444
US-11-096-568A-6822

Query Match 73.3%; Score 33; DB 7; Length 280;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
|:|:|:|
Db 108 GFEGGQTPL 116

RESULT 10
US-11-080-991-86
; Sequence 86, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-86

Query Match 73.3%; Score 33; DB 7; Length 343;

Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAP 8
| | | | |
Db 29 GAEGAEAP 36

RESULT 11

US-11-019-711-130
; Sequence 130, Application US/11019711
; Publication No. US20060009634A1

GENERAL INFORMATION:

; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/11/019,711
; CURRENT FILING DATE: 2004-12-21

; PRIOR APPLICATION NUMBER: US/10/037,417

; PRIOR FILING DATE: 2002-09-20

; PRIOR APPLICATION NUMBER: 60/260,018

; PRIOR FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: 60/260,360

; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/272,411

; PRIOR FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 60/272,817

; PRIOR FILING DATE: 2001-03-02

; PRIOR APPLICATION NUMBER: 60/291,186

; PRIOR FILING DATE: 2001-05-15

; PRIOR APPLICATION NUMBER: 60/303,231

; PRIOR FILING DATE: 2001-07-05

; PRIOR APPLICATION NUMBER: 60/305,060

; PRIOR FILING DATE: 2001-07-12

; PRIOR APPLICATION NUMBER: 60/318,405

; PRIOR FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/318,700

; PRIOR FILING DATE: 2001-09-12

; NUMBER OF SEQ ID NOS: 227

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 130

; LENGTH: 343

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-019-711-130

Query Match 73.3%; Score 33; DB 7; Length 343;
Best Local Similarity 75.0%; Pred. No. 28;

Matches 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAP 8
| | | | |
Db 29 GAEGAEAP 36

RESULT 12

US-10-821-234-1043
; Sequence 1043, Application US/10821234
; Publication No. US20050255114A1

GENERAL INFORMATION:

; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1043
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1043

Query Match 73.3%; Score 33; DB 6; Length 393;

Best Local Similarity 75.0%; Pred. No. 33;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAP 8
| | | | |
Db 79 GAEGAEAP 86

RESULT 13

US-11-052-554A-148
; Sequence 148, Application US/11052554A
; Publication No. US20050288666A1

GENERAL INFORMATION:

; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148
; LENGTH: 749
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-148

Query Match 73.3%; Score 33; DB 7; Length 749;

Best Local Similarity 75.0%; Pred. No. 69;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAP 8
| | | | |
Db 362 GLDGANAP 369

RESULT 14

US-10-467-657-7734

; Sequence 7734, Application US/10467657
; Publication No. US20050260581A1

; GENERAL INFORMATION:

; APPLICANT: CHIRON SPA

; APPLICANT: FONTANA Maria Rita

; APPLICANT: PIZZA Mariagrazia

; APPLICANT: MASIGNANI Vega

; APPLICANT: MONACI Elisabetta

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 9218

; SOFTWARE: SeqWin99, version 1.04

; SEQ ID NO 7734

; LENGTH: 144

; TYPE: PRT

; ORGANISM: Neisseria gonorrhoeae

US-10-467-7734

Query Match 71.1%; Score 32; DB 6; Length 144;

Best Local Similarity 66.7%; Pred. No. 16;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9

Db 49 GFEGGQMPL 57

RESULT 15

US-11-194-246-420

; Sequence 420, Application US/11194246

; Publication No. US20050272089A1

; GENERAL INFORMATION:

; APPLICANT: Mott, John

; APPLICANT: Trepod, Catherine

; APPLICANT: Arvidson, Staffan

; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET

; FILE REFERENCE: 00592.US1 (M&R 268.05920101)

; CURRENT APPLICATION NUMBER: US/11/194,246

; CURRENT FILING DATE: 2005-08-01

; PRIOR APPLICATION NUMBER: US/10/274,586

; PRIOR FILING DATE: 2002-10-21

; PRIOR APPLICATION NUMBER: US 60/345,438

; PRIOR FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 621

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 420

; LENGTH: 144

; TYPE: PRT

; ORGANISM: HAEMOPHILUS INFLUENZAE

US-11-194-246-420

Query Match 71.1%; Score 32; DB 7; Length 144;

Best Local Similarity 66.7%; Pred. No. 16;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9

Db 49 GFEGGQMPL 57

Search completed: March 17, 2006, 23:42:02

Job time : 12.6667 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:28:08 ; Search time 19.3333 Seconds
(without alignments)
44.791 Million cell updates/sec

Title: US-09-856-812B-50

Perfect score: 45

Sequence: 1 GLEGAQAFL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	369	2 I38659	melanoma antigen M
2	38	84.4	218	2 T47706	hypothetical prote
3	37	82.2	338	2 B82499	hypothetical prote
4	36	80.0	360	2 D85508	hypothetical prote
5	36	80.0	360	2 D90657	hypothetical prote
6	36	80.0	362	2 S77244	biotin synthase (B
7	36	80.0	584	2 B82810	ABC transporter ni
8	36	80.0	588	1 E64061	aspartate-tRNA lig
9	36	80.0	598	2 AE0250	aspartate-tRNA lig
10	35	77.8	114	2 E27397	Na+/K+-exchanging
11	35	77.8	114	2 A70562	hypothetical prote
12	35	77.8	216	2 S60048	chlorophyll a/c-bi
13	35	77.8	220	2 S20970	Na+/K+-exchanging
14	35	77.8	1021	1 PWSHNA	Na+/K+-exchanging
15	35	77.8	1021	1 S04630	Na+/K+-exchanging
16	35	77.8	1021	2 B24862	Na+/K+-exchanging
17	35	77.8	1023	1 A24639	Na+/K+-exchanging
18	35	77.8	1023	1 S24650	Na+/K+-exchanging
19	35	77.8	1023	2 A24414	Na+/K+-exchanging
20	34	75.6	314	2 JC2360	melanoma antigen M
21	34	75.6	314	2 I68889	melanoma antigen M
22	34	75.6	314	2 I54519	melanoma antigen M
23	34	75.6	314	2 JC2361	melanoma antigen M
24	34	75.6	317	2 I38661	melanoma antigen M
25	34	75.6	349	2 AC0437	conserved hypothet
26	34	75.6	449	1 B43698	paired box transcr
27	34	75.6	1445	2 A59437	KIAA1204 protein [
28	34	75.6	1513	2 T23681	hypothetical prote
29	34	75.6	1562	2 T43022	ATP-binding multid

ALIGNMENTS

RESULT 1

I38659

melanoma antigen MAGE-10 - human

C:Species: Homo sapiens (man)

C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004

C:Accession: I38659

R:De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Br

oon, T.

Immunogenetics 40, 360-369, 1994

A>Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fam

A:Reference number: I38659; MUID:95012457; PMID:7927540

A:Accession: I38659

A>Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: DNA

A:Residues: 1-369 <RES>

A:Cross-references: UNIPROT:P43363; UNIPARC:UPI00000000CS7; EMBL:U10685; NID:g533510; PID

C:Genetics:

A:Gene: GDB:MAGEA10; MAGE10

A:Cross-references: GDB:331126

A:Map position: Xq28-Xq28

A:Introns: #status absent

C:Superfamily: tumor associated protein MAGE

Query Match 100.0%; Score 45; DB 2; Length 369;

Best Local Similarity 100.0%; Pred. No. 0.22;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLEGAQAFL 9

|||||||

Db 24 GLEGAQAFL 32

RESULT 2

T47706

hypothetical protein F116.80 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C:Accession: T47706

R:Genes, V.; Wurmbach, E.; Drzonek, H.; Ansoorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.F

submitted to the Protein Sequence Database, March 2000

A:Reference number: Z24473

A:Accession: T47706

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-218 <BEN>

A:Cross-references: UNIPROT:Q9M055; UNIPARC:UPI00000A44FC; EMBL:AL161667

A:Experimental source: cultivar Columbia; BAC clone F1116

C:Genetics:

A:Map position: 3

A:Introns: 11/1; 54/3; 140/3

A>Note: F1116.80

```
Query Match      84.4%; Score 38; DB 2; Length 218;
Best Local Similarity 77.8%; Pred. No. 3.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GLEGAQAAPL 9
DB      136 GLDGQAAPL 144
      |||:|||||
      |||:|||||

RESULT 3
B82499
hypothetical protein VCA0111 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: B82499
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bacs, S.; Qin, H.; Dragoi, I.; Sellers, F.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: B82499
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-338 <HEI>
A:Cross-references: UNIPROT:Q9KN54; UNIPARC:UPI00000C3423; GB:AE004353; GB:AE003853; NID
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCA0111
A:Map position: 2

Query Match      82.2%; Score 37; DB 2; Length 338;
Best Local Similarity 77.8%; Pred. No. 8.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GLEGAQAAPL 9
DB      93 GLSGAQSPL 101
      |||:|||||
      |||:|||||

RESULT 4
D85508
hypothetical protein Z0259 [imported] - Escherichia coli (strain O157:H7, substrain EDLS
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: D85508
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: D85508
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-360 <STO>
A:Cross-references: UNIPROT:Q9X7U7; UNIPARC:UPI00000D09F4; GB:AE005174; NID:g12512965; E
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z0259

Query Match      80.0%; Score 36; DB 2; Length 360;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLEGAQAAPL 9
DB      104 GLGGSQSPL 112
      |||:|||||
      |||:|||||

RESULT 5
D90657
hypothetical protein ECs0228 [imported] - Escherichia coli (strain O157:H7, substrain R1
C:Species: Escherichia coli
```

```
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
A:Accession: D90657
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ighii, K.; Yokoyama, K.; Han, C.G.;
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: D90657
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-360 <HAY>
A:Cross-references: UNIPROT:Q9X7U7; UNIPARC:UPI00000D09F4; GB:BA000007; PIDN:BA833651.1;
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECs0228

Query Match      80.0%; Score 36; DB 2; Length 360;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 GLEGAQAAPL 9
DB      104 GLGGSQSPL 112
      |||:|||||
      |||:|||||

RESULT 6
S77244
biotin synthase (EC 2.8.1.6) bioB slrl364 [similarity] - Synechocystis sp. (strain PCC 6
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S77244
R:Kanko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S77244
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-362 <KAN>
A:Cross-references: UNIPROT:P73538; UNIPARC:UPI0000126965; EMBL:D90907; GB:AB001339; NIT
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Gene: bioB
A:Start codon: GTG
C:Superfamily: biotin synthetase
C:Keywords: 2Fe-2S; biotin biosynthesis; iron-sulfur protein; metalloprotein; sulfutra
F:88,92,95,230/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match      80.0%; Score 36; DB 2; Length 362;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 GLEGAQAAPL 9
DB      348 GLEGGEAPL 356
      |||:|||||
      |||:|||||

RESULT 7
B82810
ABC transporter nitrate permease XF0411 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: B82810
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: B82810
A>Status: preliminary
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A:Molecule type: DNA
A:Residues: 1-584 <SIM>
A:Cross-references: UNIPROT:Q9PG91; UNIPARC:UPI000000C23D7; GB:AE003892; GB:AE003849; NID
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briónes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Canargo, L.E.A.; Carraro, D.M.; Carver, H
de-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laigh
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
P.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0411

Query Match 80.0%; Score 36; DB 2; Length 584;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
| | | | |
Db 44 GAEGARAPL 52

RESULT 8
E84061
aspartate-tRNA ligase (EC 6.1.1.12) - Haemophilus influenzae (strain Rd KW20)
N:Alternate names: aspartyl-tRNA synthetase
C:Species: Haemophilus influenzae
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: E64061
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J
Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: E64061
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-588 <TIG>
A:Cross-references: UNIPROT:P43817; UNIPARC:UPI0000136396; GB:U32717; GB:L42023; NID:915
C:Genetics:
A:Gene: asps
C:Function:
A:Description: activates amino acid and transfers it to specific tRNA molecule
A:Pathway: protein biosynthesis
C:Superfamily: lysine-tRNA ligase
C:Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis

Query Match 80.0%; Score 36; DB 1; Length 588;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
| | | | |
Db 361 GLEGVQSPI 369

RESULT 9
AE0250
aspartate-tRNA ligase (EC 6.1.1.12) [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
A:Accession: AE0250
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AE0250
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-598 <KUR>
A:Cross-references: UNIPROT:Q8ZEY0; UNIPARC:UPI00001363C3; GB:AL590842; PIDN:CAC90865.1
C:Genetics:
A:Gene: asps
C:Superfamily: lysine-tRNA ligase
C:Keywords: ligase

Query Match 80.0%; Score 36; DB 2; Length 598;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
| | | | |
Db 360 GLEGVQSPI 368

RESULT 10
E27397
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain 5 - human (fragments)
N:Alternate names: sodium/potassium transporting ATPase alpha chain
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1991 #text_change 31-Dec-2004
C:Accession: E27397
R:Sverdlov, E.D.; Monastyrskaya, G.S.; Broude, N.E.; Ushkaryov, Y.A.; Allikmets, R.L.;
tina, M.B.; Sverdlov, V.E.; Modyanov, N.N.; Ovchinnikov, Y.A.
FEBS Lett. 217, 275-278, 1987
A:Title: The family of human Na+ K+-ATPase genes. No less than five genes and/or pseudo
A:Reference number: A27397; MUID:87247232; PMID:3036582
A:Accession: E27397
A:Molecule type: mRNA
A:Residues: 1-114 <SVE>
A:Cross-references: UNIPROT:P54707; UNIPARC:UPI0000175F03; GB:M27572
A:Note: the authors translated the codon TAC for residue 8 as Val
C:Superfamily: Na(+)/K(+)-transporting ATPase alpha chain; ATPase nucleotide-binding do
C:Keywords: ATP; hydrolase

Query Match 77.8%; Score 35; DB 2; Length 114;
Best Local Similarity 66.7%; Pred. No. 7.5;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
| | | | |
Db 24 GLEGGQTPI 32

RESULT 11
A70562
hypothetical protein Rv3632 - Mycobacterium tuberculosis (strain H37Rv)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: A70562
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98299387; PMID:9634230
A:Accession: A70562
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-114 <COL>
A:Cross-references: UNIPROT:O06375; UNIPARC:UPI00000D100D; GB:Z95436; GB:AL123456; NID:
A:Experimental source: strain H37Rv
C:Genetics:

A:Gene: Rv3632

Query Match 77.8%; Score 35; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSGAQAP 8
|||||

Db 104 LSGAQAP 110

RESULT 12

S60048 chlorophyll a/c-binding protein precursor - Giraudyopsis stellifer

N:Alternate names: light-harvesting complex protein cac

C:Species: Giraudyopsis stellifer

C:Date: 24-Aug-1996 #sequence_revision 08-Nov-1996 #text_change 08-Nov-1996

C:Accession: S60048; S71151

R:Passaquet, C.; Lichtl, C.

Plant Mol. Biol. 29, 135-148, 1995

A:Title: Molecular study of a light-harvesting apoprotein of Giraudyopsis stellifer (Chr

A:Reference number: S60048; MUID:96017620; PMID:7579159

A:Accession: S60048

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-216 <PAS>

A:Cross-references: UNIPARC:UPI000017CA67

R:Passaquet, C.C.

submitted to the EMBL Data Library, December 1994

A:Reference number: S71151

A:Accession: S71151

A:Molecule type: DNA

A:Residues: 42-137, 'I', 139-175, 'R', 177-216 <PAW>

A:Cross-references: UNIPARC:UPI000017CA68; EMBL:246920

C:Genetics:

A:Gene: cac

A:Genome: nuclear

C:Keywords: Chloroplast

Query Match 77.8%; Score 35; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EGAQAPL 9
|||||

Db 47 EGAQAPL 53

RESULT 13

S20970

Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - dog (fragment)

C:Species: Canis lupus familiaris (dog)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004

C:Accession: S20970

R:Canessa, C.M.; Horisberger, J.D.; Louvard, D.; Rossier, B.C.

EMBO J. 11, 1681-1687, 1992

A:Title: Mutation of a cysteine in the first transmembrane segment of Na,K-ATPase alpha

A:Reference number: S20970; MUID:92258376; PMID:1316269

A:Accession: S20970

A:Molecule type: mRNA

A:Residues: 1-220 <CAN>

A:Cross-references: UNIPARC:UPI0000087D24; GB:X66173; GB:S35173; NID:9417599; PIDN:CA046

C:Superfamily: Na(+)/K(+)-transporting ATPase alpha chain; ATPase nucleotide-binding do

C:Keywords: ATP; hydrolase

Query Match 77.8%; Score 35; DB 2; Length 220;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
|||||

Db 183 GLEGGQTPI 191

RESULT 14

PWSHNA

Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain precursor - sheep

N:Alternate names: sodium pump alpha chain; sodium/potassium-dependent ATPase alpha chain

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 31-Dec-2004

C:Accession: A01074; A35426

R:Shull, G.E.; Schwartz, A.; Lingrel, J.B.

Nature 316, 691-695, 1985

A:Title: Amino-acid sequence of the catalytic subunit of the (Na(+)+K(+)) ATPase deduced

A:Reference number: A01074; MUID:85296299; PMID:2993903

A:Accession: A01074

A:Molecule type: mRNA

A:Residues: 1-1021 <SHU>

A:Cross-references: UNIPROT:P04074; UNIPARC:UPI0000124FBE; GB:X02813; NID:gl205; PIDN:CI

J. Biol. Chem. 265, 10260-10265, 1990

A:Title: Lysine 480 is an essential residue in the putative ATP site of lamb kidney (Na,

A:Reference number: A35426; MUID:90285144; PMID:2162343

A:Accession: A35426

A>Status: preliminary

A:Molecule type: protein

A:Residues: 475-492 <HIN>

A:Cross-references: UNIPARC:UPI0000172E76

C:Comment: This is the catalytic component of the active enzyme, which catalyzes the hy

rates the electrochemical gradient of sodium and potassium, providing the energy for a

n function.

C:Comment: This enzyme is specifically inhibited by cardiac glycosides such as digoxin

C:Superfamily: Na(+)/K(+)-transporting ATPase alpha chain; ATPase nucleotide-binding do

C:Keywords: ATP; hydrolase; phosphoprotein; potassium transport; sodium transport; tran

F:6-1021/Product: Na+/K+-transporting ATPase alpha chain #status predicted <MAT>

F:94-115/Domain: transmembrane #status predicted <TM1>

F:128-144/Domain: transmembrane #status predicted <TM2>

F:289-311/Domain: transmembrane #status predicted <TM3>

F:318-346/Domain: transmembrane #status predicted <TM4>

F:585-781/Domain: ATPase nucleotide-binding domain homology <ATN>

F:785-808/Domain: transmembrane #status predicted <TM5>

F:847-872/Domain: transmembrane #status predicted <TM6>

F:951-976/Domain: transmembrane #status predicted <TM7>

F:315/Binding site: cardiac glycoside (irp) #status predicted

F:374/Active site: Asp (aspartylphosphate intermediate) #status predicted

F:506/Binding site: ATP (Lys) #status predicted

Query Match 77.8%; Score 35; DB 1; Length 1021;
Best Local Similarity 66.7%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9

|||||

Db 274 GLEGGQTPI 282

RESULT 15

S04630

Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain - horse

C:Species: Equus caballus (domestic horse)

C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 31-Dec-2004

C:Accession: S04630

R:Kano, I.; Nagai, F.; Satoh, K.; Ushiyama, K.; Nakao, T.; Kano, K.

FEBS Lett. 250, 91-98, 1989

A:Title: Structure of the alpha(1) subunit of horse Na,K-ATPase gene.

A:Reference number: S04630; MUID:89290042; PMID:2544461

A:Accession: S04630

A:Molecule type: DNA

A:Residues: 1-1021 <KAN>

A:Cross-references: UNIPROT:P18907; UNIPARC:UPI0000134FBA; EMBL:X16773; NID:gl010; PIDN

C:Genetics:

A:Introns: 4/3; 39/3; 59/3; 127/3; 165/3; 210/3; 250/1; 339/3; 406/1; 442/3; 487/3; 552/

C:Superfamily: Na(+)/K(+)-transporting ATPase alpha chain; ATPase nucleotide-binding do

C:Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium trans

F:6-1021/Product: Na+/K+-transporting ATPase alpha-1 chain #status predicted <MAT>

F:6-93/Domain: intracellular #status predicted <INT1>

F:94-118/Domain: transmembrane #status predicted <TM1>
 F:128-147/Domain: transmembrane #status predicted <TM2>
 F:148-288/Domain: intracellular #status predicted <INT2>
 F:289-311/Domain: transmembrane #status predicted <TM3>
 F:318-346/Domain: transmembrane #status predicted <TM4>
 F:347-784/Domain: intracellular #status predicted <INT3>
 F:585-781/Domain: ATPase nucleotide-binding domain homology <ATN>
 F:785-808/Domain: transmembrane #status predicted <TM5>
 F:847-872/Domain: transmembrane #status predicted <TM6>
 F:873-950/Domain: intracellular #status predicted <INT4>
 F:951-976/Domain: transmembrane #status predicted <TM7>
 F:977-1021/Domain: extracellular #status predicted <EXT>
 F:374/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F:506/Binding site: Asp (Lys) #status predicted
 F:715,719,724/Active site: Asp, Asp, Lys #status predicted

Query Match 77.8%; Score 35; DB 1; Length 1021;
 Best Local Similarity 66.7%; Pred. No. 70;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GLEGAQAPL 9
 Db 274 GLEGGQTPI 282

Search completed: March 17, 2006, 23:34:55
 Job time : 21.3333 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:21:42 ; Search time 123 Seconds
(without alignments)
51.624 Million cell updates/sec

Title: US-09-856-812b-50
Perfect score: 45
Sequence: 1 GLEGAQAPL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_05.80.*

1: uniprot_spprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	369	1	MAGAA_HUMAN
2	38	84.4	218	2	Q9M055 ARATH
3	38	84.4	2316	2	Q58GK8_PIG
4	38	84.4	2411	2	Q58G70_PIG
5	38	84.4	2513	1	FAS_BOVIN
6	37	82.2	233	2	Q61K70_DROME
7	37	82.2	338	2	Q9KN54_VIBCH
8	37	82.2	417	2	Q8XW11_RALSO
9	36	80.0	188	2	Q6SKB9_ARTAU
10	36	80.0	188	2	Q93624_PSESD
11	36	80.0	360	2	Q8X7U7_EC057
12	36	80.0	362	1	BIOB_SYNY3
13	36	80.0	484	2	Q7SG78_NEUCR
14	36	80.0	584	2	Q9FG91_XYLFA
15	36	80.0	588	1	SYD_HAEIN
16	36	80.0	588	2	Q4QNM1_HAB18
17	36	80.0	590	1	SYD_MANSN
18	36	80.0	590	1	SYD_PHOLL
19	36	80.0	598	1	SYD_YERPE
20	36	80.0	598	1	SYD_YERPS
21	36	80.0	617	2	Q6M987_NEUCR
22	36	80.0	915	2	Q91W97_MOUSE
23	36	80.0	1439	2	Q7R295_NEUCR
24	35	77.8	114	2	Q7RW28_MYCHO
25	35	77.8	114	2	O06375_MYCTU
26	35	77.8	209	2	Q8FNL9_COREF
27	35	77.8	220	2	O08735_9CARN
28	35	77.8	276	2	Q872D3_PSESM
29	35	77.8	280	2	Q8HYW7_BOVIN
30	35	77.8	306	2	Q871Q1_NEUCR
31	35	77.8	321	2	Q48722_TETNG

32	35	77.8	323	2	Q5TYR4_BRARE	Q5TYR4 brachydanio
33	35	77.8	331	2	Q503L5_BRARE	Q503L5 brachydanio
34	35	77.8	390	2	Q4WPQ0_ASPFU	Q4WPQ0 aspergillus
35	35	77.8	390	2	Q5PY60_HUMAN	Q5PY60 homo sapien
36	35	77.8	584	2	Q87AZ7_XYLFT	Q87AZ7 xylella fas
37	35	77.8	599	1	SYD_BRWCT	Q6d497 erwinia car
38	35	77.8	599	1	SYD_METCA	Q60714 methylococc
39	35	77.8	992	2	QSRBX4_PONPY	Q5rbx4 pongo pygma
40	35	77.8	1021	1	ATIAL_CANPA	P50997 canis famil
41	35	77.8	1021	1	ATIAL_HORSE	P18907 equus cabal
42	35	77.8	1021	1	ATIAL_PIG	P05024 sus scrofa
43	35	77.8	1021	1	ATIAL_SHEEP	P04074 ovis aries
44	35	77.8	1023	1	ATIAL_BUFMA	P30714 bufo marinu
45	35	77.8	1023	1	ATIAL_HUMAN	P05023 homo sapien

ALIGNMENTS

RESULT 1
MAGAA_HUMAN STANDARD; PRT; 369 AA.
AC P43363;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Melanoma-associated antigen 10 (MAGE-10 antigen).
GN Name=MAGE10; Synonyms=MAGE10;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95012457; PubMed=7927540;
RA de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,
RA de Smet C., Brasseur F., van der Bruggen P., Leche B., Lurquin C.,
RA Brasseur R., Chomez P., de Backer O., Caveness W., Boon T.;
RT "Structure, chromosomal localization, and expression of 12 genes of
the MAGE family";
RL Immunogenetics 40:360-369(1994).

[2]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
TISSUE=Skin;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McWain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S., Krzywinski M.I., Skalek U., Smalls D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Not known, though may play a role in embryonal
development and tumor transformation or aspects of tumor
progression.
-!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
such as melanoma, head and neck squamous cell carcinoma, lung
carcinoma and breast carcinoma, but not in normal tissues except
for testes and placenta.

```

CC -!- SIMILARITY: Contains 1 MAGE domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U10685; AAC68869.1; -, Genomic DNA.
CC EMBL; BC004105; AAH04105.1; -, mRNA.
CC PIR; I38659; I38659.
CC Ensembl; ENSG00000124260; Homo sapiens.
CC HGNC; HGNC:6797; MAGRA10.
CC H-InvDB; HIX0017116; -.
CC MIM; 300343; -.
CC InterPro; IPR002190; MAGE.
CC PANTHER; PTHR11736; MAGE; 2.
CC Pfam; PF01454; MAGE; 1.
CC PROSITE; PS50838; MAGE; 1.
KW Antigen; Multigene family; Tumor antigen.
FT DOMAIN 134 333 MAGE.
FT COMPIAS 54 62 Poly-Ser.
SQ SEQUENCE 369 AA; 40767 MW; 16FA3301CAB716A6 CRC64;

Query Match 100.0%; Score 45; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 2.7; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 GLEGAQAPL 9
Db 24 GLEGAQAPL 32

RESULT 2
Q9M055 ARATH PRELIMINARY; PRT; 218 AA.
AC Q9M055;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein F1116_80.
GN Names:F1116_80;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Benes V., Wurbach E., Drzonek H., Ansoerge W., Mewes H.W., Rudd S.,
RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AL161667; CAB81592.1; -, Genomic DNA.
RL PIR; T47706; T47706.
RL InterPro; IPR006566; FBD.
RL SMART; SM00579; FBD; 2.
KW Hypothetical protein.
SQ SEQUENCE 218 AA; 25389 MW; 133629BD83D20722 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 218;
Best Local Similarity 77.8%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
Db 136 GLDGVAQL 144

RESULT 3

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Q58GK8 FIG
ID Q58GK8 FIG PRELIMINARY; PRT; 2316 AA.
AC Q58GK8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Fatty acid synthase (Fragment).
GN Name=FASN;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Munoz G., Ovilio C., Rodriguez C., Silio L.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY952929; AAX51683.1; -, mRNA.
DR SMR; Q58GK8; 2001-2074, 2098-2316.
DR GO; GO:0048037; F-cofactor binding; IEA.
DR GO; GO:0016788; F-hydrolase activity, acting on ester bonds; IEA.
DR GO; GO:0016491; F-oxidoreductase activity; IEA.
DR GO; GO:0031177; F-phosphopantetheine binding; IEA.
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. .; IEA.
DR GO; GO:0016740; F-transferase activity; IEA.
DR GO; GO:0008270; F-zinc ion binding; IEA.
DR GO; GO:0009058; F-biosynthesis; IEA.
DR GO; GO:0006633; F:fatty acid biosynthesis; IEA.
DR InterPro; IPR001227; Ac transferase.
DR InterPro; IPR002085; ADH_SF_Zn.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR000794; Ketoacyl synth.
DR InterPro; IPR006163; Phappanteth_bind.
DR InterPro; IPR006162; Ppantne S.
DR InterPro; IPR000051; SAM_bind.
DR InterPro; IPR001031; Thioesterase.
DR Pfam; PF00698; Acyl transf 1; 1.
DR Pfam; PF00106; adh short; 1.
DR Pfam; PF00107; ADH_zinc_N; 1.
DR Pfam; PF00109; ketoacyl-synt C; 1.
DR Pfam; PF02801; Ketoacyl-synt; 1.
DR Pfam; PF00550; PP-binding; 1.
DR Pfam; PF00975; Thioesterase; 1.
DR PROSITE; PS50075; ACP DOMAIN; 1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
DR PROSITE; PS00012; PHOSPHOPANTHEINE; 1.
KW Fatty acid biosynthesis; Multifunctional enzyme; NAD; NADP;
KW Phosphopantetheine; Transferase.
FT NON_TER 1 2316
FT NON_TER 2316 2316
SQ SEQUENCE 2316 AA; 251137 MW; 165391CEB6CFC9AD CRC64;

Query Match 84.4%; Score 38; DB 2; Length 2316;
Best Local Similarity 87.5%; Pred. No. 4.4e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLEGAQAP 8
Db 1045 GLDGAQAP 1052

RESULT 4
Q58G70 FIG
ID Q58G70 FIG PRELIMINARY; PRT; 2411 AA.
AC Q58G70;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Fatty acid synthase (Fragment).
GN Name=FASN;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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FT ACT SITE 2483 2483 Thioesterase (By similarity).
FT BINDING 1706 1706 Pyridoxal phosphate (covalent) (By
FT BINDING 2158 2158 similarity).
FT BINDING 2158 2158 Phosphopantetheine (covalent) (By
FT MOD_RES 1 1 N-acetylmethionine (By similarity).
FT SEQUENCE 2513 AA; 274554 MW; D75B09DB855DFDAB CRC64;

Query Match 84.4%; Score 38; DB 1; Length 2513;
Best Local Similarity 87.5%; Pred. No. 4.8e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLEGQAAP 8
Db 1167 GLDGAQAP 1174
||:|||||

RESULT 6
Q6IKT0 DROME PRELIMINARY; PRT; 233 AA.
ID Q6IKT0 DROME PRELIMINARY; PRT; 233 AA.
AC Q6IKT0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE HDC11519.
ORFNames=HDC11519;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
NUCLEOTIDE SEQUENCE.
RP PubMed=14709175; DOI=10.1186/gb-2003-5-1-r3;
RA Hild M., Beckmann B., Haas S.A., Koch B., Solovjev V., Busold C.,
RA Fellenberg K., Boutros M., Vingron M., Sauer F., Hoheisel J.D.,
RA Paro R.;
RT "An integrated gene annotation and transcriptional profiling approach
RT towards the full gene content of the drosophila genome.";
RL Genome Biol. 5:RESEARCH0003.1-RESEARCH0003.17(2003).
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK002286; DAA03129.1; -; Genomic DNA.
SQ SEQUENCE 233 AA; 26432 MW; FC0A69B00C38BF6A CRC64;

Query Match 82.2%; Score 37; DB 2; Length 233;
Best Local Similarity 77.8%; Pred. No. 67;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGQAAPL 9
Db 200 GLEGSAPL 208
||||:||||

RESULT 7
Q9KN54_VIBCH PRELIMINARY; PRT; 338 AA.
ID Q9KN54_VIBCH PRELIMINARY; PRT; 338 AA.
AC Q9KN54;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein VCA0111.
GN OrderedLocusNames=VCA0111;
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=666;
RN [1]
NUCLEOTIDE SEQUENCE.
RP STRAIN=E1 Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

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RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
RA Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,
RA Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
RA Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
RA Mekalanos J.J., Venter J.C., Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; AE004353; AAF96025.1; -; Genomic_DNA.
DR FIR; B82499; B82499.
DR TIGR; VCA0111; -.
DR InterPro; IPR010732; DUF1305.
DR Pfam; PF06996; DUF1305; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 338 AA; 38367 MW; A0AF1A7F20F1F37E CRC64;

Query Match 82.2%; Score 37; DB 2; Length 338;
Best Local Similarity 77.8%; Pred. No. 98;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGQAAPL 9
Db 93 GLSQAQAPL 101
||||:||||

RESULT 8
Q8XWMI_RALSO PRELIMINARY; PRT; 417 AA.
ID Q8XWMI_RALSO PRELIMINARY; PRT; 417 AA.
AC Q8XWMI;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein RSC2453.
GN OrderedLocusNames=RSC2453; ORFNames=RS01153;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
NUCLEOTIDE SEQUENCE.
RP STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choiane N., Claudel-Renard C., Cunnac S., Demange N.,
RA Caspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Sigulier P., Tiebaut P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646070; CAD16160.1; -; Genomic_DNA.
DR HSSP; O50082; I1XK.
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR001678; Fmu NOL1/Nop2p.
DR InterPro; IPR006174; RsmE_mtfase.
DR InterPro; IPR000051; SAM_Bind.
DR Pfam; PF01189; Noll_Nop2_Fmu; 1.
DR ProDom; PD005242; NueB_region; 1.
KW Complete proteome; Hypothetical protein; Methyltransferase;
KW Transferase.
SQ SEQUENCE 417 AA; 45413 MW; E60990D227C17A20 CRC64;

Query Match 82.2%; Score 37; DB 2; Length 417;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGQAAPL 9
Db 171 GLEGAPAPL 179
||:|||||

RESULT 9

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Q6SKB9 ARTAU
ID Q6SKB9 ARTAU PRELIMINARY; PRT; 188 AA.
AC Q6SKB9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transcriptional regulator.
OS Arthrobacter aureus.
OG Plasmid pMAL.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococccineae; Micrococcaceae; Arthrobacter.
OX NCBI_TaxID=43663;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TC1;
RX PubMed=15240330; DOI=10.1128/AEM.70.7.4402-4407.2004;
RA Sajjaphan K., Shapir N., Wackett L.P., Palmer M., Blackmon B.,
RT Tomkins J., Sadowsky M.J.;
EA "Arthrobacter aureusens TC1 Atrazine Catabolism Genes trzN, atzB, and
atcZ Are Linked on a 160-Kilobase Region and Are Functional in
RT Escherichia coli.";
RT Appl. Environ. Microbiol. 70:4402-4407(2004).
RL EMBL; AV456696; AAS20053.1; -; Genomic DNA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001647; HTH_Tetr.
DR Pfam; PF00440; Tetr.N; 1.
DR PRINTS; PR00455; HTH_TETR.
DR PROSITE; PS50977; HTH_TETR_2; 1.
KW DNA-binding; Plasmid; Transcription; Transcription regulation.
SQ SEQUENCE 188 AA; 20488 MW; 5E2A6D3C048317C3 CRC64;

Query Match 80.0%; Score 36; DB 2; Length 188;
Best Local Similarity 87.5%; Pred. No. 85;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEGAQAAPL 9
DB 77 LEGAQAAPL 84
||||:|

RESULT 10
Q936Z4 PSESD PRELIMINARY; PRT; 188 AA.
AC Q936Z4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative transcriptional regulator.
GN Name=orf66;
OS Pseudomonas sp. (strain ADP).
OG Plasmid pADP-1.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=47660;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ADP;
RA Martinez B.M., Tomkins J., Wackett L.P., Wing R., Sadowsky M.J.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBSJ databases.
CC -1- FUNCTION: Repressor involved in choline regulation of the bet
genes (By similarity).
CC -1- PATHWAY: Betaine biosynthesis from choline; regulation.
DR EMBL; U66917; AAK50298.1; -; Genomic DNA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR001647; HTH_Tetr.
DR Pfam; PF00440; Tetr.N; 1.
DR PRINTS; PR00455; HTH_TETR.
DR PROSITE; PS50977; HTH_TETR_2; 1.
KW DNA-binding; Plasmid; Transcription; Transcription regulation.
SQ SEQUENCE 188 AA; 20488 MW; 5E2A6D3C048317C3 CRC64;

Query Match 80.0%; Score 36; DB 2; Length 188;
Best Local Similarity 87.5%; Pred. No. 85;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEGAQAAPL 9
DB 77 LEGAQAAPL 84
||||:|

RESULT 11
Q8X7U7 ECOS7 PRELIMINARY; PRT; 360 AA.
AC Q8X7U7; Q7AH18;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE No significant matches (Hypothetical protein EC50228).
GN OrderedLocusNames=EC50228, 20259;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.P., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=O157:H7 / Sakai / RMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo B., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL; AE005174; AAG54528.1; -; Genomic DNA.
DR EMBL; BA000007; BAB33651.1; -; Genomic DNA.
DR PIR; D85508; D85508.
DR PIR; D90657; D90657.
DR InterPro; IPR010732; DUF1305.
DR Pfam; PF06996; DUF1305; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 360 AA; 40229 MW; 3409DC46669705A CRC64;

Query Match 80.0%; Score 36; DB 2; Length 360;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLEGAQAAPL 9
DB 104 GLEGAQAAPL 112
||||:|

RESULT 12
BIOB_SYNY3
ID BIOB_SYNY3 STANDARD; PRT; 362 AA.
AC P73538;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Biotin synthase (EC 2.8.1.6) (Biotin synthetase).
GN Name=biob; OrderedLocusNames=glr1364;

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OS Synchocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
OX NCBI_TaxID=1148;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugiyama M., Saeamato S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpō S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synchocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -!- CATALYTIC ACTIVITY: Dethiobiotin + sulfur = biotin.
CC -!- COFACTOR: Binds 1 4Fe-4S cluster coordinated with 3 cysteines and
CC an exchangeable S-adenosyl-L-methionine (By similarity).
CC -!- COFACTOR: Binds 1 2Fe-2S cluster coordinated with 3 cysteines and
CC 1 arginine (By similarity).
CC -!- PATHWAY: Cofactor biosynthesis; biotin biosynthesis; biotin from
CC 6-carboxyhexanoyl-CoA: step 4 [final step].
CC -!- SIMILARITY: Belongs to the biotin and lipoic acid synthetases
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: BA000022; BAA17578.1; -; Genomic_DNA.
CC FIR: S77244; S77244.
CC InterPro: IPR010722; BATS.
CC InterPro: IPR002684; Biotin_synth.
CC InterPro: IPR006638; Elp3/MiaB/NiFB.
CC InterPro: IPR007197; Radical_SAM.
CC Pfam: PF06968; BATS; 1. SAM.
CC Pfam: PF04055; Radical_SAM; 1.
CC PIRSF: PIRSF001619; Biotin_synth; 1.
CC SMART: SM00729; Elp3; 1.
CC TIGRFAMs: TIGR00433; bioB; 1.
CC 2Fe-2S; 4Fe-4S; Biotin biosynthesis; Complete proteome; Iron;
KW Iron-sulfur; Metal-binding; Transference.
FT METAL 88 88 Iron-sulfur 1 (4Fe-4S-S-AdoMet) (By
FT similarity).
FT METAL 92 92 Iron-sulfur 1 (4Fe-4S-S-AdoMet) (By
FT similarity).
FT METAL 95 95 Iron-sulfur 1 (4Fe-4S-S-AdoMet) (By
FT similarity).
FT METAL 133 133 Iron-sulfur 2 (2Fe-2S) (By similarity).
FT METAL 170 170 Iron-sulfur 2 (2Fe-2S) (By similarity).
FT METAL 230 230 Iron-sulfur 2 (2Fe-2S) (By similarity).
FT METAL 300 300 Iron-sulfur 2 (2Fe-2S) (By similarity).
SQ SEQUENCE 362 AA; 39350 MW; BF7A16PB1CBC68B4 CRC64;
Query Match 80.0%; Score 36; DB 1; Length 362;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLEGGAAPL 9
Db 348 GLEGGAPEI 356
RESULT 13
Q7SG78 NEUCR
ID Q7SG78 NEUCR PRELIMINARY; PRT; 484 AA.
AC Q7SG78;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Predicted protein (Hypothetical protein B1014.150).

GN Name=NCU02486.1; Synonyms=B1014.150;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd K., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysseis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Kryatova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Geman S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nuebaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA German Neurospora genome project;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL: BABX01000012; EAA35844.1; -; Genomic_DNA.
CC EMBL: BX842631; CAE76400.1; -; Genomic_DNA.
CC InterPro: IPR002110; ANK.
CC Pfam: PF00023; ANK; 3.
CC PRINTS: PR01415; ANKYRIN.
CC PROSITE: PS0297; ANK_RP_REGION; 1.
CC PROSITE: PS0088; ANK_REPEAT; 1.
KW ANK repeat; Hypothetical protein; Repeat.
SQ SEQUENCE 484 AA; 53217 MW; 3007A9908AC68180 CRC64;
Query Match 80.0%; Score 36; DB 2; Length 484;
Best Local Similarity 87.5%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLEGGAAP 8
Db 3 GLEGGAAP 10
RESULT 14
Q9PG91 XYLFA
ID Q9PG91 XYLFA PRELIMINARY; PRT; 584 AA.
AC Q9PG91;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ABC transporter nitrate permease.
GN OrderedLocustNames=Xf0411;
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=9a5c;
RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,

RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barro M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.P., Camargo A.A., Camargo L.B.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Praga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Teai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen *Xylella fastidiosa*.";
RL Nature 406:151-159(2000).
CC -!- FUNCTION: Part of a binding-protein-dependent transport system.
CC -!- Probably responsible for the translocation of the substrate across
CC the membrane (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family.
DR EMBL; AE003892; AAF83221.1; -; Genomic_DNA.
DR PIR; B82810; B82810.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000515; BPD transp.
DR Pfam; PF00528; BPD transp.1; 2.
DR PROSITE; PS50928; ABC_TM1; 2.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 584 AA; 64732 MW; BE163366BFCDC4 CRC64;

Query Match 80.0%; Score 36; DB 2; Length 584;
Best Local Similarity 77.8%; Pred. No. 2.7e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
| | | | |
Db 44 GAEGARAPL 52

RESULT 15
SYD HAEIN STANDARD; PRT; 588 AA.
AC P43817;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Aspartyl-tRNA synthetase (EC 6.1.1.12) (Aspartate--tRNA ligase)
DE (AspRS).
GN Name=aspS; OrderedLocusNames=HI0317;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of *Haemophilus influenzae*
RT Rd.";
RL Science 269:496-512(1995).
CC -!- CATALYTIC ACTIVITY: ATP + L-aspartate + tRNA(Asp) = AMP +
CC diphosphate + L-aspartyl-tRNA(Asp).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the class-II aminoacyl-tRNA synthetase
CC family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U32717; AAC21981.1; -; Genomic_DNA.
DR PIR; E64061; E64061.
DR HSSP; P21889; LEQR.
DR SMR; P43817; 2-586.
DR TIGR; HI0317; -.
DR HAMAP; MF_00044; -; 1.
DR InterPro; IPR004524; Asps_bact.
DR InterPro; IPR004115; GAD.
DR InterPro; IPR012340; OB_NA_bd_sub.
DR InterPro; IPR004365; OB tRNA NA bd.
DR InterPro; IPR004364; tRNA-synt_2.
DR InterPro; IPR002312; tRNA-synt_asp.
DR InterPro; IPR006195; tRNA_ligase_II.
DR PANTHER; PTHR10218:SF2; Asps_bact; 2.
DR Pfam; PF02938; GAD; 1.
DR Pfam; PF01352; tRNA-synt_2; 1.
DR Pfam; PF01336; tRNA-anti_1.
DR PRINTS; PR01042; TRNASYNTHASP.
DR TIGRFAMs; TIGR00459; asps_bact; 1.
DR PROSITE; PS50862; AA tRNA_LIGASE_II; 1.
KW Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;
KW Nucleotide-binding; Protein biosynthesis.
SQ SEQUENCE 588 AA; 66639 MW; C53850C75270395A CRC64;

Query Match 80.0%; Score 36; DB 1; Length 588;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEGAQAPL 9
| | | | |
Db 361 GLEGVQSPI 369

Search completed: March 17, 2006, 23:34:02
Job time : 130 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 22:57:21 ; Search time 184 Seconds
(without alignments)
881.145 Million cell updates/sec

Title: US-09-856-812B-1
Perfect score: 369
Sequence: 1 MPRAPKRCMPEDLQSQS.....DTTAMASSSATGFSFSYPE 369

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 556551

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1990s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	2.7	10	3 AAY71489	Aay71489 Human MAG
2	10	2.7	10	3 AAY71529	Aay71529 Human MAG
3	10	2.7	10	3 AAY92310	Aay92310 MAGE-A1-d
4	10	2.7	10	8 ADM68734	Adm68734 Human MAG
5	10	2.7	10	8 ADM64725	Adm64725 HLA bindi
6	10	2.7	10	8 ADO43813	Ado43813 Human MAG
7	10	2.7	10	8 ADP80397	Adp80397 Human HLA
8	9	2.4	9	2 AAR79845	Aar79845 Tumour re
9	9	2.4	9	2 AAR79846	Aar79846 Tumour re
10	9	2.4	9	2 AAR79847	Aar79847 Tumour re
11	9	2.4	9	2 AAY47277	Aay47277 Immunogen
12	9	2.4	9	3 AAY71528	Aay71528 Human MAG
13	9	2.4	9	3 AAY71487	Aay71487 Human MAG
14	9	2.4	9	3 AAY71491	Aay71491 Human MAG
15	9	2.4	9	3 AAY71492	Aay71492 Human MAG
16	9	2.4	9	3 AAY92269	Aay92269 MAGE-A1 a
17	9	2.4	9	4 AAB31307	Aab31307 Exemplary
18	9	2.4	9	4 AAB31323	Aab31323 Exemplary
19	9	2.4	9	5 AAO17088	Aao17088 Human mag
20	9	2.4	9	5 AAE31265	Aae31265 Human mag
21	9	2.4	9	5 AAE31269	Aae31269 Human mag
22	9	2.4	9	5 AAE31261	Aae31261 Human mag
23	9	2.4	9	5 AAE31268	Aae31268 Human mag
24	9	2.4	9	5 AAE31267	Aae31267 Human mag

25	9	2.4	9	5 AAE31270	Aae31270 Human mag
26	9	2.4	9	5 AAE31271	Aae31271 Human mag
27	9	2.4	9	5 AAE31259	Aae31259 Human mag
28	9	2.4	9	5 AAE31272	Aae31272 Human mag
29	9	2.4	9	5 AAE31401	Aae31401 Human MAG
30	9	2.4	9	5 AAE31215	Aae31215 Human mag
31	9	2.4	9	5 AAE31263	Aae31263 Human mag
32	9	2.4	9	5 AAE31264	Aae31264 Human mag
33	9	2.4	9	5 AAE31257	Aae31257 Human mag
34	9	2.4	9	5 AAE31258	Aae31258 Human mag
35	9	2.4	9	5 AAE31262	Aae31262 Human mag
36	9	2.4	9	5 AAE31266	Aae31266 Human mag
37	9	2.4	9	5 AAE31217	Aae31217 Human mag
38	9	2.4	9	5 AAE31216	Aae31216 Human mag
39	9	2.4	9	6 ABJ19876	Abj19876 MHC bindi
40	9	2.4	9	6 ABP74235	Abp74235 Human MAG
41	9	2.4	9	6 ABP74381	Abp74381 Human MAG
42	9	2.4	9	7 ADC09240	Adc09240 Epitope w
43	9	2.4	9	7 ADC09094	Adc09094 Epitope w
44	9	2.4	9	8 ADE98042	Ade98042 Immunogen
45	9	2.4	9	8 ADG89586	Adg89586 Class I H

ALIGNMENTS

RESULT 1
AAY71489
ID AAY71489 standard; peptide; 10 AA.
XX
AC AAY71489;
XX
DT 12-OCT-2000 (first entry)
XX
DE Human MAGE-A10 decapeptide-1.
XX
KW MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
KW Immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
KW cancer; TNF; tumour necrosis factor; vaccine; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200032769-A2.
XX
PD 08-JUN-2000.
XX
PF 26-NOV-1999; 99WO-IB002018.
XX
PR 27-NOV-1998; 98GB-00026143.
XX (LUDW-) LUDWIG INST CANCER RES.
XX Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
XX WPI; 2000-412317/35.
XX
PT Novel polypeptides expressed in tumor cells useful for treating cancers
PT have an ability to complex with a major histocompatibility complex
PT molecule and comprises a specific unbroken amino acid sequence.
XX
XX Claim 9; Page 37; 80pp; English.
XX
XX The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
XX decapeptide sequences, that function as tumour rejection antigens (TRAe).
XX These peptides are capable of forming a complex with major
XX histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
XX Antigen), that are recognised by T-lymphocytes and elicit an immune
XX response from cytolytic T-lymphocytes (CTL). They function as an immune
XX response stimulator. Tumour rejection antigens are useful in prophylaxis,
XX therapy and diagnosis of tumours and are effective in controlling or
XX preventing tumour growth. The present peptide sequence is the human MAGE-
XX A10 decapeptide-1, that corresponds to residues 254-263 of the MAGE-A10

CC protein. This peptide can serve as a tumour rejection antigen (TRA) and
 CC in combination with adjuvants, can produce vaccines useful for treating a
 CC variety of tumours that express MAGE-A10

XX SQ Sequence 10 AA;

Query Match 2.7%; Score 10; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.056; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 GLYDGMHEHLI 263
 DB 1 GLYDGMHEHLI 10
 |||||

RESULT 2
 AAY71529
 ID AAY71529 standard; peptide; 10 AA.

XX AC AAY71529;

XX DT 12-OCT-2000 (first entry)

XX DE Human MAGE-A10 decapeptide-2.

XX KW MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
 KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
 KW immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
 KW cancer; TNF; tumour necrosis factor; vaccine; cytostatic.

XX OS Homo sapiens.

XX XX WO200032769-A2.

XX PD 08-JUN-2000.

XX PF 26-NOV-1999; 99WO-IB002018.

XX PR 27-NOV-1998; 98GB-00026143.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;

XX XX WPI; 2000-412317/35.

XX Novel polypeptides expressed in tumor cells useful for treating cancers
 PT have an ability to complex with a major histocompatibility complex
 PT molecule and comprises a specific unbroken amino acid sequence.

XX PS Example 3; Page 32; 80pp; English.

XX The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
 CC decapeptide sequences, that function as tumour rejection antigens (TRAs).
 CC These peptides are capable of forming a complex with major
 CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
 CC Antigen), that are recognised by T-lymphocytes and elicit an immune
 CC response from cytolytic T-lymphocytes (CTL). They function as an immune
 CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
 CC therapy and diagnosis of tumours and are effective in controlling or
 CC preventing tumour growth. The present peptide sequence is the human MAGE-
 CC A10 decapeptide-2, that corresponds to residues 182-191 of the MAGE-A10
 CC protein. This peptide conform to the HLA-A2.1 peptide binding motif and
 CC can serve as a tumour rejection antigen (TRA). This peptide failed to
 CC confer recognition by the CTLs even after LB1751-EBV cells were treated
 CC with monoclonal antibody MA2.1

XX SQ Sequence 10 AA;

Query Match 2.7%; Score 10; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.056;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 182 CMLLVFGIDV 191
 DB 1 CMLLVFGIDV 10
 |||||

RESULT 3
 AAY92310

ID AAY92310 standard; peptide; 10 AA.

XX AC AAY92310;

XX DT 10-AUG-2000 (first entry)

XX DE MAGE-A1-derived antigenic 10-mer peptide epitope.

XX KW MAGE-A4; antigen; epitope; cytotoxic T lymphocyte; CTL; complex;
 KW human leukocyte antigen; HLA.

XX OS Homo sapiens.

XX XX WO200020445-A2.

XX PD 13-APR-2000.

XX PF 15-SEP-1999; 99WO-IB001664.

XX PR 02-OCT-1998; 98US-00165863.

XX PR 09-APR-1999; 99US-00289350.

XX PA (CHAU/) CHAUX P.

XX PA (LUIT/) LUITEN R.

XX PA (DEMO/) DEMOTTE N.

XX PA (DUFE/) DUFFOUR M.

XX PA (LURQ/) LURQUIN C.

XX PA (TRAV/) TRAVERSARI C.

XX PA (STRO/) STROOBANT V.

XX PA (CORN/) CORNELIS G R.

XX PA (BOON/) BOON-FALLEUR T.

XX PA (VBRU/) VAN DER BRUGGEN P.

XX PA (SCHU/) SCHULTZ E.

XX PA (WARN/) WARNIER G.

XX XX WPI; 2000-303739/26.

XX Isolation of cytotoxic T-lymphocytes clones by successive steps of
 PT stimulation and testing of lymphocytes with antigen presenting cells
 PT which present antigens derived from different expression systems.

XX PS Example 8; Page 58; 99pp; English.

XX A novel method of isolation of cytotoxic T-lymphocytes (CTL) clones
 CC comprises successive steps of stimulation and testing of lymphocytes with
 CC antigen presenting cells (APCs) which present antigens derived from
 CC different expression systems. The CTL clones isolated recognize specific
 CC antigenic peptides of proteins, preferably of the MAGE family. The APC is
 CC autologous and each expression systems is different from at least one of
 CC the other expression systems, therefore isolating a cytotoxic T cell
 CC clone specific for the protein. The method can also be used to identify
 CC an antigenic peptide epitope. Isolated CTL clones specific for a
 CC peptide/human leukocyte antigen (HLA) complex are claimed. The CTL cells
 CC specific for the complexes, peptides or cells which present the complexes
 CC on the cell surface are useful for treating pathological conditions
 CC characterized by abnormal expression of the complexes

XX SQ Sequence 10 AA;

Query Match 2.7%; Score 10; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.056;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 SDPARYEFLW 298
 Db 1 SDPARYEFLW 10
 RESULT 4
 ADM68734
 ID ADM68734 standard; peptide; 10 AA.
 XX
 AC ADM68734;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human MAGE-2-related peptide SeqID83.
 XX
 KW MAGE-C2; antigenic; MAGE family; tumour rejection antigen precursor;
 KW TRAP; cytostatic; gene therapy; HLA-A2; cancer; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004029071-A2.
 XX
 PD 08-APR-2004.
 XX
 PF 26-SEP-2003; 2003WO-US030031.
 XX
 PR 27-SEP-2002; 2002US-0413844P.
 PR 18-DEC-2002; 2002US-0413983P.
 PR 02-APR-2003; 2003US-0459263P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Ma W, Germeau C, Van Den Eynde B, Coulie P, Falleur TB;
 XX
 DR WPI; 2004-305144/28.
 XX
 PT New peptide derived from MAGE-C2 and that binds to HLA-A2, useful for
 PT preparing a composition for treating a disorder characterized by the
 PT presence of complexes of HLA-A2 and MAGE-C2 molecules, e.g., cancer.
 XX
 PS Example 3; SEQ ID NO 83; 115pp; English.
 XX
 CC This invention relates to novel isolated peptides derived from MAGE-C2
 CC which are antigenic. The peptides are derived from the MAGE family of
 CC tumour rejection antigen precursors (TRAP molecules). The invention may
 CC be useful for the production of compounds with a cytostatic activity or
 CC for gene therapy. The peptide is useful for preparing a composition for
 CC treating a disorder characterized by the presence of complexes of HLA-A2
 CC and MAGE-C2 molecules, for example cancer. The present sequence is that
 CC of a human MAGE-C2-related peptide which was used in the exemplification
 CC of the invention.
 XX
 SQ Sequence 10 AA;
 Query Match 2.7%; Score 10; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.056; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 185 LVFGIDVKEV 194
 Db 1 LVFGIDVKEV 10
 RESULT 5
 ADN64725
 ID ADN64725 standard; peptide; 10 AA.
 XX
 AC ADN64725;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE HLA binding peptide #1325.

XX
 KW cytostatic; hepatotropic; virucide; antiinflammatory; anti-HIV;
 KW gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome;
 KW prostate specific antigen; prostate specific membrane antigen;
 KW hepatitis B virus antigen; hepatitis C virus antigen;
 KW malignant melanoma antigen; MAGE; Epstein Barr virus; cancer;
 KW prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;
 KW chondyoma acuminatum.
 XX
 OS Unidentified.
 XX
 PN WO2004031211-A2.
 XX
 PD 15-APR-2004.
 XX
 PF 03-OCT-2003; 2003WO-US031308.
 XX
 PR 03-OCT-2002; 2002US-0416207P.
 PR 08-OCT-2002; 2002US-0417269P.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Sidney J, Southwood S, Sette A;
 XX
 DR WPI; 2004-347953/32.
 XX
 PT New composition of peptides and nucleic acids capable of binding Major
 PT Histocompatibility Complex molecules, useful for diagnosing, preventing
 PT or treating viral infections or cancer, such as prostate cancer,
 PT hepatitis B or AIDS.
 XX
 PS Claim 1; SEQ ID NO 1325; 186pp; English.
 XX
 CC The invention relates to a novel composition comprising one or more
 CC peptides or nucleic acids encoding an HLA binding peptide. The
 CC composition further comprises an HTL epitope. It also comprises a spacer
 CC molecule, a carrier, an MHC targeting sequence or a lipid. The peptides
 CC are incorporated as part of a liposome. The peptide is from an antigen
 CC selected from prostate specific antigen (PSA), prostate specific membrane
 CC antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV)
 CC antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, human
 CC immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2),
 CC Papilloma virus, Laesa virus, Mycobacterium tuberculosis (MT), p53,
 CC murine p53 (mp53), CEA, HER2/neu, and tyrosine kinase related protein
 CC (TKP). The composition is useful for preventing or treating viral
 CC infections or cancer, such as prostate cancer, hepatitis B, hepatitis C,
 CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondyoma
 CC acuminatum. The composition is also used for diagnosing such diseases.
 CC This sequence represents a peptide of the invention.
 XX
 SQ Sequence 10 AA;
 Query Match 2.7%; Score 10; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.056; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 277 QENYLEYRQV 286
 Db 1 QENYLEYRQV 10
 RESULT 6
 ADO43813
 ID ADO43813 standard; peptide; 10 AA.
 XX
 AC ADO43813;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Human MAGE HLA class I-binding peptide #12.
 XX
 KW Human; MAGE-A4; human leukocyte antigen; HLA class I-binding peptide;
 KW HLA-B37; CD8+ cytotoxic T lymphocyte; cancer; melanoma; myeloma;

CC strong complex with HLA-2 which may be used diagnostically and as an
 CC immunogen in the production of antibodies. They may also be used as
 CC targets for the generation of cytolytic T cell clones. This cytolytic T
 CC cell clone is used to treat a cancerous condition characterised by the
 CC fact that the cancer cells present the HLA-2/ peptide complex on their
 CC surface
 CC
 SQ Sequence 9 AA;

Query Match 2.4%; Score 9; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 FLLEKYQMK 152
 DB 1 FLLEKYQMK 9
 |||||

RESULT 9

AAR79846
 ID AAR79846 standard; peptide; 9 AA.
 XX
 AC AAR79846;

DT 08-MAY-1996 (first entry)

DE Tumour rejection antigen peptide #10.

KW Tumour rejection antigen; MAGE tumour rejection precursor; complex;
 KW HLA-2; immunogen; antibody; cytolytic T cell clone.

OS Synthetic.

PN WO9525740-A1.

PD 28-SEP-1995.

PF 22-MAR-1995; 95WO-US003657.

PR 24-MAR-1994; 94US-00217186.

PR 17-JUN-1994; 94US-00261160.

PR 15-AUG-1994; 94US-00290381.

XX (LUDW-) LUDWIG INST CANCER RES.

PA (UYOX-) UNIV OXFORD.

PA (UYLE-) RIJKSUNIV LEIDEN.

XX Townsend A, Bastin J, Boon-Falleur T, Van Der Bruggen P, Coulie P;
 PI Gajewski T, Melief CJ, Visseren MW, Kast WM;

XX WPI; 1995-344584/44.

XX Isolated peptide(s) which complex with HLA-A2 - used as immunogens for
 PT the prodn. of antibodies, or as targets for the generation of cytolytic T
 PT cell clones...

XX Claim 15; Page 23; 44pp; English.

XX The peptides given in AAR79845-47 represent tumour rejection antigens
 CC derived from MAGE tumour rejection precursor. These peptides form a
 CC strong complex with HLA-2 which may be used diagnostically and as an
 CC immunogen in the production of antibodies. They may also be used as
 CC targets for the generation of cytolytic T cell clones. This cytolytic T
 CC cell clone is used to treat a cancerous condition characterised by the
 CC fact that the cancer cells present the HLA-2/ peptide complex on their
 CC surface
 CC

XX Sequence 9 AA;

Query Match 2.4%; Score 9; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GLEGAQAPL 32
 DB 1 GLEGAQAPL 9
 |||||

RESULT 10

AAR79847
 ID AAR79847 standard; peptide; 9 AA.
 XX
 AC AAR79847;

DT 08-MAY-1996 (first entry)

XX Tumour rejection antigen peptide #11.

KW Tumour rejection antigen; MAGE tumour rejection precursor; complex;
 KW HLA-2; immunogen; antibody; cytolytic T cell clone.

OS Synthetic.

PN WO9525740-A1.

PD 28-SEP-1995.

PF 22-MAR-1995; 95WO-US003657.

PR 24-MAR-1994; 94US-00217186.

PR 17-JUN-1994; 94US-00261160.

PR 15-AUG-1994; 94US-00290381.

XX (LUDW-) LUDWIG INST CANCER RES.

PA (UYOX-) UNIV OXFORD.

PA (UYLE-) RIJKSUNIV LEIDEN.

XX Townsend A, Bastin J, Boon-Falleur T, Van Der Bruggen P, Coulie P;
 PI Gajewski T, Melief CJ, Visseren MW, Kast WM;

XX WPI; 1995-344584/44.

XX Isolated peptide(s) which complex with HLA-A2 - used as immunogens for
 PT the prodn. of antibodies, or as targets for the generation of cytolytic T
 PT cell clones.

XX Claim 15; Page 23; 44pp; English.

XX The peptides given in AAR79845-47 represent tumour rejection antigens
 CC derived from MAGE tumour rejection precursor. These peptides form a
 CC strong complex with HLA-2 which may be used diagnostically and as an
 CC immunogen in the production of antibodies. They may also be used as
 CC targets for the generation of cytolytic T cell clones. This cytolytic T
 CC cell clone is used to treat a cancerous condition characterised by the
 CC fact that the cancer cells present the HLA-2/ peptide complex on their
 CC surface
 CC

XX Sequence 9 AA;

Query Match 2.4%; Score 9; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 FIEGYCTPE 243
 DB 1 FIEGYCTPE 9
 |||||

RESULT 11

AAY47277
 ID AAY47277 standard; peptide; 9 AA.
 XX
 AC AAY47277;

DT 01-DEC-1999 (first entry)

XX

DE Immunogenic peptide having a human leukocyte antigen binding motif #1888.
 XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9945954-A1.
 XX
 PD 16-SEP-1999.
 XX
 PF 13-MAR-1998; 98WO-US005039.
 XX
 PR 13-MAR-1998; 98WO-US005039.
 XX
 PA (EPTM-) EPTMUNE INC.
 XX
 PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
 XX WPI; 1999-551214/46.
 DR
 XX New immunogenic peptides with HLA binding motif, useful in treatment and
 PT diagnosis of cancers and viral diseases.
 PT
 XX Claim 1; Page 101; 150pp; English.
 PS
 CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also known
 CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
 CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
 CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
 CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
 CC (CTLs) which destroy antigen-bearing cells are normally induced by an
 CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
 CC than the intact foreign antigen itself, and are particularly important in
 CC tumour rejection and in fighting viral infections. The peptides are
 CC therefore useful therapeutically to treat or prevent viral infections and
 CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
 CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
 CC elicit an immune response in individuals susceptible or otherwise at risk
 CC of viral infection or cancer, or used to treat chronic or acute
 CC conditions. They are also useful diagnostically, and can be used to
 CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
 CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
 CC patient. The polynucleotides encoding the immunogenic peptides are also
 CC useful therapeutically and for immunisation as above
 XX
 SQ Sequence 9 AA;
 Query Match 2.4%; Score 9; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 294 YEFLWGPR 302
 DB 1 YEFLWGPR 9
 |||||
 RESULT 12
 AAY71528
 ID AAY71528 standard; peptide; 9 AA.
 XX
 AC AAY71528;
 XX
 DT 12-OCT-2000 (first entry)
 DE Human MAGE-A10 nonapeptide-5.
 XX
 KW MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;

KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
 KW immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
 XX cancer; TNP; tumour necrosis factor; vaccine; cytostatic.
 OS Homo sapiens.
 XX WO200032769-A2.
 PN
 XX 08-JUN-2000.
 PD
 XX 26-NOV-1999; 99WO-IB002018.
 PF
 XX 27-NOV-1998; 98GB-00026143.
 PR
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 XX Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
 PI WPI; 2000-412317/35.
 XX
 DR Novel polypeptides expressed in tumor cells useful for treating cancers
 PT have an ability to complex with a major histocompatibility complex
 PT molecule and comprises a specific unbroken amino acid sequence.
 PT
 XX Example 3; Page 31; 80pp; English.
 PS
 XX The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
 CC decapeptide sequences, that function as tumour rejection antigens (TRAs).
 CC These peptides are capable of forming a complex with major
 CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
 CC Antigen), that are recognised by T-lymphocytes and elicit an immune
 CC response from cytolytic T-lymphocytes (CTL). They function as an immune
 CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
 CC preventing tumour growth. The present peptide sequence is the human MAGE-
 CC A10 nonapeptide-5, that corresponds to residues 183-191 of the MAGE-A10
 CC protein. This peptide conform to the HLA-A2.1 peptide binding motif and
 CC can serve as a tumour rejection antigen (TRA). This peptide failed to
 CC confer recognition by the CTLs even after LB1751-EBV cells were treated
 CC with monoclonal antibody MA2.1
 XX
 SQ Sequence 9 AA;
 Query Match 2.4%; Score 9; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 183 MLLVFGIDV 191
 DB 1 MLLVFGIDV 9
 |||||
 RESULT 13
 AAY71487
 ID AAY71487 standard; peptide; 9 AA.
 XX
 AC AAY71487;
 XX
 DT 12-OCT-2000 (first entry)
 DE Human MAGE-A10 nonapeptide-1.
 XX
 KW MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
 KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
 KW immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
 KW cancer; TNP; tumour necrosis factor; vaccine; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200032769-A2.
 XX
 PD 08-JUN-2000.
 XX

PF 26-NOV-1999; 99WO-IB002018.
XX
PR 27-NOV-1998; 98GB-00026143.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
XX
DR WPI; 2000-412317/35.
XX
PT Novel polypeptides expressed in tumor cells useful for treating cancers
PT have an ability to complex with a major histocompatibility complex
PT molecule and comprises a specific unbroken amino acid sequence.
XX
PS Claim 8; Page 36; 80pp; English.
XX
CC The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
CC decapeptide sequences, that function as tumour rejection antigens (TRA).
CC These peptides are capable of forming a complex with major
CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
CC Antigen), that are recognised by T-lymphocytes and elicit an immune
CC response from cytolytic T-lymphocytes (CTL). They function as an immune
CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
CC therapy and diagnosis of tumours and are effective in controlling or
CC preventing tumour growth. The present peptide sequence is the human MAGE-
CC A10 nonapeptide-1, that corresponds to residues 254-262 of the MAGE-A10
CC protein. This peptide can serve as a tumour rejection antigen (TRA) and
CC in combination with adjuvants, can produce vaccines useful for treating a
CC variety of tumours that express MAGE-A10
XX
SQ Sequence 9 AA;
Query Match 2.4%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 254 GLYDGMHL 262
DB 1 GLYDGMHL 9
RESULT 14
AA71491
ID AAY71491 standard; peptide; 9 AA.
XX
AC AAY71491;
XX
DT 12-OCT-2000 (first entry)
XX
DE Human MAGE-A10 nonapeptide-2.
XX
KW MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
KW immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
KW cancer; TNF; tumour necrosis factor; vaccine; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200032769-A2.
XX
PD 08-JUN-2000.
XX
PF 26-NOV-1999; 99WO-IB002018.
XX
PR 27-NOV-1998; 98GB-00026143.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
XX
DR WPI; 2000-412317/35.
XX
PT Novel polypeptides expressed in tumor cells useful for treating cancers

PT have an ability to complex with a major histocompatibility complex
PT molecule and comprises a specific unbroken amino acid sequence.
XX
PS Claim 5; Page 36; 80pp; English.
XX
CC The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
CC decapeptide sequences, that function as tumour rejection antigens (TRA).
CC These peptides are capable of forming a complex with major
CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
CC Antigen), that are recognised by T-lymphocytes and elicit an immune
CC response from cytolytic T-lymphocytes (CTL). They function as an immune
CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
CC therapy and diagnosis of tumours and are effective in controlling or
CC preventing tumour growth. The present peptide sequence is the human MAGE-
CC A10 nonapeptide-2, that corresponds to residues 144-152 of the MAGE-A10
CC protein. This peptide can serve as a tumour rejection antigen (TRA) and
CC in combination with adjuvants, can produce vaccines useful for treating a
CC variety of tumours that express MAGE-A10
XX
SQ Sequence 9 AA;
Query Match 2.4%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 144 FLLFKYQMK 152
DB 1 FLLFKYQMK 9
RESULT 15
AA71492
ID AAY71492 standard; peptide; 9 AA.
XX
AC AAY71492;
XX
DT 12-OCT-2000 (first entry)
XX
DE Human MAGE-A10 nonapeptide-3.
XX
KW MAGE-A10; human; Tumour Rejection Antigen; TRA; Human Leucocyte Antigen;
KW HLA; Major Histocompatibility Complex; MHC; cytolytic T-lymphocyte; CTL;
KW immune response stimulator; prophylaxis; therapy; diagnosis; tumour;
KW cancer; TNF; tumour necrosis factor; vaccine; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200032769-A2.
XX
PD 08-JUN-2000.
XX
PF 26-NOV-1999; 99WO-IB002018.
XX
PR 27-NOV-1998; 98GB-00026143.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Huang L, Van Pel A, Brasseur F, De Plaen E, Boon T;
XX
DR WPI; 2000-412317/35.
XX
PT Novel polypeptides expressed in tumor cells useful for treating cancers
PT have an ability to complex with a major histocompatibility complex
PT molecule and comprises a specific unbroken amino acid sequence.
XX
PS Claim 5; Page 36; 80pp; English.
XX
CC The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and
CC decapeptide sequences, that function as tumour rejection antigens (TRA).
CC These peptides are capable of forming a complex with major
CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte
CC Antigen), that are recognised by T-lymphocytes and elicit an immune
CC response from cytolytic T-lymphocytes (CTL). They function as an immune
CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
CC therapy and diagnosis of tumours and are effective in controlling or
CC preventing tumour growth. The present peptide sequence is the human MAGE-
CC A10 nonapeptide-2, that corresponds to residues 144-152 of the MAGE-A10
CC protein. This peptide can serve as a tumour rejection antigen (TRA) and
CC in combination with adjuvants, can produce vaccines useful for treating a
CC variety of tumours that express MAGE-A10

CC response stimulator. Tumour rejection antigens are useful in prophylaxis,
CC therapy and diagnosis of tumours and are effective in controlling or
CC preventing tumour growth. The present peptide sequence is the human MAGE-
CC A10 nonapeptide-3, that corresponds to residues 235-243 of the MAGE-A10
CC protein. This peptide can serve as a tumour rejection antigen (TRA) and
CC in combination with adjuvants, can produce vaccines useful for treating a
CC variety of tumours that express MAGE-A10

XX
SQ Sequence 9 AA;
Query Match 2.4%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 235 FIEGYCTPE 243
|||||
Db 1 FIEGYCTPE 9

Search completed: March 17, 2006, 23:00:41
Job time : 185 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:04:51 ; Search time 47 Seconds
(without alignments)
649.092 Million cell updates/sec

Title: US-09-856-812B-1
Perfect score: 369
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Scoring table: OLIGO 3
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

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Total number of hits satisfying chosen parameters: 130918

Minimum DB seq length: 0
Maximum-DB seq length: 10

Post-processing: Listing first 45 summaries

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6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	2.7	10	2	US-09-165-863-41
2	10	2.7	10	2	US-09-289-350-41
3	10	2.7	10	2	US-09-806-769-41
4	9	2.4	9	2	US-09-165-863-42
5	9	2.4	9	2	US-09-289-350-42
6	9	2.4	9	2	US-09-533-499B-18
7	9	2.4	9	2	US-09-533-499B-19
8	9	2.4	9	2	US-09-533-499B-20
9	9	2.4	9	2	US-09-806-769-42
10	9	2.4	9	2	US-09-865-548A-39
11	8	2.2	9	1	US-08-465-167A-35
12	8	2.2	9	1	US-08-465-167A-38
13	8	2.2	9	2	US-08-159-339A-97
14	8	2.2	10	1	US-08-159-339A-98
15	8	2.2	10	1	US-08-465-167A-48
16	8	2.2	10	2	US-08-159-339A-96
17	7	1.9	9	1	US-08-217-188A-47
18	7	1.9	9	1	US-08-195-186A-4
19	7	1.9	9	1	US-08-217-186-6
20	7	1.9	9	1	US-08-261-160A-6
21	7	1.9	9	1	US-08-687-226-47
22	7	1.9	9	1	US-08-106-981-11
23	7	1.9	9	1	US-08-465-167A-5
24	7	1.9	9	1	US-08-787-547-50
25	7	1.9	9	1	US-08-787-547-52
26	7	1.9	9	1	US-08-498-461-9
27	7	1.9	9	1	US-08-290-381A-6

28	7	1.9	9	1	US-08-902-516-22	Sequence 22, Appl
29	7	1.9	9	1	US-08-902-516-24	Sequence 24, Appl
30	7	1.9	9	1	US-09-036-582-2	Sequence 2, Appl
31	7	1.9	9	1	US-09-036-582-4	Sequence 4, Appl
32	7	1.9	9	2	US-08-880-963-19	Sequence 19, Appl
33	7	1.9	9	2	US-08-667-725B-47	Sequence 47, Appl
34	7	1.9	9	2	US-08-785-831-47	Sequence 47, Appl
35	7	1.9	9	2	US-09-064-964-9	Sequence 9, Appl
36	7	1.9	9	2	US-09-007-748-47	Sequence 47, Appl
37	7	1.9	9	2	US-09-183-931-28	Sequence 28, Appl
38	7	1.9	9	2	US-09-183-931-30	Sequence 30, Appl
39	7	1.9	9	2	US-09-183-931-35	Sequence 35, Appl
40	7	1.9	9	2	US-09-183-931-38	Sequence 38, Appl
41	7	1.9	9	2	US-09-183-706-5	Sequence 5, Appl
42	7	1.9	9	2	US-09-183-706-7	Sequence 7, Appl
43	7	1.9	9	2	US-09-162-934-2	Sequence 2, Appl
44	7	1.9	9	2	US-09-061-388-19	Sequence 19, Appl
45	7	1.9	9	2	US-09-166-448-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-09-165-863-41
; Sequence 41, Application US/09165863
; Patent No. 6407063
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Duffour, Marie-Therese
; APPLICANT: Demotte, Nathalie
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Cornelis, Guy
; APPLICANT: Stroobant, Vincent
; APPLICANT: Lurquin, Christophe
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Chau, Pascal
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; FILE OF INVENTION: PROCEDURE
; FILE REFERENCE: 11727
; CURRENT APPLICATION NUMBER: US/09/165,863
; CURRENT FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 10
; TYPE: PPT
; ORGANISM: Human MAGE-A1 peptide
US-09-165-863-41

Query Match 2.7%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.019; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 SDPARYEFLW 298
Db 1 SDPARYEFLW 10
|||||

RESULT 2
US-09-289-350-41
; Sequence 41, Application US/09289350
; Patent No. 6531451
; GENERAL INFORMATION:
; APPLICANT: Chau, Pascal
; APPLICANT: Luiten, Rosalie
; APPLICANT: Demotte, Nathalie
; APPLICANT: Duffour, Marie-Therese
; APPLICANT: Lurquin, Christophe
; APPLICANT: Traversari, Catia
; APPLICANT: Stroobant, Vincent
; APPLICANT: Cornelis, Guy R.
; APPLICANT: Boon-Falleur, Thierry

```
; APPLICANT: Van Der Bruggen, Pierre
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; FILE OF INVENTION: PROCEDURE
; FILE REFERENCE: 117272
; CURRENT APPLICATION NUMBER: US/09/289,350
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/165,863
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human MAGE-A1 peptide
US-09-289-350-41

Query Match          2.7%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      289 SDPARYEFLW 298
Db      1 SDPARYEFLW 10
|||||

RESULT 3
US-09-806-769-41
; Sequence 41, Application US/09806769
; Patent No. 6710172
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Luiten, Rosalie
; APPLICANT: Demotte, Nathalie
; APPLICANT: Deffour, Marie-Therese
; APPLICANT: Lurquin, Christophe
; APPLICANT: Traversari, Catia
; APPLICANT: Stroobant, Vincent
; APPLICANT: Cornelis, Guy R.
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Van Der Bruggen, Pierre
; APPLICANT: Schultz, Erwin
; APPLICANT: Warnier, Guy
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; FILE OF INVENTION: PROCEDURE
; FILE REFERENCE: 117272
; CURRENT APPLICATION NUMBER: US/09/806,769
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 09/165,863
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 09/289,350
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/806,769
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human MAGE-A1 peptide
US-09-806-769-41

Query Match          2.7%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      289 SDPARYEFLW 298
Db      1 SDPARYEFLW 10
|||||

RESULT 4
US-09-165-863-42
; Sequence 42, Application US/09165863
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; Patent No. 6407063
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Duffour, Marie-Therese
; APPLICANT: Demotte, Nathalie
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Cornelis, Guy
; APPLICANT: Stroobant, Vincent
; APPLICANT: Lurquin, Christophe
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Chaux, Pascal
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; FILE OF INVENTION: PROCEDURE
; FILE REFERENCE: 11727
; CURRENT APPLICATION NUMBER: US/09/165,863
; CURRENT FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human MAGE-A1 peptide
US-09-165-863-42

Query Match          2.4%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      290 DPARYEFLW 298
Db      1 DPARYEFLW 9
|||||

RESULT 5
US-09-289-350-42
; Sequence 42, Application US/09289350
; Patent No. 6531451
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Luiten, Rosalie
; APPLICANT: Demotte, Nathalie
; APPLICANT: Deffour, Marie-Therese
; APPLICANT: Lurquin, Christophe
; APPLICANT: Traversari, Catia
; APPLICANT: Stroobant, Vincent
; APPLICANT: Cornelis, Guy R.
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Van Der Bruggen, Pierre
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; FILE OF INVENTION: PROCEDURE
; FILE REFERENCE: 117272
; CURRENT APPLICATION NUMBER: US/09/289,350
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/165,863
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human MAGE-A1 peptide
US-09-289-350-42

Query Match          2.4%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      290 DPARYEFLW 298
Db      1 DPARYEFLW 9
|||||
```

RESULT 6

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US-09-533-499B-18
; Sequence 18, Application US/09533499B
; Patent No. 6682731
; GENERAL INFORMATION:
; APPLICANT: Townsend, Alan; Bastin, Judy; Boon-Falleur, Thierry; van der
; Bruggen, Pierre; Coullie, Pierre; Gajewski, Thomas; Melief,
; Cornelis J.M.; Visseren, M.W.; Kast, W.M.
; TITLE OF INVENTION: ISOLATED PEPTIDES DERIVED FROM MAGE TUMOR
; REJECTION ANTIGEN PRECURSORS WHICH COMPLEX WITH
; HLA-A2 MOLECULES
;
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/533,499B
; FILING DATE: 23-Mar-2000
; CLASSIFICATION: 530
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/722,115
; FILING DATE: February 6, 1997
; APPLICATION NUMBER: 08/290,381
; FILING DATE: 15-August-1994
; APPLICATION NUMBER: 08/261,160
; FILING DATE: 17-June-1994
; APPLICATION NUMBER: 08/217,186
; FILING DATE: 24-March-1994
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-March-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6682731man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5327.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-533-499B-18
;
; Query Match 2.4%; Score 9; DB 2; Length 9;
; Best Local Similarity 100.0%; Pred. No. 4.6e+05;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 144 FLLFKYQMK 152
; DB 1 FLLFKYQMK 9
;
; RESULT 7
US-09-533-499B-19
; Sequence 19, Application US/09533499B
; Patent No. 6682731
; GENERAL INFORMATION:
; APPLICANT: Townsend, Alan; Bastin, Judy; Boon-Falleur, Thierry; van der
; Bruggen, Pierre; Coullie, Pierre; Gajewski, Thomas; Melief,
; Cornelis J.M.; Visseren, M.W.; Kast, W.M.
; TITLE OF INVENTION: ISOLATED PEPTIDES DERIVED FROM MAGE TUMOR
; REJECTION ANTIGEN PRECURSORS WHICH COMPLEX WITH
; HLA-A2 MOLECULES
;
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/533,499B
; FILING DATE: 23-Mar-2000
; CLASSIFICATION: 530
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/722,115
; FILING DATE: February 6, 1997
; APPLICATION NUMBER: 08/290,381
; FILING DATE: 15-August-1994
; APPLICATION NUMBER: 08/261,160
; FILING DATE: 17-June-1994
; APPLICATION NUMBER: 08/217,186
; FILING DATE: 24-March-1994
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-March-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6682731man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5327.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-533-499B-18
;
; Query Match 2.4%; Score 9; DB 2; Length 9;
; Best Local Similarity 100.0%; Pred. No. 4.6e+05;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 144 FLLFKYQMK 152
; DB 1 FLLFKYQMK 9
;
; RESULT 7
US-09-533-499B-19
; Sequence 19, Application US/09533499B
; Patent No. 6682731
; GENERAL INFORMATION:
; APPLICANT: Townsend, Alan; Bastin, Judy; Boon-Falleur, Thierry; van der
; Bruggen, Pierre; Coullie, Pierre; Gajewski, Thomas; Melief,
; Cornelis J.M.; Visseren, M.W.; Kast, W.M.
; TITLE OF INVENTION: ISOLATED PEPTIDES DERIVED FROM MAGE TUMOR
; REJECTION ANTIGEN PRECURSORS WHICH COMPLEX WITH
; HLA-A2 MOLECULES
;
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/533,499B
; FILING DATE: 23-Mar-2000
; CLASSIFICATION: 530
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/722,115
; FILING DATE: February 6, 1997
; APPLICATION NUMBER: 08/290,381
; FILING DATE: 15-August-1994
; APPLICATION NUMBER: 08/261,160
; FILING DATE: 17-June-1994
; APPLICATION NUMBER: 08/217,186
; FILING DATE: 24-March-1994
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-March-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6682731man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5327.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-533-499B-19
;
; Query Match 2.4%; Score 9; DB 2; Length 9;
; Best Local Similarity 100.0%; Pred. No. 4.6e+05;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 235 FIEGYCTPE 243
; DB 1 FIEGYCTPE 9
;
; RESULT 8
US-09-533-499B-20
; Sequence 20, Application US/09533499B
; Patent No. 6682731
; GENERAL INFORMATION:
; APPLICANT: Townsend, Alan; Bastin, Judy; Boon-Falleur, Thierry; van der
; Bruggen, Pierre; Coullie, Pierre; Gajewski, Thomas; Melief,
; Cornelis J.M.; Visseren, M.W.; Kast, W.M.
; TITLE OF INVENTION: ISOLATED PEPTIDES DERIVED FROM MAGE TUMOR
; REJECTION ANTIGEN PRECURSORS WHICH COMPLEX WITH
; HLA-A2 MOLECULES
;
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
```

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/533,499B
; FILING DATE: 23-Mar-2000
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/722,115
; FILING DATE: February 6, 1997
; APPLICATION NUMBER: 08/290,381
; FILING DATE: 15-August-1994
; APPLICATION NUMBER: 08/261,160
; FILING DATE: 17-June-1994
; APPLICATION NUMBER: 08/217,186
; FILING DATE: 24-March-1994
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-March-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6682731man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5327.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-533-499B-20

Query Match                2.4%; Score 9; DB 2; Length 9;
Best Local Similarity      100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      24  GLEGAQAPL 32
Db      1  GLEGAQAPL 9

RESULT 9
US-09-806-769-42
; Sequence 42, Application US/09806769
; Patent No. 6710172
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Luiten, Rosalie
; APPLICANT: Demotte, Nathalie
; APPLICANT: Deffour, Marie-Therese
; APPLICANT: Lurquin, Christophe
; APPLICANT: Traversari, Catia
; APPLICANT: Stroobant, Vincent
; APPLICANT: Cornelis, Guy R.
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Van Der Bruggen, Pierre
; APPLICANT: Schultz, Erwin
; APPLICANT: Warnier, Guy
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; FILE REFERENCE: 11727zv
; CURRENT APPLICATION NUMBER: US/09/806,769
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 09/165,863
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 09/289,350
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/806,769
; PRIOR FILING DATE: 2001-04-02

;
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human MAGE-A1 peptide
US-09-806-769-42

Query Match                2.4%; Score 9; DB 2; Length 9;
Best Local Similarity      100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      290 DPARYEFLLW 298
Db      1  DPARYEFLLW 9

RESULT 10
US-09-865-548A-39
; Sequence 39, Application US/09865548A
; Patent No. 6867283
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULES
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-39

Query Match                2.4%; Score 9; DB 2; Length 9;
Best Local Similarity      100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      254 GLYDGMHHL 262
Db      1  GLYDGMHHL 9

RESULT 11
US-08-465-167A-35
; Sequence 35, Application US/08465167A
; Patent No. 5750395
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Sette, Alessandro D.
; APPLICANT: Sidney, John C.
; TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 98111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; 
```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/103,623
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60-1
TELEPHONE: 206-467-9600
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-167A-35

Query Match 2.2%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 SDPARYEP 296
Db 2 SDPARYEP 9

RESULT 12
US-08-465-167A-38
Sequence 38, Application US/08465167A
Patent No. 5750395
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Livingston, Brian D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sidney, John C.
TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 98111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/103,623
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-167A-38

Query Match 2.2%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 EPLMGFRA 302
Db 1 EPLMGFRA 8

RESULT 13
US-08-159-339A-97
Sequence 97, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Eteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-0050300S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-97

Query Match 2.2%; Score 8; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 LESVIKRY 169
|||||
Db 2 LESVIKRY 9

RESULT 14
US-08-159-339A-98
; Sequence 98, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Eteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-98

Query Match 2.2%; Score 8; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 185 LVFGIDVK 192
|||||
Db 2 LVFGIDVK 9

RESULT 15
US-08-465-167A-48
; Sequence 48, Application US/08465167A
; Patent No. 5750395
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.

; APPLICANT: Livingston, Brian D.
; APPLICANT: Sette, Alessandro D.
; APPLICANT: Sidney, John C.
; TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 98111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,167A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/103,623
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-60-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-465-167A-48
Query Match 2.2%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 289 SDPARYEF 296
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Db 3 SDPARYEF 10

Search completed: March 17, 2006, 23:06:11
Job time : 47 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 23:05:32 ; Search time 160 Seconds
(without alignments)
963.619 Million cell updates/sec

Title: US-09-856-812B-1
Perfect score: 369
Sequence: 1 MPRAKRCRQMPEDLSQS.....DTTAWASASSATGFSFSYPE 369

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Searched: 1867569 seqs, 417829326 residues

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Total number of hits satisfying chosen parameters: 232507

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : Published Applications_AA_Main:*
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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	2.7	10	4	US-10-218-095-59
2	10	2.7	10	4	US-10-753-158-41
3	10	2.7	10	4	US-10-670-472A-83
4	9	2.4	9	3	US-09-933-708-3
5	9	2.4	9	3	US-09-865-548A-39
6	9	2.4	9	4	US-10-117-937-119
7	9	2.4	9	4	US-10-117-937-265
8	9	2.4	9	4	US-10-164-121A-13
9	9	2.4	9	4	US-10-164-078A-12
10	9	2.4	9	4	US-10-447-161-14
11	9	2.4	9	4	US-10-447-161-29
12	9	2.4	9	4	US-10-149-135-238
13	9	2.4	9	4	US-10-149-135-429
14	9	2.4	9	4	US-10-149-135-2050
15	9	2.4	9	4	US-10-149-135-2080
16	9	2.4	9	4	US-10-149-135-2106
17	9	2.4	9	4	US-10-149-135-2135
18	9	2.4	9	4	US-10-156-527-21
19	9	2.4	9	4	US-10-753-158-42
20	9	2.4	9	4	US-10-670-472A-6
21	9	2.4	9	5	US-10-651-616-24
22	9	2.4	9	5	US-10-362-715-8
23	9	2.4	9	5	US-10-705-459-39
24	9	2.4	9	5	US-10-776-521B-392
25	9	2.4	9	5	US-10-941-150A-13
26	9	2.4	9	6	US-11-067-064-119
27	9	2.4	9	6	US-11-067-064-265

28 9 2.4 9 6 US-11-067-159-119 Sequence 119, App
29 9 2.4 9 6 US-11-067-159-265 Sequence 265, App
30 30 2.4 10 3 US-09-572-270A-530 Sequence 530, App
31 9 2.4 10 3 US-09-572-270A-532 Sequence 532, App
32 9 2.4 10 3 US-09-572-270A-536 Sequence 536, App
33 9 2.4 10 3 US-09-572-270A-548 Sequence 548, App
34 9 2.4 10 3 US-09-572-270A-552 Sequence 552, App
35 9 2.4 10 3 US-09-572-270A-554 Sequence 554, App
36 9 2.4 10 3 US-09-573-822C-517 Sequence 517, App
37 9 2.4 10 3 US-09-573-822C-519 Sequence 519, App
38 9 2.4 10 3 US-09-573-822C-521 Sequence 521, App
39 9 2.4 10 3 US-09-573-822C-523 Sequence 523, App
40 9 2.4 10 3 US-09-573-822C-525 Sequence 525, App
41 9 2.4 10 3 US-09-573-822C-527 Sequence 527, App
42 9 2.4 10 3 US-09-573-822C-529 Sequence 529, App
43 9 2.4 10 3 US-09-573-822C-531 Sequence 531, App
44 9 2.4 10 3 US-09-573-822C-533 Sequence 533, App
45 9 2.4 10 3 US-09-573-822C-535 Sequence 535, App

ALIGNMENTS

RESULT 1
US-10-218-095-59
; Sequence 59, Application US/10218095
; Publication No. US20040033541A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Stroobant, Vincent
; APPLICANT: Russo, Vincenzo
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: MAGE-A4 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: L00461/70137
; CURRENT APPLICATION NUMBER: US/10/218,095
; CURRENT FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-218-095-59

Query Match 2.7% Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 180 SECMLLVFGI 189
Db 1 SECMLLVFGI 10
|||||||

RESULT 2
US-10-753-158-41
; Sequence 41, Application US/10753158
; Publication No. US20040185033A1
; GENERAL INFORMATION:
; APPLICANT: Chau, Pascal
; APPLICANT: Luiten, Rosalie
; APPLICANT: Demotte, Nathalie
; APPLICANT: Deyfour, Marie-Therese
; APPLICANT: Lurquin, Christophe
; APPLICANT: Traversari, Catia
; APPLICANT: Stroobant, Vincent
; APPLICANT: Cornellis, Guy R.
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Van Der Bruggen, Pierre
; APPLICANT: Schultz, Erwin
; APPLICANT: Warnier, Guy
; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL
; PROCEDURE

;
; FILE REFERENCE: 11727z
; CURRENT APPLICATION NUMBER: US/10/753,158
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US/09/806,769
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/165,863
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 09/289,350
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/806,769
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human MAGE-A1 peptide
US-10-753-158-41

Query Match 2.7%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 289 SDPARYEFLW 298
Db 1 SDPARYEFLW 10
|||||

RESULT 3
US-10-670-472A-83
; Sequence 83, Application US/10670472A
; Publication No. US20040214779A1
; GENERAL INFORMATION:
; APPLICANT: MA, Wenbin
; APPLICANT: GERMEAU, Catherine
; APPLICANT: VAN DEN EYNDE, Benoit
; APPLICANT: COULIE, Pierre
; APPLICANT: BOON-PALLEUR, Thierry
; TITLE OF INVENTION: MAGE C2 ANTI-GENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5780.2 US
; CURRENT APPLICATION NUMBER: US/10/670,472A
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/413,844
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/433,983
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 60/459,263
; PRIOR FILING DATE: 2003-04-02
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-670-472A-83

Query Match 2.7%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 185 LVFGIDVKEV 194
Db 1 LVFGIDVKEV 10
|||||

RESULT 4
US-09-933-708-3
; Sequence 3, Application US/09933708
; Publication No. US2002009013A1
; GENERAL INFORMATION:
; APPLICANT: PICCARELLO, THOMAS
; APPLICANT: OLON, LAWRENCE P.
; APPLICANT: KIRK, RANDAL J.

;
; TITLE OF INVENTION: ACTIVE AGENT DELIVERY SYSTEMS AND METHODS FOR
; TITLE OF INVENTION: PROTECTING AND ADMINISTERING ACTIVE AGENTS
; FILE REFERENCE: 54719.000028
; CURRENT APPLICATION NUMBER: US/09/933,708
; CURRENT FILING DATE: 2003-04-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(9)
; OTHER INFORMATION: This peptide may encompass 4-9 residues
US-09-933-708-3

Query Match 2.4%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 SSSSSSSSS 62
Db 1 SSSSSSSSS 9
|||||

RESULT 5
US-09-865-548A-39
; Sequence 39, Application US/09865548A
; Publication No. US20030096298A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECUL
; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-39

Query Match 2.4%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 254 GLYDGMHEHL 262
Db 1 GLYDGMHEHL 9
|||||

RESULT 6
US-10-117-937-119
; Sequence 119, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping

; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-119

Query Match 2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPRKLLT 272
Db 1 YGEPRKLLT 9

RESULT 7
US-10-117-937-265
; Sequence 265, Application US/10117937
; Publication No. US2003022039A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 265
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-265

Query Match 2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 LVFGIDVKE 193
Db 1 LVFGIDVKE 9

RESULT 8
US-10-164-121A-13
; Sequence 13, Application US/10164121A
; Publication No. US20030228308A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Boon, Thierry
; APPLICANT: Van der Bruggen, Pierre

; APPLICANT: Traversari, Catra
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-Cw6 Molecules And Uses There
; FILE REFERENCE: LUD-5771
; CURRENT APPLICATION NUMBER: US/10/164,121A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-121A-13

Query Match 2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 GLYDGMHEHL 262
Db 1 GLYDGMHEHL 9

RESULT 9
US-10-164-078A-12
; Sequence 12, Application US/10164078A
; Publication No. US20030228325A1
; GENERAL INFORMATION:
; APPLICANT: Bilsborough, Janine
; APPLICANT: Schultz, Erwin
; APPLICANT: Panichelli, Christophe
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Boon, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B18 Molecules And Uses There
; FILE REFERENCE: LUD-5756
; CURRENT APPLICATION NUMBER: US/10/164,078A
; CURRENT FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-078A-12

Query Match 2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 GLYDGMHEHL 262
Db 1 GLYDGMHEHL 9

RESULT 10
US-10-447-161-14
; Sequence 14, Application US/10447161
; Publication No. US2004002314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide

US-10-447-161-14

Query Match 2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 DPARYEFW 298
Db 1 DPARYEFW 9
|||||

RESULT 11

US-10-447-161-29
; Sequence 29, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-29

Query Match 2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 GLYDGMHL 262
Db 1 GLYDGMHL 9
|||||

RESULT 12

US-10-149-135-238
; Sequence 238, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05

; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 238
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-238

Query Match 2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 284 RQVPGSDPA 292
Db 1 RQVPGSDPA 9
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RESULT 13

US-10-149-135-429
; Sequence 429, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 429
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-429

Query Match 2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 284 RQVPGSDPA 292
Db 1 RQVPGSDPA 9
|||||

RESULT 14

US-10-149-135-2050
; Sequence 2050, Application US/10149135
; Publication No. US20040053822A1

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; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2050
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2050

Query Match          2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      281 LEYRQVPGS 289
DB      1 LEYRQVPGS 9

RESULT 15
US-10-149-135-2080
; Sequence 2080, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
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; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2080
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2080

Query Match          2.4%; Score 9; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      276 VOENYLEYR 284
DB      1 VOENYLEYR 9

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OM protein - protein search, using sw model

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(without alignments)
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Title: US-09-856-812B-1
Perfect score: 369
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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

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(Maximum DB seq length: 10)

Post-processing: Listing first 45 summaries

- Database : Published Applications AA.New.*
- 1: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 4: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 5: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	2.7	10	7	US-11-044-051-83
2	9	2.4	9	6	US-10-994-204-11
3	9	2.4	9	7	US-11-032-498-14
4	9	2.4	9	7	US-11-044-051-6
5	8	2.2	9	7	US-11-044-051-48
6	8	2.2	10	7	US-11-044-051-86
7	7	1.9	9	6	US-10-517-784-33
8	7	1.9	9	6	US-10-962-951-12
9	7	1.9	9	7	US-11-032-498-8
10	7	1.9	9	7	US-11-032-498-11
11	7	1.9	9	7	US-11-044-051-49
12	7	1.9	9	7	US-11-044-051-50
13	7	1.9	9	7	US-11-044-051-5
14	7	1.9	9	7	US-11-240-341-5
15	7	1.9	9	7	US-11-240-341-7
16	6	1.6	6	8	US-10-510-101-114
17	6	1.6	6	6	US-10-517-784-30
18	6	1.6	9	6	US-10-510-101-23
19	6	1.6	9	7	US-11-032-498-20
20	6	1.6	9	7	US-11-044-051-8
21	6	1.6	9	7	US-11-044-051-10
22	6	1.6	9	7	US-11-240-341-4
23	6	1.6	9	7	US-11-188-849-1
24	5	1.4	9	6	US-10-491-096-100
25	5	1.4	9	6	US-10-491-096-165

ALIGNMENTS

RESULT 1

US-11-044-051-83
; Sequence 83, Application US/11044051
; Publication No. US2005025553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: GODELAINE, Danisla
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 83
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-044-051-83

Query Match 2.7%; Score 10; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 LVFGIDVKEV 194
DB 1 LVFGIDVKEV 10
|||||||

RESULT 2

US-10-994-204-11
; Sequence 11, Application US/10994204
; Publication No. US20050271679A1
; GENERAL INFORMATION:
; APPLICANT: DADAGLIO, GILLES
; APPLICANT: LECLEERC, CLAUDE
; APPLICANT: LADANT, DANIEL
; APPLICANT: VAN DEN EYNDE, BENOIT
; APPLICANT: MOREL, SANDRA
; APPLICANT: BAUCHE, CECILE
; TITLE OF INVENTION: RECOMBINANT ADENYLATE CYCLASE TOXIN OF BORDETTELLA
; TITLE OF INVENTION: INDUCES T CELL RESPONSES AGAINST TUMORAL ANTIGENS
; FILE REFERENCE: 03495.0327
; CURRENT APPLICATION NUMBER: US/10/994,204

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; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: 60/523,632
; PRIOR FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-994-204-11

Query Match          2.4%; Score 9; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 GLYDGMGHEHL 262
DB 1 GLYDGMGHEHL 9

RESULT 3
US-11-032-498-14
; Sequence 14, Application US/11032498
; Publication No. US20050249743A1
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Van der Bruggen, Pierre
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-A24 Molecule and Uses Thereof
; FILE REFERENCE: LUD 5881
; CURRENT APPLICATION NUMBER: US/11/032,498
; PRIOR FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: US 60/535,751
; PRIOR FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MAGS-A10 peptide
US-11-032-498-14

Query Match          2.4%; Score 9; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 GLYDGMGHEHL 262
DB 1 GLYDGMGHEHL 9

RESULT 4
US-11-044-051-6
; Sequence 6, Application US/11044051
; Publication No. US2005025553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: GODELAINE, DanisLe
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGS C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459,263
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
US-11-044-051-6
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; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-044-051-6

Query Match          2.4%; Score 9; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 333 ALKDEEERA 341
DB 1 ALKDEEERA 9

RESULT 5
US-11-044-051-48
; Sequence 48, Application US/11044051
; Publication No. US2005025553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: GODELAINE, DanisLe
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGS C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459,263
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 9
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Antigenic peptide
US-11-044-051-48

Query Match          2.2%; Score 8; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 333 ALKDEEER 340
DB 1 ALKDEEER 8

RESULT 6
US-11-044-051-86
; Sequence 86, Application US/11044051
; Publication No. US2005025553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: GODELAINE, DanisLe
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGS C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459,263
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 86
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-044-051-86
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Query Match          2.2%; Score 8; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 8; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

Qy 187 FGIDVKEV 194
Db 3 FGIDVKEV 10

RESULT 7
US-10-517-784-33
; Sequence 33, Application US/10517784
; Publication No. US20060003315A1
; GENERAL INFORMATION:
; APPLICANT: MARGALIT, Alon
; TITLE OF INVENTION: MEMBRANE-ANCHORED BETA-2 MICROGLOBULIN COVALENTLY LINKED TO MHC
; TITLE OF INVENTION: PEPTIDE EPITOPES
; FILE REFERENCE: GAVISH-004 US
; CURRENT APPLICATION NUMBER: US/10/517,784
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US 60/388,273
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/IL03/00501
; PRIOR FILING DATE: 2003-06-12
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-517-784-33

Query Match          1.9%; Score 7; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

Qy 296 FLWGPRA 302
Db 1 FLWGPRA 7

RESULT 8
US-10-962-951-12
; Sequence 12, Application US/10962951
; Publication No. US20060029610A1
; GENERAL INFORMATION:
; APPLICANT: Argon, Yair
; APPLICANT: Gidalevitz, Tali
; APPLICANT: Biswas, Chhanda
; APPLICANT: Simen, Birgitte B.
; APPLICANT: Wanderling, Sherry
; APPLICANT: Ostrovsky, Olga
; TITLE OF INVENTION: GRP94-BASED COMPOSITIONS AND METHODS OF
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: 3460-CHOP C-206US
; CURRENT APPLICATION NUMBER: US/10/962,951
; CURRENT FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US/10/844,711
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/469,723
; PRIOR FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/477,990
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: 60/478,149
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: 60/556,362
; PRIOR FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: 60/566,363
; PRIOR FILING DATE: 2004-04-28
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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MAGE 3
US-10-962-951-12

Query Match          1.9%; Score 7; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

Qy 296 FLWGPRA 302
Db 1 FLWGPRA 7

RESULT 9
US-10-602-663-31
; Sequence 31, Application US/10602663
; Publication No. US20060040347A1
; GENERAL INFORMATION:
; APPLICANT: CHARNEAU, PIERRE
; APPLICANT: ZENNOU, VERONIQUE
; APPLICANT: FIRAT, HUSEYIN
; TITLE OF INVENTION: USE OF TRIPLEX STRUCTURE DNA SEQUENCES FOR TRANSFERRING
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 03495.0199
; CURRENT APPLICATION NUMBER: US/10/602,663
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US/09/688,990
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: PCT/FR99/00974
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Melanoma
; OTHER INFORMATION: peptide
US-10-602-663-31

Query Match          1.9%; Score 7; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

Qy 296 FLWGPRA 302
Db 1 FLWGPRA 7

RESULT 10
US-11-032-498-8
; Sequence 8, Application US/11032498
; Publication No. US20050249743A1
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Van der Bruggen, Pierre
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-A24 Molecule and Uses Thereof
; FILE REFERENCE: LUD 5881
; CURRENT APPLICATION NUMBER: US/11/032,498
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: US 60/535,751
; PRIOR FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 9
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; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: MAGA-A3 peptide
US-11-032-498-8

Query Match 1.9%; Score 7; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 FLWGPRA 302
Db 1 FLWGPRA 7

RESULT 11
US-11-032-498-11
; Sequence 11, Application US/11032498
; Publication No. US20050249743A1
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Van der Bruggen, Pierre
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-A24 Molecule and Uses Thereof
; FILE REFERENCE: LUD 5881
; CURRENT APPLICATION NUMBER: US/11/032,498
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: US 60/535,751
; PRIOR FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MAGA-A12 peptide
US-11-032-498-11

Query Match 1.9%; Score 7; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 FLWGPRA 302
Db 1 FLWGPRA 7

RESULT 12
US-11-044-051-49
; Sequence 49, Application US/11044051
; Publication No. US2005025553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: GODELAINE, DanisLe
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; TITLE OF INVENTION: MAGA C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459,263
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 9
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Antigenic peptide
US-11-044-051-49

Query Match 1.9%; Score 7; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 333 ALKDEEE 339
Db 1 ALKDEEE 7

RESULT 13
US-11-044-051-50
; Sequence 50, Application US/11044051
; Publication No. US2005025553A1
; GENERAL INFORMATION:
; APPLICANT: VAN PEL, Aline
; APPLICANT: GODELAINE, DanisLe
; APPLICANT: CARRASCO, Javier
; APPLICANT: BRASSEUR, Francis
; APPLICANT: BOON-FALLEUR, Thierry
; TITLE OF INVENTION: MAGA C2 ANTIGENIC PEPTIDES AND USES THEREOF
; FILE REFERENCE: LUD 5888 US
; CURRENT APPLICATION NUMBER: US/11/044,051
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/459,263
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 9
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Antigenic peptide
US-11-044-051-50

Query Match 1.9%; Score 7; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 333 ALKDEEE 339
Db 1 ALKDEEE 7

RESULT 14
US-11-240-341-5
; Sequence 5, Application US/11240341
; Publication No. US20060024742A1
; GENERAL INFORMATION:
; APPLICANT: Martelage, Valerie
; APPLICANT: De Smet, Charles
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: L0461.70047US01
; CURRENT APPLICATION NUMBER: US/11/240,341
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US 09/183,789
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: US 09/060,706
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-240-341-5

Query Match 1.9%; Score 7; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 YGEPRKL 270


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Db          3 YGPRKL 9
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RESULT 15
US-11-240-341-7
; Sequence 7, Application US/11240341
; Publication No. US20060024742A1
; GENERAL INFORMATION:
; APPLICANT: Martelange, Valerie
; APPLICANT: De Smet, Charles
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: L0461.70047US01
; CURRENT APPLICATION NUMBER: US/11/240,341
; PRIOR FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US 09/183,789
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: US 09/060,706
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-240-341-7

Query Match      1.9%; Score 7; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      296 FLWGPRA 302
Db      1 FLWGPRA 7

Search completed: March 17, 2006, 23:09:26
Job time : 23 secs
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RESULT 3
PT0593
T-cell receptor beta chain V-D-J region (159-1P) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0593
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0593
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEE>
A:Cross-references: UNIPARC:UPI000017C83F
A:Experimental source: day 19 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      1.1%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      38 ASSS 41
      |||||
Db      1 ASSS 4

RESULT 4
A35039
hypothetical collagen alpha 2(I) intron 2 protein 1 - chicken
C:Species: Gallus gallus (chicken)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: A35039
R;Bennett, V.D.; Adams, S.L.
J. Biol. Chem. 265, 2223-2230, 1990
A:Title: Identification of a cartilage-specific promoter within intron 2 of the chick al
A:Reference number: A35039; MUID:90130479; PMID:1688851
A:Accession: A35039
A:Molecule type: mRNA
A:Residues: 1-6 <BEN>
A:Cross-references: UNIPARC:UPI000017CEB1; GB:M33382; NID:G211043
A:Note: This ORF is not translated in GenBank entry CHKA21CG
C:Comment: This sequence is the translation of a cartilage specific alternative transcri
C:Keywords: alternative splicing; cartilage

Query Match      1.1%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      98 ASLP 101
      |||||
Db      2 ASLP 5

RESULT 5
A11483
aspartate transaminase (EC 2.6.1.1), mitochondrial - sheep (fragment)
N:Alternate names: aspartate aminotransferase, mitochondrial
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 20-Aug-1999
C:Accession: A11483
R;Campos-Cavieres, M.; Milstein, C.P.
Biochem. J. 147, 275-281, 1975
A:Title: The sequences of the coenzyme-binding peptide in the cytoplasmic and the mitoch
A:Reference number: A11483; MUID:76039441; PMID:1180894
A:Accession: A11483
A:Molecule type: protein
A:Residues: 1-7 <CAM>
A:Cross-references: UNIPARC:UPI000017C59C
A:Experimental source: liver
C:Keywords: aminotransferase; mitochondrion; phosphoprotein; pyridoxal phosphate
F/2/Binding site: pyridoxal phosphate (lys) (covalent) #status experimental
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Query Match      1.1%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      253 MGLY 256
      |||||
Db      4 MGLY 7

RESULT 6
B39040
calsequestrin, fast skeletal muscle - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997
C:Accession: B39040
R;Cata, S.E.; Jones, L.R.
J. Biol. Chem. 266, 391-398, 1991
A:Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein
A:Reference number: A39040; MUID:91093153; PMID:1985907
A:Accession: B39040
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-7 <CAL>
A:Cross-references: UNIPARC:UPI000017C5BC
C:Keywords: phosphoprotein; skeletal muscle

Query Match      1.1%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 BEDL 16
      |||||
Db      3 BEDL 6

RESULT 7
PT0691
T-cell receptor beta chain V-D-J region (154-2K) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0691
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0691
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-8 <FEE>
A:Cross-references: UNIPARC:UPI000017C83D
A:Experimental source: day 18 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      1.1%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      265 GEPR 268
      |||||
Db      3 GEPR 6

RESULT 8
S29272
tocopherol-binding protein, 81K - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 12-Apr-1996
C:Accession: S29272
R;Nalecz, K.A.; Nalecz, M.J.; Azzi, A.
Eur. J. Biochem. 209, 37-42, 1992
A:Title: Isolation of tocopherol-binding proteins from the cytosol of smooth muscle A7r:
A:Reference number: S29272; MUID:93011150; PMID:1396710
A:Accession: S29272
```

A:Molecule type: protein
 A:Residues: 1-8 <NAL>
 A:Cross-references: UNIPARC:UPI000017CA08
 A:Experimental source: smooth muscle A7r5 cells

Query Match 1.1%; Score 4; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PEED 15
 ||||
 Db 1 PEED 4

RESULT 9

S65647
 2-hydroxyglutaryl-CoA dehydratase - Acidaminococcus fermentans (fragment)
 C:Species: Acidaminococcus fermentans
 C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S65647
 R:Mueller, U.; Buckel, W.
 Eur. J. Biochem. 230, 698-704, 1995
 A:Title: Activation of (R)-2-hydroxyglutaryl-CoA dehydratase from Acidaminococcus fermentans
 A:Reference number: S65647; MUID:95331308; PMID:7607244
 A:Accession: S65647
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-8 <MUE>
 A:Cross-references: UNIPROT:Q7M1C5; UNIPARC:UPI000017AB76

Query Match 1.1%; Score 4; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 GIDV 191
 ||||
 Db 4 GIDV 7

RESULT 10

I57018
 gene Cftr protein - mouse (fragment)
 C:Species: Mus sp. (mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C:Accession: I57018
 R:Dorin, J.R.; Stevenson, B.J.; Fleming, S.; Alton, E.W.; Dickinson, P.; Porteous, D.J.
 Mamm. Genome 5, 465-472, 1994
 A:Title: Long-term survival of the exon 10 insertional cystic fibrosis mutant mouse is a result of a compensatory mutation in the CFTR gene
 A:Reference number: I57018; MUID:95037043; PMID:7949729
 A:Accession: I57018
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-8 <RES>
 A:Cross-references: UNIPROT:Q7M056; UNIPARC:UPI000017C895; GB:S74246; NID:g710482
 C:Genetics: Cftr
 A:Gene: Cftr

Query Match 1.1%; Score 4; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 LPDS 126
 ||||
 Db 1 LPDS 4

RESULT 11

B45796
 dihydroliipoamide S-succinyltransferase (EC 2.3.1.61) - Pseudomonas fluorescens (fragment)
 C:Species: Pseudomonas fluorescens
 C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
 C:Accession: B45796
 R:Benen, J.A.E.; Van Berkel, W.J.H.; Van Dongen, W.M.A.M.; Mueller, F.; De Kok, A.

J. Gen. Microbiol. 135, 1787-1797, 1989

A:Title: Molecular cloning and sequence determination of the lpd gene encoding lipopamidase
 A:Reference number: A45796; MUID:90132584; PMID:2515251
 A:Accession: B45796
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-9 <BEN>
 A:Cross-references: UNIPROT:Q51765; UNIPARC:UPI00000BD216; GB:M28356; NID:g151343; PIDN
 C:Superfamily: dihydroliipoamide acetyltransferase; lipoyl/biotin-binding homology
 C:Keywords: acyltransferase; coenzyme A; lipopamide; tricarboxylic acid cycle

Query Match 1.1%; Score 4; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 DPAR 293
 ||||
 Db 1 DPAR 4

RESULT 12

PT0670
 T-cell receptor beta chain V-D-J region (121-1BN) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0670
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0670
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-9 <FEE>
 A:Cross-references: UNIPARC:UPI000017C7EC
 A:Experimental source: day 4 postnatal thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 1.1%; Score 4; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ASSS 41
 ||||
 Db 1 ASSS 4

RESULT 13

PH0902
 T-cell receptor beta chain V-D-J region (hybridoma S23F4F4) - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 C:Accession: PH0902
 R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
 J. Exp. Med. 174, 1467-1476, 1991
 A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis
 A:Reference number: PH0891; MUID:92078857; PMID:1836012
 A:Accession: PH0902
 A:Molecule type: mRNA
 A:Residues: 1-9 <GOL>
 A:Cross-references: UNIPARC:UPI000017C9F1
 A:Experimental source: myelin basic protein-immunized T-cell
 C:Keywords: T-cell receptor

Query Match 1.1%; Score 4; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 SSTS 43
 ||||
 Db 3 SSTS 6

RESULT 14

B41983
orf downstream to bacterioferritin - Azotobacter vinelandii (fragment)
C:Species: Azotobacter vinelandii
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B41983
R:Grossman, M.J.; Hinton, S.M.; Minak-Bernero, V.; Slaughtter, C.; Stiefel, E.I.
Proc. Natl. Acad. Sci. U.S.A. 89, 2419-2423, 1992
A:Title: Unification of the ferritin family of proteins.
A:Reference number: A41983; MUID:92196129; PMID:1549605
A:Accession: B41983
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-9 <GRO>
A:Cross-references: UNIPROT:P25825; UNIPARC:UPI000013A327; GB:M83692; NID:gi42297; PIDN:
A>Note: sequence extracted from NCBI backbone (NCBIP:88442)

Query Match 1.1%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 TSTS 45
|||
Db 6 TSTS 9

RESULT 15

S19617
globin - polychaete (Eudistylia vancouveri) (fragment)
N:Alternate names: chlorocruorin
C:Species: Eudistylia vancouveri
C:Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 05-Dec-1998
C:Accession: S19617
R:Qabar, A.N.; Stern, M.S.; Walz, D.A.; Chiu, J.T.; Timkovich, R.; Wall, J.S.; Kapp, O.H.
J. Mol. Biol. 222, 1109-1129, 1991
A:Title: Hierarchy of globin complexes. The quaternary structure of the extracellular ch
A:Reference number: S19532; MUID:92106333; PMID:1762147
A:Accession: S19617
A:Molecule type: protein
A:Residues: 1-10 <QAB>
A:Cross-references: UNIPARC:UPI000017BD6E
A:Experimental source: plume
C:Complex: dodecamers, each consisting of a trimer of tetramers of globin chains; dodeca
C:Keywords: calcium; dodecamer; heme; homotetramer; oxygen carrier

Query Match 1.1%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 LEGA 28
|||
Db 2 LEGA 5

Search completed: March 17, 2006, 23:05:19
Job time : 40 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 22:57:46 ; Search time 227 Seconds
(without alignments)
1146.872 Million cell updates/sec

Title: US-09-856-812B-1
Perfect score: 369
Sequence: 1 MPAPKRCRCPEDLQSQS.....DTTASASSATGTSFSYPE 369

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3063

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	5	1.4	Q70Y81_9LAMI	Q70Y81 plectranth
2	5	1.4	Q9FXL0_LILLO	Q9FXL0 lilium long
3	4	1.1	BIOA_CITFR	P13071 citrobacter
4	4	1.1	P70804_AZOVI	P70804 azotobacter
5	4	1.1	Q9P285_HUMAN	Q9P285 homo sapien
6	4	1.1	Q53TM6_HUMAN	Q53TM6 homo sapien
7	4	1.1	P82324_PEA	P82324 pisum sativ
8	4	1.1	O87471_HABIN	O87471 haemophilus
9	4	1.1	Q7M1C5_ACIFE	Q7M1C5 acidaminoco
10	4	1.1	Q78DX6_RAT	Q78DX6 rattus norv
11	4	1.1	Q7M056_9MURI	Q7M056 mus sp. gen
12	4	1.1	Q35835_9MURI	Q35835 rattus sp.
13	4	1.1	RTJ3_BOVIN	P82926 bos taurus
14	4	1.1	YBFR_AZOVI	P25825 azotobacter
15	4	1.1	Q51LX3_MAGGR	Q51LX3 magnaporthe
16	4	1.1	Q15891_HUMAN	Q15891 homo sapien
17	4	1.1	Q6QF45_HUMAN	Q6QF45 homo sapien
18	4	1.1	Q9UCS8_HUMAN	Q9UCS8 homo sapien
19	4	1.1	Q28112_BOVIN	Q28112 bos taurus
20	4	1.1	Q5ZES4_BOVIN	Q5ZES4 bos taurus
21	4	1.1	Q42452_WHEAT	Q42452 triticum ae
22	4	1.1	P83529_LACSN	P83529 lactobacill
23	4	1.1	Q5UAH1_XANMA	Q5UAH1 xanthomonas
24	4	1.1	Q51765_PSEFL	Q51765 pseudomonas
25	4	1.1	Q81182_MOUSE	Q81182 mus musculu
26	4	1.1	Q72P19_9HIVI	Q72P19 human immun
27	4	1.1	AMFN_HELAM	P81731 helicoverpa
28	4	1.1	CATB_SHEEP	P83205 ovis aries
29	4	1.1	DYS2_LIMDU	P82080 limnodynaet
30	4	1.1	PNEU_RAT	P21996 rattus norv
31	4	1.1	Q6LDE2_HUMAN	Q6LDE2 homo sapien

32 4 1.1 10 2 Q9UCQ8_HUMAN Q9UCQ8 homo sapien
33 4 1.1 10 2 Q25356_LOCOMI Q25356 locusta mig
34 4 1.1 10 2 Q8MJ78_BOSMU Q8MJ78 bos mutus g
35 4 1.1 10 2 Q8LLJ0_ORYSA Q8LLJ0 oryza sativ
36 4 1.1 10 2 QSBS2_9POAL Q5ABE2 thamochoort
37 4 1.1 10 2 Q8GDC0_ECOLI Q8GDC0 escherichia
38 4 1.1 10 2 Q9R7J9_HELPY Q9R7J9 helicobacte
39 4 1.1 10 2 P90391_TYLCV P90391 tomato yell
40 4 1.1 10 2 Q53EE9_9NEOB Q53EE9 eleutheroda
41 4 1.1 10 2 Q64980_AVIMB Q64980 avian myelo
42 4 1.1 10 2 Q88082_SIVCZ Q88082 chimpanzee
43 3 0.8 5 1 AP21_EISFO P84182 eisenia foe
44 3 0.8 5 1 FARP_CHICK P83308 gallus gall
45 3 0.8 5 1 TRAW3_ECOLI P13973 escherichia

ALIGNMENTS

RESULT 1
Q70Y81_9LAMI PRELIMINARY; PRT; 9 AA.
AC Q70Y81
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Ribosomal protein (Fragment).
OS Name=rps16;
GN Plectranthus gillettii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Plectranthus.
OX NCBI TaxID=204186;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;
RA Paton A., Springate D.A., Suddle S., Otieno D., Gray R., Harley M.M.,
RA Willis F., Simmonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basilis and allies (Ocimeae, Labiatae)
based on three plastid DNA regions."
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505385; CAD45506.1; -; Genomic DNA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1016 MW; 66D6205861A3333B CRC64;

Query Match 1.4%; Score 5; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 KTGIL 227
DB 4 KTGIL 8

RESULT 2
Q9FXL0_LILLO PRELIMINARY; PRT; 9 AA.
ID Q9FXL0_LILLO
AC Q9FXL0
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE LIM8 protein (Fragment).
OS Name=LIM8;
GN Lilium longiflorum (Trumpet lily).
OS Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.
OX NCBI TaxID=4690;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RA Uefuji H., Minami M., Takase H., Hiratsuka K.;
RT "Isolation of a Promoter that Directs Microsporogenesis-Associated
RT Gene Expression in *Lilium longiflorum*.";
RL Plant Biotechnol. 18:151-156(2001).
DR EMBL; AB050987; BAB17856.1; -; Genomic_DNA.
FT NON TER 9
SQ SEQUENCE 9 AA; 1021 MW; 6F8BD76685A6C2CB CRC64;

Query Match 1.4%; Score 5; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 VQSMP 222
DB 3 VQSMP 7

RESULT 3
BIOA_CITFR STANDARD; PRT; 5 AA.
ID BIOA_CITFR
AC P13071;
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Adenosylmethionine-8-amino-7-oxonanoate aminotransferase
DE (EC 2.6.1.62) (7,8-diamino-7-oxonanoate aminotransferase) (DAPA
DE aminotransferase) (Fragment).
GN Name=bioA;
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=89006280; PubMed=2971595; DOI=10.1016/0378-1119(88)90397-6;
RA Shuan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of *Escherichia coli*,
RT Citrobacter freundii and *Salmonella typhimurium* biotin operons.";
RL Gene 67:203-211(1988).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
CC oxonanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
CC diaminonanoate.
CC -!- COFACTOR: Pyridoxal phosphate.
CC -!- PATHWAY: Cofactor biosynthesis; biotin biosynthesis; biotin from
CC 6-carboxyhexanoyl-CoA: step 2.
CC -!- SUBUNIT: Homodimer.
CC -!- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent
CC aminotransferase family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

DR EMBL; M21922; -; NOT ANNOTATED_CDS; Genomic_DNA.
DR PIR; I40697; I40697.
DR InterPro; IPR005814; Aminotrans 3.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
KW Aminotransferase; Biotin biosynthesis; Pyridoxal phosphate;
KW Transferase.
FT NON TER 5
SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 1.1%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 347 TTDD 350
DB 2 TTDD 5

RESULT 4
P70804 AZOVI
ID P70804_AZOVI PRELIMINARY; PRT; 7 AA.
AC P70804;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Algt protein (Fragment).
DE Name=algt;
GN Azotobacter vinelandii.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E;
RX MEDLINE=96427318; PubMed=8830682;
RA Rehm B.H.A., Ertesvaag H., Valla S.;
RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algC) is
RT part of an alg gene cluster physically organized in a manner similar
RT to that in *Pseudomonas aeruginosa*.";
RL J. Bacteriol. 178:5884-5889(1996).
DR EMBL; X87973; CAA61230.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 7 AA; 684 MW; 71B5A5A5A2D1AED0 CRC64;

Query Match 1.1%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 SSST 42
DB 4 SSST 7

RESULT 5
Q9P285 HUMAN
ID Q9P285_HUMAN PRELIMINARY; PRT; 8 AA.
AC Q9P285;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Clotting factor VIII (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Shibata M., Shima M., Morichika S., Yoshiola A.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040872; BAA94312.1; -; Genomic_DNA.
FT NON TER 1
FT NON TER 8
FT NON TER 8
SQ SEQUENCE 8 AA; 866 MW; 1C16987AAB05BDD3 CRC64;

Query Match 1.1%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 DGME 260
DB 5 DGME 8

RESULT 6
Q53TM6 HUMAN
ID Q53TM6_HUMAN PRELIMINARY; PRT; 8 AA.
AC Q53TM6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Hypothetical protein LOC130940 (Fragment).
 GN Name=LOC130940;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Tucci S., Stoneking T., Kyung K.;
 RT "The sequence of Homo sapiens BAC clone RP11-368J13.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.H.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Wilson R.K.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC008070; AY14928.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 737 MW; EE75BDC5BDDDB6 CRC64;

Query Match 1.1%; Score 4; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 ASAS 358
 |||||
 4 ASAS 7

Db

RESULT 7
 P82324_PEA PRELIMINARY; PRT; 8 AA.
 AC P82324;
 DT 01-JUN-2000 (TRENBLrel. 14, Created)
 DT 01-JUN-2000 (TRENBLrel. 14, Last sequence update)
 DE Unknown protein from 2D-page of thylakoid (SPOT105) (Fragment).
 OS Pisum sativum (Garden pea)
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
 OX NCBI_TaxID=3888;
 RN [1]
 RP PROTEIN SEQUENCE. SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
 RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
 RX MEDLINE=20181728; PubMed=10715320; DOI=10.1105/tpc.12.3.319;
 RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
 RA Adamska I., van Wijk K.J.;
 RT "Proteomics of the chloroplast: systematic identification and
 RT targeting analysis of luminal and peripheral thylakoid proteins.";
 RL Plant Cell 12:319-341(2000).
 CC -|- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR
 CC PERIPHERY.
 CC -|- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
 CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.7, ITS MW IS: 16.8 kDa.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0009579; C:thylakoid; IEA.
 KW Chloroplast; Thylakoid.
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 839 MW; DDC68B5DDC2D2D5 CRC64;

Query Match 1.1%; Score 4; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 SWVA 98
 |||||

Db 1 SWVA 4

RESULT 8

087471_HAEIN PRELIMINARY; PRT; 8 AA.
 AC 087471;
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DE HiFA (Fragment).
 GN Name=hiFA;
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Eagan;
 RX MEDLINE=98389689; PubMed=9721313;
 RA Mhlanga-Mutangadura T., Morlin G., Smith A.L., Eisenstark A.,
 RA Golomb M.;
 RT "Evolution of the major pilus gene cluster of Haemophilus
 RT influenzae.";
 RL J. Bacteriol. 180:4593-4703(1998).
 DR EMBL; AF071762; AAC35830.1; -; Genomic_DNA.
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 876 MW; DAB44451A7272325 CRC64;

Query Match 1.1%; Score 4; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 269 KLLT 272
 |||||

Db 2 KLLT 5

RESULT 9

Q7M1C5_ACIFE PRELIMINARY; PRT; 8 AA.
 AC Q7M1C5;
 DT 01-MAR-2004 (TRENBLrel. 26, Created)
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
 DE 2-hydroxyglutaryl-CoA dehydratase (Fragment).
 OS Acidaminococcus fermentans.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Acidaminococcaceae;
 OC Acidaminococcus.
 OX NCBI_TaxID=905;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=9531308; PubMed=7607244;
 RA Mueller U., Buckel W.;
 RT "Activation of (R)-2-hydroxyglutaryl-CoA dehydratase from
 RT Acidaminococcus fermentans.";
 RL Pur. J. Biochem. 230:698-704(1995).
 DR Pur. J. Biochem. 230:698-704(1995).
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 761 MW; C762CAA0587731B5 CRC64;

Query Match 1.1%; Score 4; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 GIDV 191
 |||||

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Db          4 GIDV 7

RESULT 10
Q78DX6 RAT PRELIMINARY; PRT; 8 AA.
AC Q78DX6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Vasopressin V2 receptor (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX MEDLINE=95396550; PubMed=7667072;
RA Mandon B., Bellanger A.C., Elalouf J.M.;
RT "Inverse-PCR-mediated cloning of the promoter for the rat vasopressin
RT V2 receptor gene.";
RL Pfluegers Arch. 430:12-18(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RA Elalouf J.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; X83264; CAA58238.1; -; Genomic DNA.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER
SQ SEQUENCE 8 AA; 849 MW; ECA2D1B5A2C72726 CRC64;

Query Match 1.1%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 MLLV 186
DB 1 MLLV 4

RESULT 11
Q7M056 9MURI PRELIMINARY; PRT; 8 AA.
AC Q7M056
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Gene Ctr protein (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95037043; PubMed=7949729;
RA Dorin J.R., Stevenson B.J., Fleming S., Alton E.W., Dickinson P.,
RA Porcous D.J.;
RT "Long-term survival of the exon 10 insertion cystic fibrosis mutant
RT mouse is a consequence of the low level residual wild-type Ctr gene
RT expression.";
RL Mamm. Genome 5:465-472(1994).
DR PIR; I57018; I57018.1
FT NON_TER
SQ SEQUENCE 8 AA; 874 MW; 180EA5A775BAB767 CRC64;

Query Match 1.1%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db          4 GIDV 7

RESULT 12
Q35835 9MURI PRELIMINARY; PRT; 8 AA.
AC Q35835
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE ORF1 protein.
GN Name=ORF1;
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=98008057; PubMed=9581555;
RA Hospital V., Prat A., Joulie C., Cherif D., Day R., Cohen P.;
RT "Human and rat testis express two mRNA species encoding variants of
RT NR2 convertase, a metalloendopeptidase of the insulinase family.";
RL Biochem. J. 327:773-779(1997).
DR EMBL; X93208; CAA63695.1; -; mRNA.
SQ SEQUENCE 8 AA; 886 MW; EA7EA1B1ADC5A5B6 CRC64;

Query Match 1.1%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 SSAT 362
DB 2 SSAT 5

RESULT 13
RT33 BOVIN STANDARD; PRT; 9 AA.
AC P82326
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).
GN Name=MRPS33;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123; DOI=10.1074/jbc.M100727200;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 LPDS 126
DB 1 LPDS 4

RESULT 13
RT33 BOVIN STANDARD; PRT; 9 AA.
AC P82326
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).
GN Name=MRPS33;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123; DOI=10.1074/jbc.M100727200;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC
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CC removed.
CC
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KW Direct protein sequencing; Mitochondrion; Ribonucleoprotein;
 KW Ribosomal protein.
 FT NON_TER 1
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;

Query Match 1.1%; Score 4; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 LFSE 178
 |||||

Db 1 LFSE 4
 |||||

RESULT 14

YBFR_AZ0VI

ID YBFR_AZ0VI STANDARD; PRT; 9 AA.

AC P25825; YBFR_AZ0VI STANDARD; PRT; 9 AA.

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Hypothetical protein in bfr 3'region (Fragment).

OS Azotobacter vinelandii

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Azotobacter.

OX NCBI_TaxID=354;

RN [1]_TaxID=354;

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

EX MEDLINE=92196129; PubMed=1549605;

RA Grossman M.J.; Hinton S.M.; Minak-Bernero V.; Slaughter C.,

RA Stiefel E.I.;

RT Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423 (1992).

RL "Unification of the ferritin family of proteins."

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC -----

CC NUCLEOTIDE SEQUENCE.

DR EMBL; M83692; AAA22122.1; -; Genomic_DNA.

KW PIR; B41983;

KW Hypothetical protein.

FT NON_TER 9

SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B41776D CRC64;

Query Match

Best Local Similarity 1.1%; Score 4; DB 1; Length 9;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 TSTS 45
 |||||

Db 6 TSTS 9
 |||||

RESULT 15

Q51LX3 MAGGR

ID Q51LX3_MAGGR PRELIMINARY; PRT; 9 AA.

AC Q51LX3;

DT 13-SEP-2005 (TRENBLrel. 31, Created)

DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)

DE Hypothetical protein.

GN ORFNames=MG02768.4;

OS Magnaporthe grisea 70-15.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.

OX NCBI_TaxID=242507;

RN [1]_TaxID=242507;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=70-15;

RA Birren B.; Nusbaum C.; Abebe A.; Abouelleil A.; Adekoya E.,

RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
 RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
 RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L.,
 RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
 RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
 RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
 RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
 RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
 RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G.,
 RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Hatcher A., Heller A., Higgins H.,
 RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
 RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseis M., Karlsson E.,
 RA Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
 RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
 RA Lindblad-toh K., Liu X., Lokitsang T., Lokitsang Y., Lucien O.,
 RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
 RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
 RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Menes L.,
 RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
 RA Mozes J., Mulraiv L., Munson G., Naylor J., Neves C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
 RA Norbu N., O'donnell P., Oksawo O., O'leary S., Omotosho B.,
 RA O'Neill K., Oman S., Parker S., Perrin D., Phunkhang P., Pignani B.,
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
 RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
 RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
 RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
 RA Stenson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
 RA Tensing P., Tesfaye S., Theodore J., Thoultsang Y., Tophing A.,
 RA Towey S., Tsamila T., Tsomo N., Vallee D., Vassiliev H.,
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Lander E.;
 RT "The genome sequence of Magnaporthe grisea."
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Zhu H., Blackmon B.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AACU01001555; EAA47525.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 9 AA; 1003 MW; DF9FCSA6D1F5BDC6 CRC64;

Query Match 1.1%; Score 4; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 QSQS 20
 |||||

Db 6 QSQS 9
 |||||

Search completed: March 17, 2006, 23:04:37
 Job time : 231 secs

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